



Full wwPDB EM Validation Report ⓘ

Mar 27, 2026 – 04:32 PM UTC

PDB ID : 6SCN / pdb_00006scn
EMDB ID : EMD-10143
Title : 33mer structure of the Salmonella flagella MS-ring protein FljF
Authors : Johnson, S.; Fong, Y.H.; Deme, J.C.; Furlong, E.J.; Kuhlen, L.; Lea, S.M.
Deposited on : 2019-07-24
Resolution : 3.10 Å(reported)

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We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

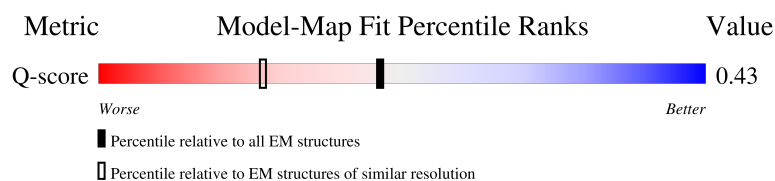
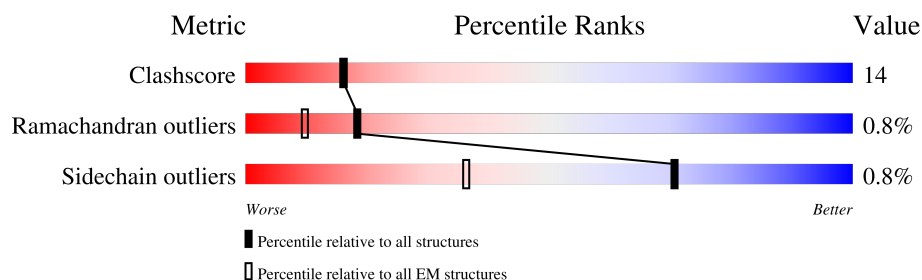
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

1 Overall quality at a glance

The following experimental techniques were used to determine the structure:
ELECTRON MICROSCOPY

The reported resolution of this entry is 3.10 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	14724 (2.60 - 3.60)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	560	 29% 14% 56%
1	B	560	 13% 33% 11% 56%
1	C	560	 32% 12% 56%
1	D	560	 30% 13% 56%

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Mol	Chain	Length	Quality of chain
1	E	560	
1	F	560	
1	G	560	
1	H	560	
1	I	560	
1	J	560	
1	K	560	
1	L	560	
1	M	560	
1	N	560	
1	O	560	
1	P	560	
1	Q	560	
1	R	560	
1	S	560	
1	T	560	
1	U	560	
1	V	560	
1	W	560	
1	X	560	
1	Y	560	
1	Z	560	
1	a	560	
1	b	560	
1	c	560	

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Mol	Chain	Length	Quality of chain
1	d	560	12%31%12%56%
1	e	560	30%13%56%
1	f	560	29%15%56%
1	g	560	21%6%72%

2 Entry composition [i](#)

There is only 1 type of molecule in this entry. The entry contains 60582 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called Flagellar M-ring protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	247	Total	C	N	O	S	0	0
			1897	1160	350	383	4		
1	B	247	Total	C	N	O	S	0	0
			1897	1160	350	383	4		
1	C	247	Total	C	N	O	S	0	0
			1897	1160	350	383	4		
1	D	247	Total	C	N	O	S	0	0
			1897	1160	350	383	4		
1	E	247	Total	C	N	O	S	0	0
			1897	1160	350	383	4		
1	F	247	Total	C	N	O	S	0	0
			1897	1160	350	383	4		
1	G	247	Total	C	N	O	S	0	0
			1897	1160	350	383	4		
1	H	247	Total	C	N	O	S	0	0
			1897	1160	350	383	4		
1	I	247	Total	C	N	O	S	0	0
			1897	1160	350	383	4		
1	J	247	Total	C	N	O	S	0	0
			1897	1160	350	383	4		
1	K	155	Total	C	N	O	S	0	0
			1224	744	230	247	3		
1	L	247	Total	C	N	O	S	0	0
			1897	1160	350	383	4		
1	M	247	Total	C	N	O	S	0	0
			1897	1160	350	383	4		
1	N	247	Total	C	N	O	S	0	0
			1897	1160	350	383	4		
1	O	247	Total	C	N	O	S	0	0
			1897	1160	350	383	4		
1	P	247	Total	C	N	O	S	0	0
			1897	1160	350	383	4		
1	Q	247	Total	C	N	O	S	0	0
			1897	1160	350	383	4		

