

# Supplementary Information, Redzic et al. (4 Figures, 1 Table)

CLUSTAL O(1.2.4) multiple sequence alignment

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G.haemolysans(WP_040464465) MRKYLEEKYNKFSRLKLTVGVCMSMTIGSFFLVSTVQPEDYVVKAAADNAIVHYKYVGEDNL 60
S.pneumoniae(WP_000417171.1) MEKYFGEKQERFSFRKLSVGLVSATISSLFFMSVLASS--SVDAQETAGVHYKYVADSEL 58
S.oralis(WP_000713080.1) MKKFFGEKQHRFSLRKLAIGLVSAISSLFFVSIASSG--TVFAQENVAVHYKYVTDTEL 58
S.Sanguis(WP_002913590.1) MKKFLGEKQTRFAFRKLA/GLVSAISSLFFVSIAGVD--SVQAQEKLVNHYKYVTDTEI 58
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G.haemolysans(WP_040464465) TDKEKELIKKEVPSVSSKEETYLVFKPTKTTQLNKLNTGLNYGVGSMMLGGM---LG 117
S.pneumoniae(WP_000417171.1) SSEEKKQLVYDIPTYVENDDETYLVYKLNLSQNLAEPLNTGSKNERQALVAGASLAALG 118
S.oralis(WP_000713080.1) SGQEKDLIVKDIPKIAEDSESTYYLVYRMDEKAQLGQLPNTGGQNSLTSVLSGGVLASIG 118
S.Sanguis(WP_002913590.1) TPQEKELIVSGVPRMPEGNEETYLVYRLNSNAGAKTLPNTGDNNSNTMMAAGLLTTIG 118
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G.haemolysans(WP_040464465) LVVVVVAKGKNKSRKILSVLVTSLGATTLELPARAMEDLQLSVYNMMDYNLKVGDKLEI 177
S.pneumoniae(WP_000417171.1) ILIFAVSKKKVKNKTVLHLVLVAGMGNV-LVSVHALENHLLNNTDYELTSGEKPLP 177
S.oralis(WP_000713080.1) FLIFVSKKKKGGKALLKVVLTGMGSL-ASSVQAIENQLLIQYNQEYQLSQGDSLPLP 177
S.Sanguis(WP_002913590.1) LVVFAVSKRKVQSKFLLTVLVGASVGGGL-ILSVDALENGSLQYNAEYQVSAGESLPS 177
* * * * *
G.haemolysans(WP_040464465) SSIPGYSFVGFINKNEAETKKEEVEKQITSQQHKKQPELKENTDENVIENKQENKTTL 237
S.pneumoniae(WP_000417171.1) KEISGYTYIGYIKEGKTTSDFEVSNQEK-----AATPTKQKVDYVNTPNFVDHPSTV 231
S.oralis(WP_000713080.1) RALSGYTYLGYIKQDKEINQQ-----ETAARDQKLDYTVQPHFQANEGGQ 222
S.Sanguis(WP_002913590.1) GEISGYTYVGYIKDESIKLLDNKIPDNQANVDKEALNQNKKLDYSVS----- 227
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G.haemolysans(WP_040464465) K-----ISDKK-----EDKKVIE--NINKKD 256
S.pneumoniae(WP_000417171.1) QAIQEQTPTSSTKPTVEVQWEKPFSTELINPRKEEKQSSDSQEQLAEHKNLETKKEEKIS 291
S.oralis(WP_000713080.1) KAGDEQKAPSSTSPADK-----IPSDLS 247
S.Sanguis(WP_002913590.1) -----FDKNGL 233
* * * * *
G.haemolysans(WP_040464465) EKKVQGVNTVNPQDEVLAGKLTPELLYSDKIETPLKYNQIIESNDQLPEGTRRIKQQG 316
S.pneumoniae(WP_000417171.1) PKEKTGVNTLNPQDEVLSGQLNKPELLYREETIETKIDFQEEIQENPDLAEGTVRVKQEG 351
S.oralis(WP_000713080.1) NQKPSGIASVDPQDEVLAGRVNKPELLYKDEIVTKLDVSEVVQENPELGTIHKVQEG 307
S.Sanguis(WP_002913590.1) KNQTVGVNTIEPQDEVLSGRVAKPELLYKETSIEIEIAYGEQIQENPDLAEGTVRVKQEG 293
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G.haemolysans(WP_040464465) KEGKKTEVIRMFTEGKEVSRELSTKTEEPVSEIIEKGTKKAVSNVITKGQKLVKPAVE 376
S.pneumoniae(WP_000417171.1) KLGKKVEIVRIFSVNKEEVSREIVSTTAPSPRIVEKGTKKTVIKEQPE----- 402
S.oralis(WP_000713080.1) RAGKKIELVRIFTVENQEISREVLSTKVEEALPRIVEKGTKKAVVPEAPQ----- 358
S.Sanguis(WP_002913590.1) KPGRKIEVVRIFTVDNAEVSREVLSTKIEEATPKIVEKGTKKLEAPSEKPV----- 344
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G.haemolysans(WP_040464465) VKPEYTGQAGAVEPVKAEVPKEYTGQAGAVEPAKVETPKEYTGQAGAVEPAKAE 436
S.pneumoniae(WP_000417171.1) -----TGVEH-----KDVQSGAIVEPAIQP 422
S.oralis(WP_000713080.1) -----SAK----- 361
S.Sanguis(WP_002913590.1) -----TSNLVQPEQVAPLPEYTGQAGAVE----- 369
* * * * *
G.haemolysans(WP_040464465) VSKEYTGQAGTIVEPAKAEVPKEYTGQAGAVEPEK-VEPQYGGVTSALVKPEKIEA 495
S.pneumoniae(WP_000417171.1) ELPEA--VSDKGEPEVQPTLPEAVVTDKG-----ETEVPQESPDTVSDKGEPEQVAP 474
S.oralis(WP_000713080.1) -----KGPETQAPLPEYTGQAGAVVAPETAEKPEYTGQAGAVEPEQVAP 409
S.Sanguis(WP_002913590.1) -----EPEQVASLPEYSGTLSGAVEPEQ-IEPEIGGVQSGAIVEPEQVTP 414
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G.haemolysans(WP_040464465) PKEYTGQAGAVEPAKAEAPKEYRGVQAGAVEPEKIESPKEYTGQAGAVEPAKAEV 555
S.pneumoniae(WP_000417171.1) LPEYKGNIEQVKPETPVEKTKEQGPEKTEEVVVKP----- 509
S.oralis(WP_000713080.1) LPEYQGTQAGAVEPEKVEP-EVGGVQSGALVEPE----- 443
S.Sanguis(WP_002913590.1) LPEYTGQAGAVVSPEQVAPLPEYTGQAGAVEP----- 449
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G.haemolysans(WP_040464465) PKEYRGVQAGAVEPEKIESPKEYTGEQSGAIVEPEKVETTKEYTGQAGALVEPEKVEA 615
S.pneumoniae(WP_000417171.1) -----TEETPVNPNEGTTEGTSIQEAENPVQPAEESTTNSEKVSPTSSE 554
S.oralis(WP_000713080.1) -----TSEKPT--YTGEQSGAIVEPEQVPTPEYRGVQAGAVVAPETAE- 485
S.Sanguis(WP_002913590.1) -----AQVTLPEYTGQAGAVEPAKPAQVTLPEYTGQAGAVEPEQV-- 492
* * * * *
G.haemolysans(WP_040464465) PKEYTGQAGAVEPEKVEPPKEYTGQAGAVEPEKVEAPKEYTGKIEPLKTNPKPTV 675
S.pneumoniae(WP_000417171.1) N-----TGEVSSNPDSSTSVGESNKPENHNSKNENSEKT----- 590
S.oralis(WP_000713080.1) -----KPEYTGQAGAVEPETQSSL----- 506
S.Sanguis(WP_002913590.1) -----TPSPEYTGQAGAVEPEQVAVSL----- 515
* * * * *
G.haemolysans(WP_040464465) ENNNTAEI NNVPKNASALLRMNFVKGNQVLSGTGSATFIAPNVLTLVAHNFINNSADNST 735
S.pneumoniae(WP_000417171.1) -----EEVPVNPNE-----GTVEGTSNQETEK----- 613
S.oralis(WP_000713080.1) -----
S.Sanguis(WP_002913590.1) -----
* * * * *
G.haemolysans(WP_040464465) GEFIDGKSKNTYEWQTPDGQKGSFTSEDIHFYNKKDYKPGFIYDLAVITLPQSTRRQHAN 795
S.pneumoniae(WP_000417171.1) -----VQP-----AEETQNTSGK 626
S.oralis(WP_000713080.1) -----PEYTGQAGA 516
S.Sanguis(WP_002913590.1) -----PEYTGQAGA 525
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G. haemolysans(WP\_040464465) LVENYSKVNVDKLNVDYGYPRGEYAHKDDTVEIEQKYANNTYGVQYQGGKAGMSGGGIF 855  
S. pneumoniae(WP\_000417171.1) IANENTG-EVSNKPSDSKPPV-EESNQ-----PEKNGT----- 657  
S. oralis(WP\_000713080.1) IVE-----PEQVTP-----L-----PEYTG----- 532  
S. Sanguis(WP\_002913590.1) IVE-----PEQVEPPQ-----EYTG----- 541

G. haemolysans(WP\_040464465) NSKGEVIGLHQNGAENRSGGLISPTQLDWIRSIKKEITPNYDALERHKDEKKDDIKE 915  
S. pneumoniae(WP\_000417171.1) -----ATKPEN---S---GN-TTSENG 672  
S. oralis(WP\_000713080.1) -----TE---QVKPEA---P---TEK-PKEKPK 550  
S. Sanguis(WP\_002913590.1) -----IE---PAAPEA---ENPTKAQEPKEQ 562

G. haemolysans(WP\_040464465) EKQVDKKLELRNINVELYTLNENKYRHVSSLSVPTNPEAYFMKVKSENFKDVMLPVKS 975  
S. pneumoniae(WP\_000417171.1) QTEPEKKLELRNVDIELYSQTNQTYRQHVSLDGPENTDYFVKVKSSAFKDVYIPVAS 732  
S. oralis(WP\_000713080.1) EKDPEKTLELRNVDLELYSQTNGTYKQHVSLDGVSPNPDYFVKVKSSSFKDVYLPVAS 610  
S. Sanguis(WP\_002913590.1) KQEPKNIELRNVDVELYSLADGKYKQHVSLDAIPSNQENYFVKVKSSKFKDVFLPISS 622

←--- linker →

G. haemolysans(WP\_040464465) IESARKDNQDVYKIVGQANDLIQHENNITLNYTYLPKTVNSENGVYTSFKNLVDAMNI 1035  
S. pneumoniae(WP\_000417171.1) ITEEKRNQGSVYKITAKAEKLQLEENKYVDNFTFYLDKKAKEENTNFTSFSNLVKAINQ 792  
S. oralis(WP\_000713080.1) ITAETKDGQPVYKITAKAEKLQLEENKYVDNFTFYLAKKARETTTTFTSFSNLVKAINQ 670  
S. Sanguis(WP\_002913590.1) IVDSTKDGQPVYKITASAEKLQDVNNKYEDNFTFYLAKKAREVNTFTSFSNLVQAINN 682