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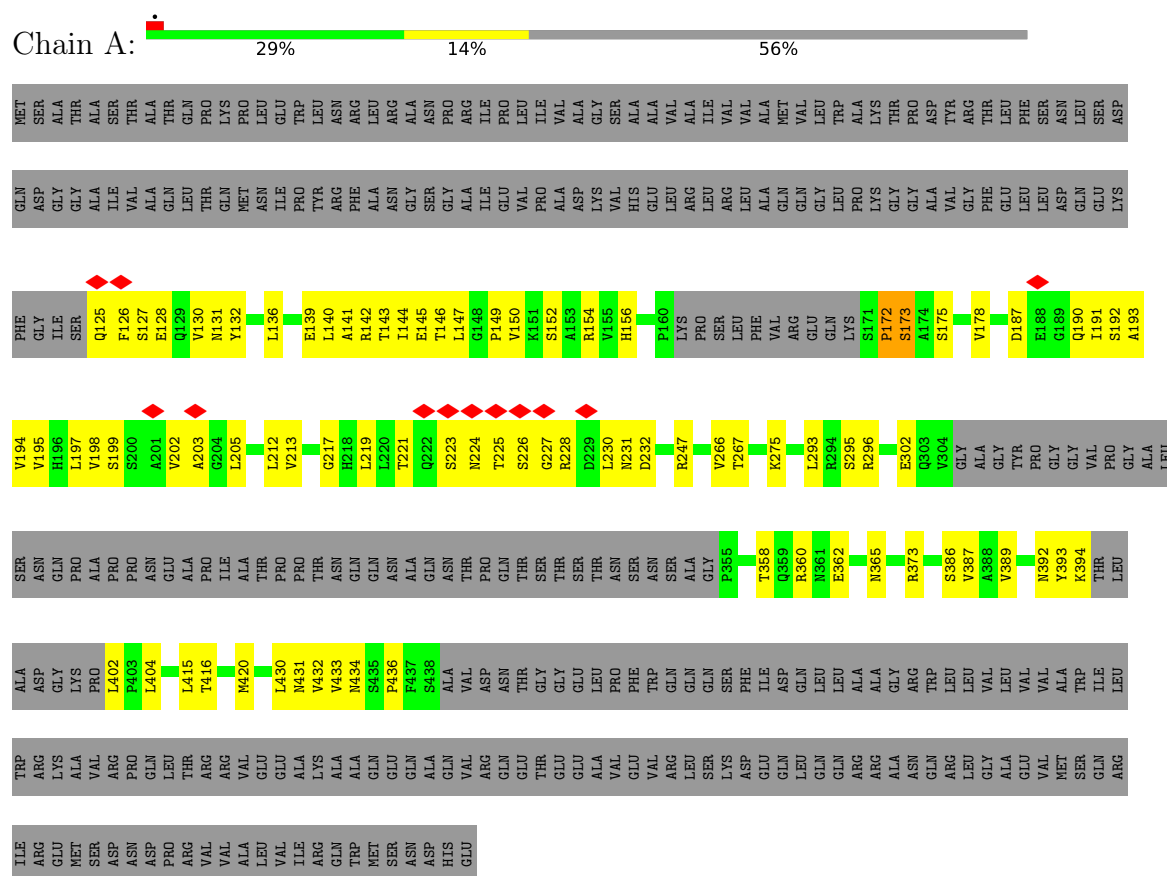
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Mol	Chain	Residues	Atoms					AltConf	Trace
1	R	247	Total	C	N	O	S	0	0
			1897	1160	350	383	4		
1	S	247	Total	C	N	O	S	0	0
			1897	1160	350	383	4		
1	T	247	Total	C	N	O	S	0	0
			1897	1160	350	383	4		
1	U	247	Total	C	N	O	S	0	0
			1897	1160	350	383	4		
1	V	155	Total	C	N	O	S	0	0
			1224	744	230	247	3		
1	W	247	Total	C	N	O	S	0	0
			1897	1160	350	383	4		
1	X	247	Total	C	N	O	S	0	0
			1897	1160	350	383	4		
1	Y	247	Total	C	N	O	S	0	0
			1897	1160	350	383	4		
1	Z	247	Total	C	N	O	S	0	0
			1897	1160	350	383	4		
1	a	247	Total	C	N	O	S	0	0
			1897	1160	350	383	4		
1	b	247	Total	C	N	O	S	0	0
			1897	1160	350	383	4		
1	c	247	Total	C	N	O	S	0	0
			1897	1160	350	383	4		
1	d	247	Total	C	N	O	S	0	0
			1897	1160	350	383	4		
1	e	247	Total	C	N	O	S	0	0
			1897	1160	350	383	4		
1	f	247	Total	C	N	O	S	0	0
			1897	1160	350	383	4		
1	g	155	Total	C	N	O	S	0	0
			1224	744	230	247	3		

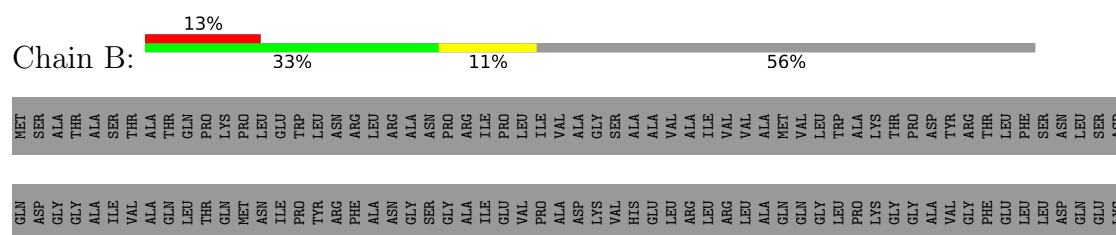
3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

• Molecule 1: Flagellar M-ring protein



• Molecule 1: Flagellar M-ring protein

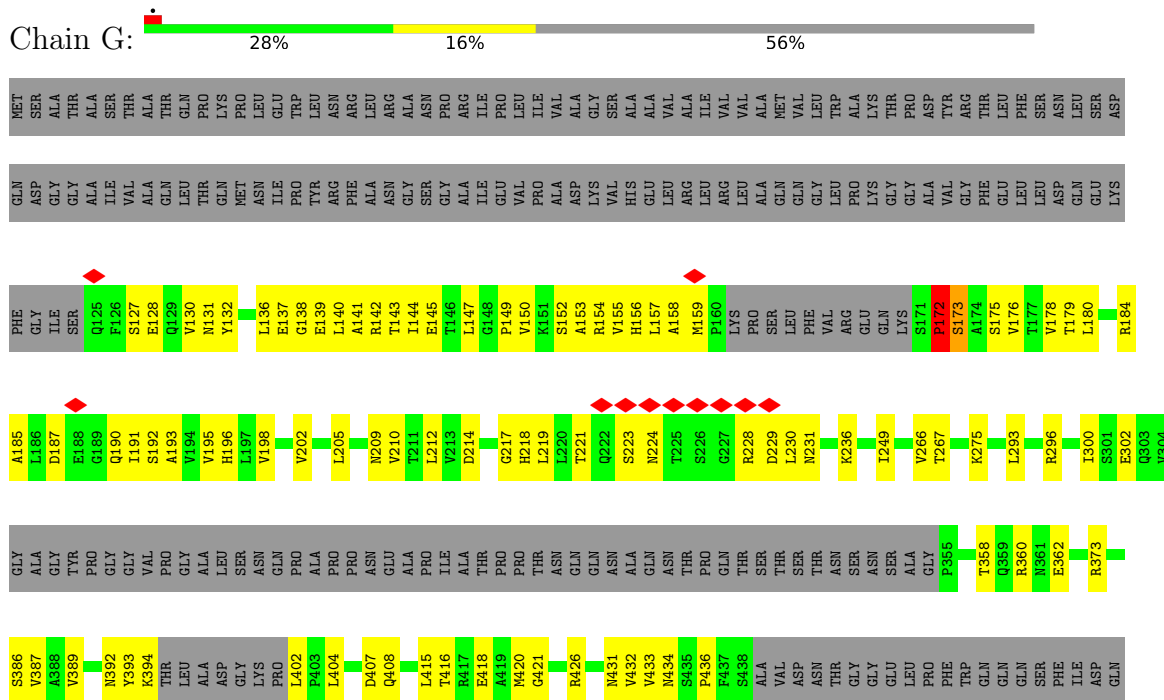




Chain F:

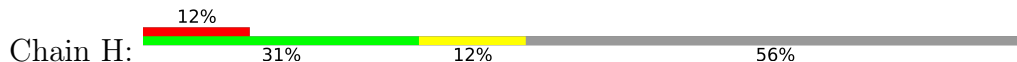


Chain G:



[illegible]

- Molecule 1: Flagellar M-ring protein



NET	SER	ALA	THR	ALA	SER	THR	ALA	THR	GLN	PRO	PRO	LYS	PRO	LEU	GLU	TRP	LEU	ASN	ARG	ARG	LEU	ARG	ALA	ALA	ASN	PRO	ARG	ILE	ILE	LEU	VAL	ALA	GLY	SER	ALA	ALA	ALA	VAL	VAL	ALA	ILE	VAL	VAL	VAL	VAL	MET	VAL	LEU	TRP	ALA	ALA	LYS	THR	PRO	ASP	TYR	ARG	THR	LEU	PHE	SER	ASN	LEU	SER	ASP
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[illegible]