G. haemolysans(WP\_040464465) NPYGTFRLGATMDAREVELSDGQESYINKEFSGKLIGENKGGYAIYNLKKPLFKALSHA 1095  
S. pneumoniae(WP\_000417171.1) NPSGTYHLAASLNANEVELGPDERSYIKDTFTGRLIGEKGDKNYAIYNLKKPLFENLSGA 852  
S. oralis(WP\_000713080.1) NLSGTYHLAASLNANEVELEPEAKSYIKGTFTGQLIGEKGDKQYAIYNLKKPLFETLSGA 730  
S. Sanguis(WP\_002913590.1) NLNGTYHLAASLNANEVELENGASSYIKGRFTGKLFSGDKGNYAIYNLKKPLFDLSAA 742

G. haemolysans(WP\_040464465) TIQDLSIKEANVSSKEDAATIAKEAKNDTTIANVHSSGVIAGERSIGGLISQVTDSTISN 1155  
S. pneumoniae(WP\_000417171.1) TVEKLSLKNVAISGKNDIGSLANEATNGTKIKQVHVDGVLAGERGVGGLLAKADQSSIAE 912  
S. oralis(WP\_000713080.1) RVEKLSLKNVVISGKDDIGSLTYEAQNGTKIKQVHVDGVLAGERGIGGLLAKADQSSITE 790  
S. Sanguis(WP\_002913590.1) TVENLTLKDVNISGKTDIGALANEANATRINNVDGVLAGERGIGGLVWKADNSKISN 802

G. haemolysans(WP\_040464465) SSFTGRITNTYDATTATYQIGGLVGLKSGVGALIEKSISSIDMATNANTGDQVVGAVGV 1215  
S. pneumoniae(WP\_000417171.1) SSKFGRIVNTYETTDAYNIGGLVGHLTGKNASIAKSKATVTISSNTNRSDQTVGGLAGLV 972  
S. oralis(WP\_000713080.1) SSKFGRINIYETTAAYNIGGLVGHLTGNKALLTKSKATVAISSNTNSSDQTVGGLAGLV 850  
S. Sanguis(WP\_002913590.1) SSKFGRIVNSYETKAPYNIGGLVGLTGINALVDKSKATITISSNADSTNQTVGGLAGLV 862

G. haemolysans(WP\_040464465) DKKATIRNSYVEGNLNNVFPFGKVGGVGNLWDRETSEVSNAGNLTNVLSDVNVVTNGNA 1275  
S. pneumoniae(WP\_000417171.1) DQDAHIQNSYAEGDINNPKHFGRVAGVAGYLWDRTSGEEKHAGELTNVLSDVNVVTNGNAI 1032  
S. oralis(WP\_000713080.1) DQDAIQDSYAEGDINNPKHFGRVAGVAGYLWDRTSNLEKHAGSLTNVLSDVNVVTNGNAI 910  
S. Sanguis(WP\_002913590.1) EKDALISNSYAEGNINNVKRFSGVAGVAGYLWDRDSSEERHAGRLHNVLSDVNVVTNGNAI 922

←----- linker-----

G. haemolysans(WP\_040464465) AGYDFNGIKATNTYSNKNKVVQVDDVEVLSKDEEQRGTVLENNIVLEKKIELVPK 1335  
S. pneumoniae(WP\_000417171.1) TGYHYTGMKVANTFSSKANRVNVTLEKDEVVSKESEFEERGTMLDASQIVSKKAEINPLT 1092  
S. oralis(WP\_000713080.1) TGYHYNDMKVDTFSSKANRVNVTLVKDEVVSKESFEERGTMLDTSQIESKKAANPLT 970  
S. Sanguis(WP\_002913590.1) SGYHYRGMRTDSYSNKNDRVYKVTLEKDEVVTKESLEERTILDVSIASKKSEINSL 982

linker-----→

G. haemolysans(WP\_040464465) NTKIEDFNFSRYETDYKNLKDADVSRRLRVYKNIKLLPFYNRETIVKYGNLVDANNTLY 1395  
S. pneumoniae(WP\_000417171.1) LPTVEPLSTSGKKDSDFSKIAHYQANRALVYKNIKLLPFYKSTIVKYGNLVKENSLLY 1152  
S. oralis(WP\_000713080.1) LPTVEPLSTSGKKDSDFSKIAHYQAKRALYKNIKLLPFYKATIVKYGNLVNENSLLY 1030  
S. Sanguis(WP\_002913590.1) APKVETLLTSTNKESDFSKVQYQASRALYKNIKLLPFYKATIVKYGNLVKEDSTLY 1042

G. haemolysans(WP\_040464465) TKDLVSVPMKDKEVISDINKNKTINKLHLYSDNTSQTLDIKYLQDFSKVAEYEJANI 1455  
S. pneumoniae(WP\_000417171.1) QKELLSAVMMKDDQVITDIVSNKQTANKLHLYNDHSSEKFDLKYQTFANLAEYNLGN 1212  
S. oralis(WP\_000713080.1) QKEVLSAVMMKDNQVITDIVSNKQTANKLHLYKDHSSKIDLQYQADFALAEYSLGDT 1090  
S. Sanguis(WP\_002913590.1) EKEILSAVMMKDNEVITDIASHKEAANKLLIHYKDHSSKLDLTYQSDFSKLAEYRVGDT 1102

G. haemolysans(WP\_040464465) KLIYTPNTLLHSYNNIVKAVLNDLKSVDYSDAVRVLDISSNIKLTLYLDEQFTKTKA 1515  
S. pneumoniae(WP\_000417171.1) GLLYTPNQFLYDRDSIVKEVLPQLKLDYQSDAIRKTLGISPEVKLTLYLEDQFSKTKQ 1272  
S. oralis(WP\_000713080.1) GLLYTPNQFLYDQSSIIKQVLPDLQNVYHSEGIRKTLGISPNVQTELYLEDQFAKTKE 1150  
S. Sanguis(WP\_002913590.1) GLIYTPNQFLQNHSSIVNLPDLKAVDYQSEAIRNTLGISSGVSLTELYLEEQFAKTKE 1162

G. haemolysans(WP\_040464465) NIEDSLKLLSADAVIAENSNSIIDNYIEKIKNKEALLGLTYLERWYFNKYDNTSAK 1575  
S. pneumoniae(WP\_000417171.1) NLGDSLKLLSADAGLAS-DNSVTRGYLVDKIKNKEALLGLTYLERWYFNKYDNTSAK 1331  
S. oralis(WP\_000713080.1) HLEDLKLKLLSADAGLAG-DNPVTKGYLVDKIKRNEKLLGLTYLERWYFNKYDNTSAK 1209  
S. Sanguis(WP\_002913590.1) NLANTLEKLLSADAVIAS-ENQTINGYVVDKIKRNEKALLGLTYLERWYFNKYDNTSAK 1221

G. haemolysans(WP\_040464465) DLVLYHLDFFGKSNSSALDNVIELGKSGFNLLAKNNVITYNVLLSKNYGTEGLFKALEG 1635

S.pneumoniae(WP\_000417171.1) DLV MYHPDFFGKNTSPLDTLIELGKSGFNLLAKNNVDYGISLASQHGATDLFSTLEH 1391  
S.oralis(WP\_000713080.1) DLVLYHLDFFGKGNASPLDTLIELGKSGFNLLAKNNVDYISLASHHGTDLFSTLEN 1269  
S.Sanguis(WP\_002913590.1) DLV MYHMDFFGKGNVSPLDLTIELGKSGFNLLAKNNVDAYNISLANNATKDLFSTLAN 1281  
\*\*\*\*\* \*\* \* ..\*\*\*\*\* \*\* \* ..\*\*

G.haemolysans(WP\_040464465) YRKVFLPNVSNNDWFKTQSKAYIVEEKSTIPEVSSKQSKQGTEHSIGVYDRLTSPSWKYQ 1695  
S.pneumoniae(WP\_000417171.1) YRKVFLPNTSNNDWFKSETKAYIVEEKSTIEEVKTKQGLAGTKYSIGVYDRITSATWKYR 1451  
S.oralis(WP\_000713080.1) YRKVFLPTTSNNDWFKKQTKAYIVEEKSNIEEVKTKQGLAGTKYSISVYDRITSATWKYR 1329  
S.Sanguis(WP\_002913590.1) YREVFLPNKTNQWFKEQTKAYIVEEKSAIDEVRVKQEQAQSKYSIGVYDRITSATWKYR 1341  
\*\*\*\*\* \*\* \* ..\*\*\*\*\* \*\* \* ..\*\*

G.haemolysans(WP\_040464465) SMVLP LLTPEEKMIFMIANISTIGFGAYDRYSSEYPKGDKLNRVFEENAQA AAKRFRO 1755  
S.pneumoniae(WP\_000417171.1) NMVLP LLT LPER-SV FVISTMSSLGFGAYDRYRSSDHKAGKALNDFVEENARETAKRQRD 1510  
S.oralis(WP\_000713080.1) NMVLP LLT LPEK-SV FVISTMSSLGFGAYDRYRNSDHKAGKALNDFVEENARETAKRQRD 1388  
S.Sanguis(WP\_002913590.1) NMVLP LLT MPER-SV FVISTISSLGFAYDRYRNEHRAGAELNKFVEDNAQETAKRQRD 1400  
\*\*\*\*\* \*\* \* ..\*\*\*\*\* \*\* \* ..\*\*

G.haemolysans(WP\_040464465) HYDYWYKILDKENKEKLFRSVLVYDAFRFGNDTN--KETQEANFETNPNVIKNFFGPAGN 1813  
S.pneumoniae(WP\_000417171.1) HYDYWYRILD EQSREKLYRTILLYDAYKFGDDTTSGKATAEAKFDSSNPAMKNFFGPVGN 1570  
S.oralis(WP\_000713080.1) HYDYWYRILDNEGREKLYRTILLYDAYKFGDDTTSGKATAEAKFDSSNPAMKNFFGPVGN 1448  
S.Sanguis(WP\_002913590.1) HYDYWYRILD EQREKLYRTILLYDAYKFGDDTTVDKATVEAQFDSSNPAMKNFFGPVGN 1460  
\*\*\*\*\* \*\* \* ..\*\*\*\*\* \*\* \* ..\*\*