PHE	GLY	ILE	SER	Q125	F126	S127	E128	Q129	V130	N131	R134	L135	L136	E137	G138	E139	L140	A141	A142	T143	I144	E145	T146	L147	G148	P149	V150	K151	S152	A153	R154	V155	H156	L157	A158	M159	S160	LYS	PRO	SER	LEU	PHE	VAL	ARG	GLU	GLN	LYS	S171	P172	S173	A174	S175	V176	T177	V178	T179	L180	A181	L182	L183	L184	L185	L186	L187	L188	L189	L190	L191	L192	L193	L194	L195	L196	L197	L198	L199	L200	L201	L202	L203	L204	L205	L206	L207	L208	L209	L210	L211	L212	L213	L214	L215	L216	L217	L218	L219	L220	L221	L222	L223	L224	L225	L226	L227	L228	L229	L230	L231	L232	L233	L234	L235	L236	L237	L238	L239	L240	L241	L242	L243	L244	L245	L246	L247	L248	L249	L250	L251	L252	L253	L254	L255	L256	L257	L258	L259	L260	L261	L262	L263	L264	L265	L266	L267	L268	L269	L270	L271	L272	L273	L274	L275	L276	L277	L278	L279	L280	L281	L282	L283	L284	L285	L286	L287	L288	L289	L290	L291	L292	L293	L294	L295	L296	L297	L298	L299	L300	L301	L302	L303	L304	L305	L306	L307	L308	L309	L310	L311	L312	L313	L314	L315	L316	L317	L318	L319	L320	L321	L322	L323	L324	L325	L326	L327	L328	L329	L330	L331	L332	L333	L334	L335	L336	L337	L338	L339	L340	L341	L342	L343	L344	L345	L346	L347	L348	L349	L350	L351	L352	L353	L354	L355	L356	L357	L358	L359	L360	L361	L362	L363	L364	L365	L366	L367	L368	L369	L370	L371	L372	L373	L374	L375	L376	L377	L378	L379	L380	L381	L382	L383	L384	L385	L386	L387	L388	L389	L390	L391	L392	L393	L394	L395	L396	L397	L398	L399	L400	L401	L402	L403	L404	L405	L406	L407	L408	L409	L410	L411	L412	L413	L414	L415	L416	L417	L418	L419	L420	L421	L422	L423	L424	L425	L426	L427	L428	L429	L430	L431	L432	L433	L434	L435	L436	L437	L438	L439	L440	L441	L442	L443	L444	L445	L446	L447	L448	L449	L450	L451	L452	L453	L454	L455	L456	L457	L458	L459	L460	L461	L462	L463	L464	L465	L466	L467	L468	L469	L470	L471	L472	L473	L474	L475	L476	L477	L478	L479	L480	L481	L482	L483	L484	L485	L486	L487	L488	L489	L490	L491	L492	L493	L494	L495	L496	L497	L498	L499	L500	L501	L502	L503	L504	L505	L506	L507	L508	L509	L510	L511	L512	L513	L514	L515	L516	L517	L518	L519	L520	L521	L522	L523	L524	L525	L526	L527	L528	L529	L530	L531	L532	L533	L534	L535	L536	L537	L538	L539	L540	L541	L542	L543	L544	L545	L546	L547	L548	L549	L550	L551	L552	L553	L554	L555	L556	L557	L558	L559	L560	L561	L562	L563	L564	L565	L566	L567	L568	L569	L570	L571	L572	L573	L574	L575	L576	L577	L578	L579	L580	L581	L582	L583	L584	L585	L586	L587	L588	L589	L590	L591	L592	L593	L594	L595	L596	L597	L598	L599	L600	L601	L602	L603	L604	L605	L606	L607	L608	L609	L610	L611	L612	L613	L614	L615	L616	L617	L618	L619	L620	L621	L622	L623	L624	L625	L626	