G.haemolysans(WP\_040464465) NVVHNKHGAYATGDAFYMYMAYRMLDKSGAVTYTHEMTHNSDREIYLG GYGRRSGLGPEFFY 1873  
S.pneumoniae(WP\_000417171.1) KV VHNQH GAYATGDGVYMSYRMLDKDGAITYTHEMTHDSDQDIYLG GYGRRNGLGPEFF 1630  
S.oralis(WP\_000713080.1) KV VHNQH GAYATGDGVYMSYRMLDKDGAITYTHEMTHDSDQDIYLG GYGRRSGLGPEFF 1508  
S.Sanguis(WP\_002913590.1) KV VHNKHGAYATGDSVYMGYRMLDKDGAITYTHEMTHDSDNEIYLG GYGRRSGLGPEFF 1520  
\*\*\*\*\* \*\* \* ..\*\*\*\*\* \*\* \* ..\*\*

G.haemolysans(WP\_040464465) AKGLLQAPDHSYDPTITINSVLKYDDS--ENSTR LQIADPTQRFTNVEDLHNYMHNMF DL 1931  
S.pneumoniae(WP\_000417171.1) AKGLLQAPDQPSDATITINSILKHSKSDSTEGSR LQVLDPTERFQNAADLQNYVHNMF DL 1690  
S.oralis(WP\_000713080.1) AKGLLQAPDQPSDATITINSILRHSKSDSTEGSR LQILDPTERFQNAADLQNYVHNMF DL 1568  
S.Sanguis(WP\_002913590.1) AKGLLQAPDHPDDATITVNSILKYDKN DASEKSR LQVLDPTKRFQNAADLKNYVHNMF DV 1580  
\*\*\*\*\* \*\* \* ..\*\*\*\*\* \*\* \* ..\*\*

G.haemolysans(WP\_040464465) IYTL EILEGRAV-AKLDYNEKNDLLRKIENIYKDP-DGNSVYATNAVRR LTSDEIKNLT 1989  
S.pneumoniae(WP\_000417171.1) IYMM EYLEGQSIVNKL SVYQKMAALRKIENKYV KDPADGNEVYATNVVKELTEAEARNLN 1750  
S.oralis(WP\_000713080.1) IYMLEYLEGQSIVNKL NVYQKMAVLRKIENKYV KDPV DNEVYATNVVKELTEAEAKLT 1628  
S.Sanguis(WP\_002913590.1) IYMLEYLEGMSIVNRLSDVQKV NALRKIENKYVRD-ADGNDVYATNVIKNITMADAQKLN 1639  
\*\*\*\*\* \*\* \* ..\*\*\*\*\* \*\* \* ..\*\*

G.haemolysans(WP\_040464465) SFDKLIENDVITRRGYIDQGEYERNGYHTINLFSPIYSALSSKIGTPGDLMGRRMAFELL 2049  
S.pneumoniae(WP\_000417171.1) SFESLIDHNILSAREYQ-SGDYERNGYTIKLFAPISALSSEKGTGPGDLMGRR IAYELL 1809  
S.oralis(WP\_000713080.1) NFDSLIDHNILSAREYQ-SGDYERNGYTIKLFAPISALSSEKGTGPGDLMGRR IAYELL 1687  
S.Sanguis(WP\_002913590.1) SFNSLIENDILSAREYK-NGDVERNGYHTIKLFSPISALSSEKGTGPGDLMGRR IAYELL 1698  
\*\*\*\*\* \*\* \* ..\*\*\*\*\* \*\* \* ..\*\*

G.haemolysans(WP\_040464465) AAKGYKEGMVPIYSNQYEKEAKDRGSKIRSYGKEIGLVTD DLVLEKVFNKYGSWVFEFK 2109  
S.pneumoniae(WP\_000417171.1) AAKGFKDGMVPIYSNQYEEDAKQQQTINLYGKERGLVTD ELVLKVFDFGKYKTWAEFKT 1869  
S.oralis(WP\_000713080.1) AAKGFKDGMVPIYSNQYEEAAKQKGTINLYGKERGLVTD ELVLDKVFEGKYASWAAFKK 1747  
S.Sanguis(WP\_002913590.1) AAKGFKDGMVPIYSNQYEDDAKQNGKTISIYKTRGLVTD DLVLRKVFNGQFNNWTEFKK 1758  
\*\*\*\*\* \*\* \* ..\*\*\*\*\* \*\* \* ..\*\*

G.haemolysans(WP\_040464465) DMYKERVEQFSKLN RVSFDPNGPWGRQKNVTVNNISVLEKMIETAVREDAEDF---TAQ 2166  
S.pneumoniae(WP\_000417171.1) AMYQERVDQFGNLKQVTFKDPKWPWSYGTKTINNVD ELQALMDQAVLKDAEG--PRWSN 1927  
S.oralis(WP\_000713080.1) AMYKERVDQFKNLKQVTFKDPKWPWSYATKTINSVTELQELMDQAVLQDAVA--PRWSD 1805  
S.Sanguis(WP\_002913590.1) AMYEERKNKFDLSLNKVTFD DTRQPWTSYATKTISTV EELQTLMD EAVLQDANDNWYSWSG 1818  
\*\*\*\*\* \*\* \* ..\*\*\*\*\* \*\* \* ..\*\*

G.haemolysans(WP\_040464465) YVPDTNSRV LK LKKAIFKAYLDQTKDFR TSIFGGK 2201  
S.pneumoniae(WP\_000417171.1) YDPEIDSAVHKLKRAIFKAYLDQTNDFR SSIFENKK 1963  
S.oralis(WP\_000713080.1) YKPEIDSAVHKLKRAIFKAYLDQTKDFR TSIFKK-- 1839  
S.Sanguis(WP\_002913590.1) YKPEYNSAVHKLKKAIFKAYLDQTKDFRKSIFENKQ 1854  
\*\*\*\*\* \*\* \* ..\*\*\*\*\* \*\* \* ..\*\*

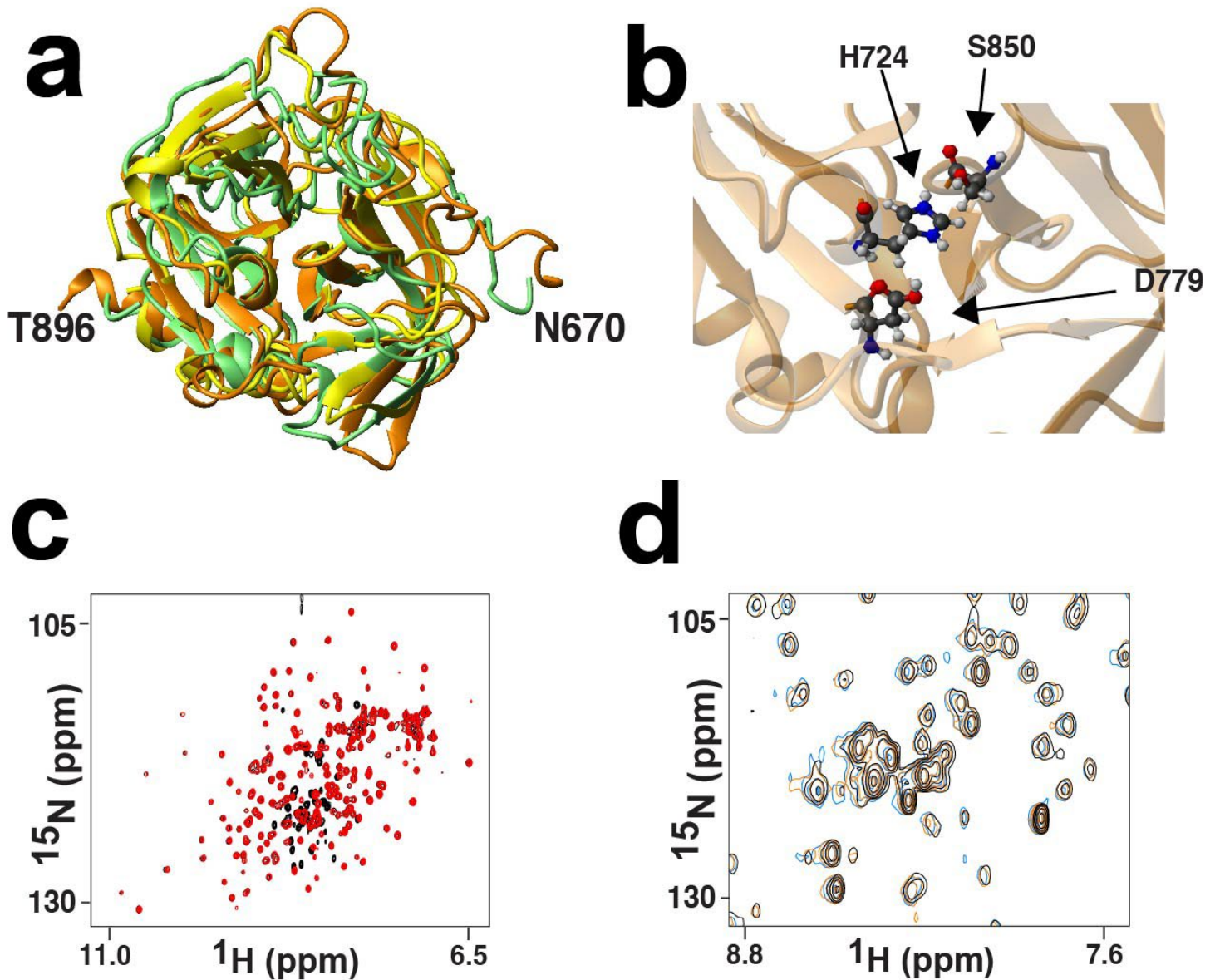
Supplementary Figure 1. Sequence comparison between four IgA1Ps. Specific regions are color-coded to match structural figures. These include the conserved LPXTG motif and the G5 domain (gray), the IgA1P NTD1 domain (yellow), the IgA1P NTD<sup>2</sup> domain (red), the IgA1P MD domain (green), the IgA1P CTD domain (purple), and the GhTrp (brown). Sequences were aligned with Clustal Omega through uniprot.org.