L627	L628	L629	L630	L631	L632	L633	L634	L635	L636	L637	L638	L639	L640	L641	L642	L643	L644	L645	L646	L647	L648	L649	L650	L651	L652	L653	L654	L655	L656	L657	L658	L659	L660	L661	L662	L663	L664	L665	L666	L667	L668	L669	L670	L671	L672	L673	L674	L675	L676	L677	L678	L679	L680	L681	L682	L683	L684	L685	L686	L687	L688	L689	L690	L691	L692	L693	L694	L695	L696	L697	L698	L699	L700	L701	L702	L703	L704	L705	L706	L707	L708	L709	L710	L711	L712	L713	L714	L715	L716	L717	L718	L719	L720	L721	L722	L723	L724	L725	L726	L727	L728	L729	L730	L731	L732	L733	L734	L735	L736	L737	L738	L739	L740	L741	L742	L743	L744	L745	L746	L747	L748	L749	L750	L751	L752	L753	L754	L755	L756	L757	L758	L759	L760	L761	L762	L763	L764	L765	L766	L767	L768	L769	L770	L771	L772	L773	L774	L775	L776	L777	L778	L779	L780	L781	L782	L783	L784	L785	L786	L787	L788	L789	L790	L791	L792	L793	L794	L795	L796	L797	L798	L799	L800	L801	L802	L803	L804	L805	L806	L807	L808	L809	L810	L811	L812	L813	L814	L815	L816	L817	L818	L819	L820	L821	L822	L823	L824	L825	L826	L827	L828	L829	L830	L831	L832	L833	L834	L835	L836	L837	L838	L839	L840	L841	L842	L843	L844	L845	L846	L847	L848	L849	L850	L851	L852	L853	L854	L855	L856	L857	L858	L859	L860	L861	L862	L863	L864	L865	L866	L867	L868	L869	L870	L871	L872	L873	L874	L875	L876	L877	L878	L879	L880	L881	L882	L883	L884	L885	L886	L887	L888	L889	L890	L891	L892	L893	L894	L895	L896	L897	L898	L899	L900	L901	L902	L903	L904	L905	L906	L907	L908	L909	L910	L911	L912	L913	L914	L915	L916	L917	L918	L919	L920	L921	L922	L923	L924	L925	L926	L927	L928	L929	L930	L931	L932	L933	L934	L935	L936	L937	L938	L939	L940	L941	L942	L943	L944	L945	L946	L947	L948	L949	L950	L951	L952	L953	L954	L955	L956	L957	L958	L959	L960	L961	L962	L963	L964	L965	L966	L967	L968	L969	L970	L971	L972	L973	L974	L975	L976	L977	L978	L979	L980	L981	L982	L983	L984	L985	L986	L987	L988	L989	L990	L991	L992	L993	L994	L995	L996	L997	L998	L999	L1000
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GLY	GLU	LEU	PRO	PHE	TRP	GLN	GLN	SER	GLN	PHE	TLE	ASP	GLN	LEU	LEU	ALA	ALA	GLY	ARG	TRP	LEU	VAL	LEU	VAL	VAL	ALA	ALA	TRP	ILE	LEU	TRP	LYS	ARG	ALA	VAL	ARG	PRO	GLN	LEU	THR	ARG	ARG	VAL	GLU	GLU	ALA	ALA	LYS	GLN	ALA	ALA	GLN	VAL	ARG	GLN	GLU	THR
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GLU GLU GLU VAL VAL VAL ARG LEU SER LYS ASP GLU GLN GLN GLN GLN ARG ALA ALA ASN GLN GLN ARG LEU GLY GLU ALA GLU VAL VAL MET MET SER SER GLN ARG ARG ARG ARG ARG MET MET SER ASP ASN ASP PRO PRO ARG ARG VAL VAL ALA LEU VAL ILE ILE GLU GLU MET MET SER ASP ASN ASP ASP TRP MET SER ASN ASP HIS GLU

- Molecule 1: Flagellar M-ring protein

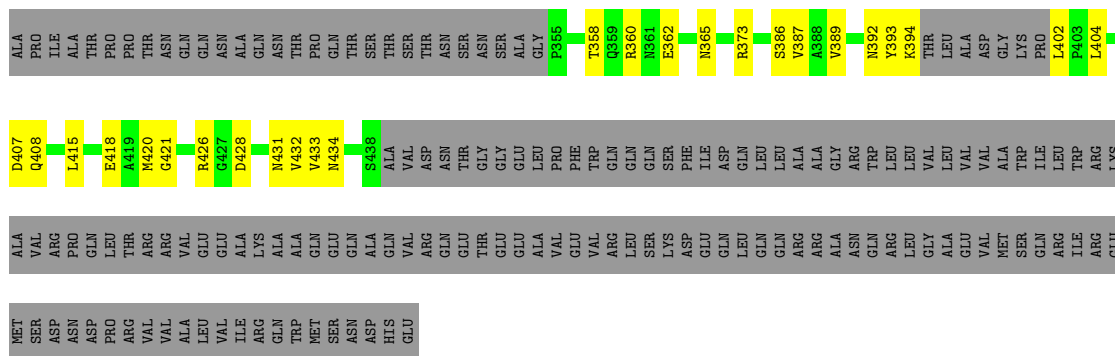


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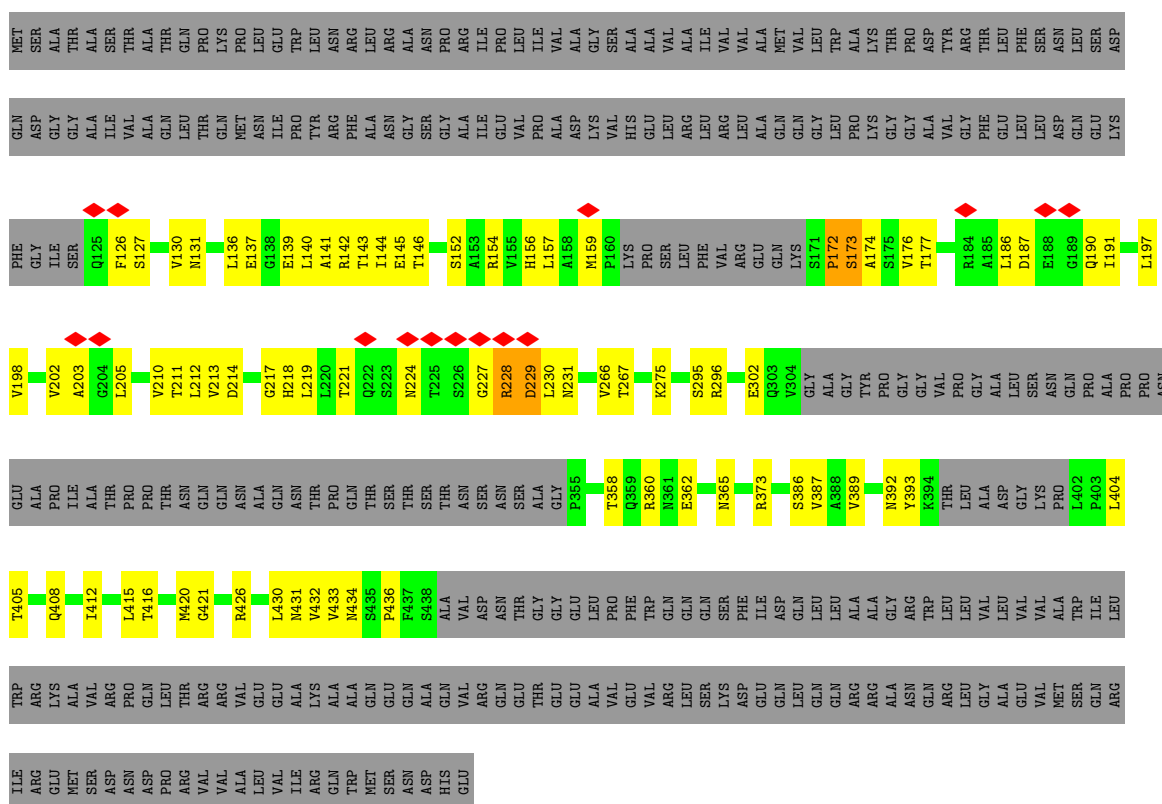