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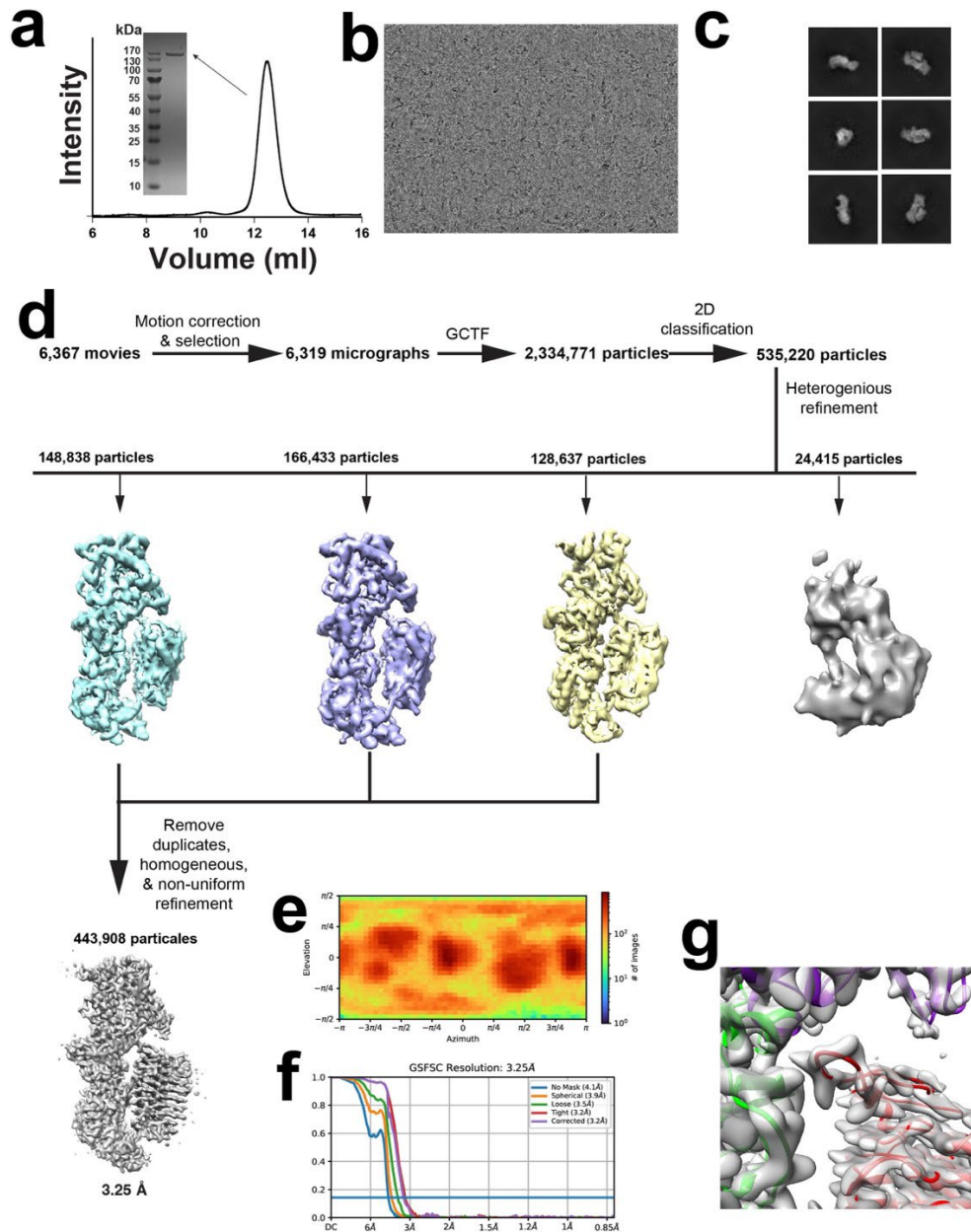
G.haemolysans(WP_040464465)   GIQAGALVEPEKVEAPKEYTGVQAGAVEPEKVEPPKEYTGVQAGAVEPEKVEAPKEYT 660
1agj(WP_001065781.1) -----EVSAEEIK--KHEEKWNKYGVNA-----FNLPKELF 30
                               ** * .. * ..**.* ..**
G.haemolysans(WP_040464465)   GKIEPLKTEENPKPTVENNTAEINNVPKNASALLRMNFVKGNQVLSGTGSATFIAPNVLL 720
1agj(WP_001065781.1)   SKVDEK-----DRQKYPY---NTIGNVFVKGQTSATG----VLIGKNTVL 68
                               *:: .. * : ****: * : *:*
G.haemolysans(WP_040464465)   TVAHINFINNSADNSTGEFIGDKSKNTYEWQTPDGQKGSFTSEDIHFYNNKKDYPKGFIYDL 780
1agj(WP_001065781.1)   TNRHIAKFANGDPSKVSFRP--SINTDDNGNTETPYGEYEVKE----ILQEPFGAGVDL 121
                               * * ..**.* ** * : : * : : * * **
G.haemolysans(WP_040464465)   AVITLPQSTRRQ-----HANLVENYSKVNVDKLNQVGYPRGEYAHLKDTTVEIEQKYA 834
1agj(WP_001065781.1)   ALIRLKPQNGVSLGDKISPAKIGTSDNLKDGDKLELIGYPFDHKVNQMH---RSEIELT 178
                               *.* * .. : : : : ****: ** * : : * : :
G.haemolysans(WP_040464465)   NNTYGVQYQG-GKAGMSGGGIFNSKGEVIGLHQNGAENRSGG--LILSPTQLDWIRSIK 891
1agj(WP_001065781.1)   TLRGLRYYGFTVPGNSGSGIFNSGELVGIHSSKVSHTLDREHQINYGVGIGNYVKRIIN 238
                               : : ** * ** ***** ** * : : : : : : **
G.haemolysans(WP_040464465)   GKEITPNYDALERHKDEKDDIKEEKQVDKLELRNISNVELYTLNENKYRHVSSLSSVP 951
1agj(WP_001065781.1)   EKNE----- 242

```

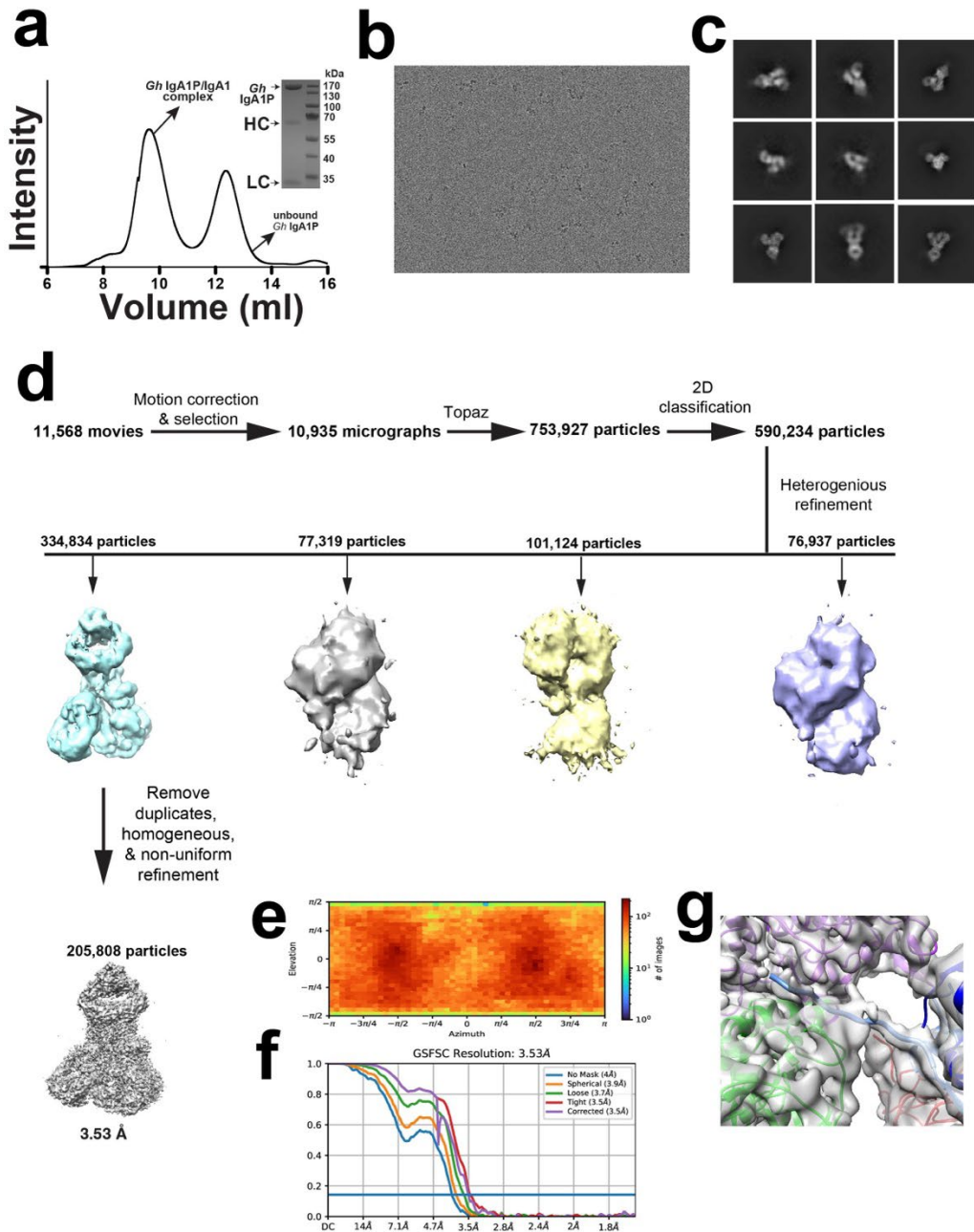
Supplementary Figure 2. Sequence comparison between trypsin-like domains. Sequence alignment between the *G. haemolysans* GhTrp domain (brown) and closest solved structure of *Staphylococcus aureus* epidermolytic toxin A (ETA, PDB entry 1agj). The conserved catalytic triad is highlighted (yellow). Sequences were aligned with Clustal Omega through uniprot.org.