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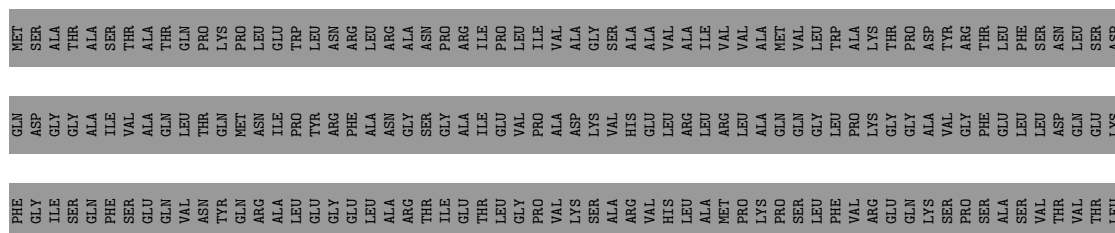
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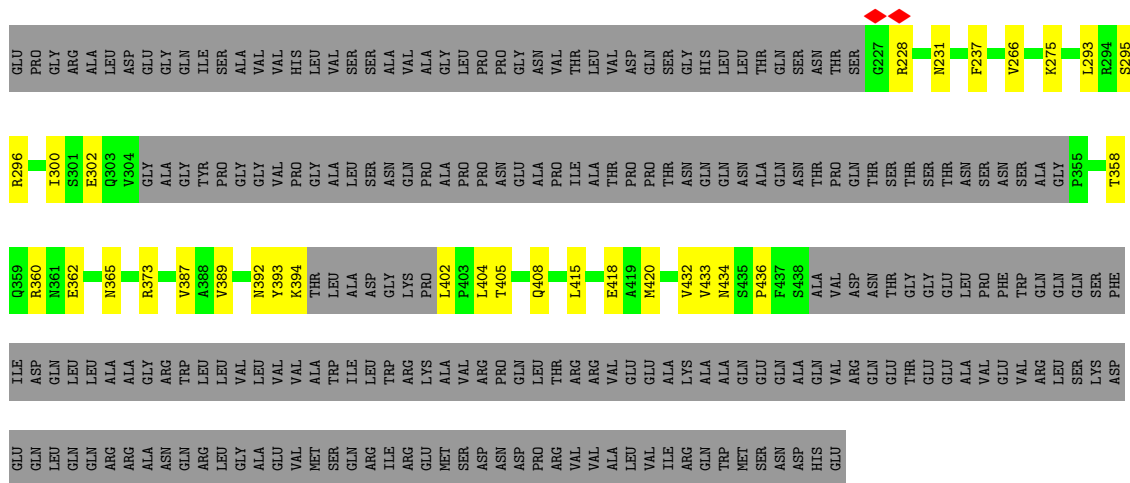