Supplementary Figure 3. Structural interrogation of the *G. haemolysans* trypsin-like domain, GhTrp. a) Overlay of three independently determined models of GhTrp that included SWISS-MODEL (yellow), I-TASSER model (green), and Rosetta model (orange). b) The catalytic triad of H724, D779, and S850 is shown within the Rosetta model. c)  $^{15}\text{N}$ -HSQC spectra of GhTrp residues 684-896 (red) is shown along with the overlay of the N-terminally extended construct of GhTrp residues 651-896 (black). d)  $^{15}\text{N}$ -HSQC spectra of GhTrp residues 651-891 alone (black) and with 50  $\mu\text{M}$  (blue) and 100  $\mu\text{M}$  (orange) unlabelled *G. haemolysans* IgA1P region (residues 907-2201).



Supplementary Figure 4. Purification and workflow for cryo-EM data processing for substrate free *G. haemolysans* IgA1P. a) Analytical size exclusion chromatography to assess purity of substrate-free *G. haemolysans* IgA1P residues 907-2201 together with an SDS-PAGE gel analysis of this single elution peak. b) Raw cryo-EM micrograph c) Representative 2D class averages of substrate-free *G. haemolysans* IgA1P residues 907-2201. d) EM data processing workflow. e) Angular distribution of the final reconstruction. f) Local resolution map of the final density. g) Density and corresponding model for the active site.



Supplementary Figure 5. Purification and workflow for cryo-EM data processing for substrate bound *G. haemolysans* IgA1P in complex with IgA1. a) Analytical size exclusion chromatography to assess purity of the *G. haemolysans* IgA1P residues 907-2201 complex with IgA1 together with an SDS-PAGE gel analysis of the elution peak indicating the presence of IgA1P, IgA1-HC, and IgA1-LC. b) Raw cryo-EM micrograph c) Representative 2D class averages of substrate-free *G. haemolysans* IgA1P residues 907-2201. d) EM data processing workflow. e) Angular distribution of the final reconstruction. f) Local resolution map of the final density. g) Density and corresponding model for the active site within the complex.