- Molecule 1: Flagellar M-ring protein

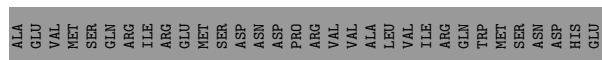
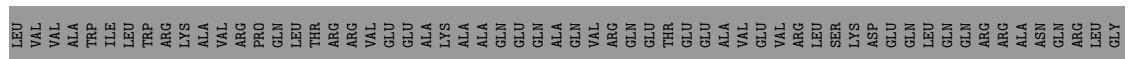
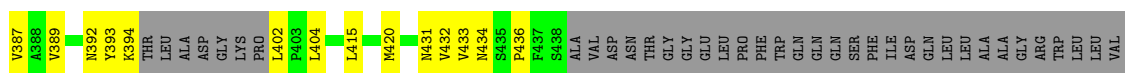
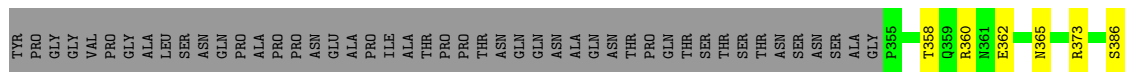
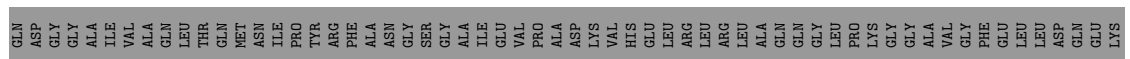
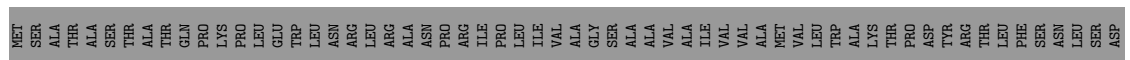


- Molecule 1: Flagellar M-ring protein

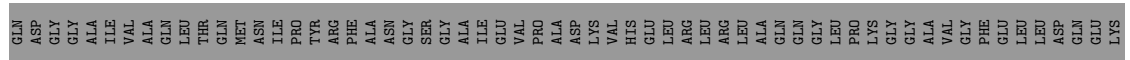
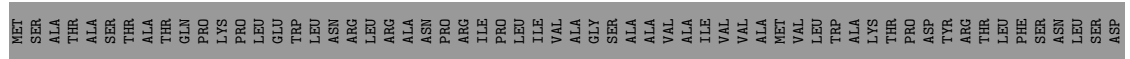
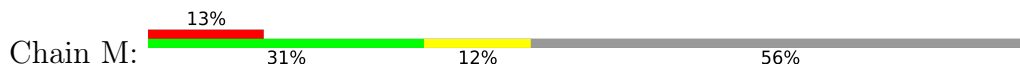


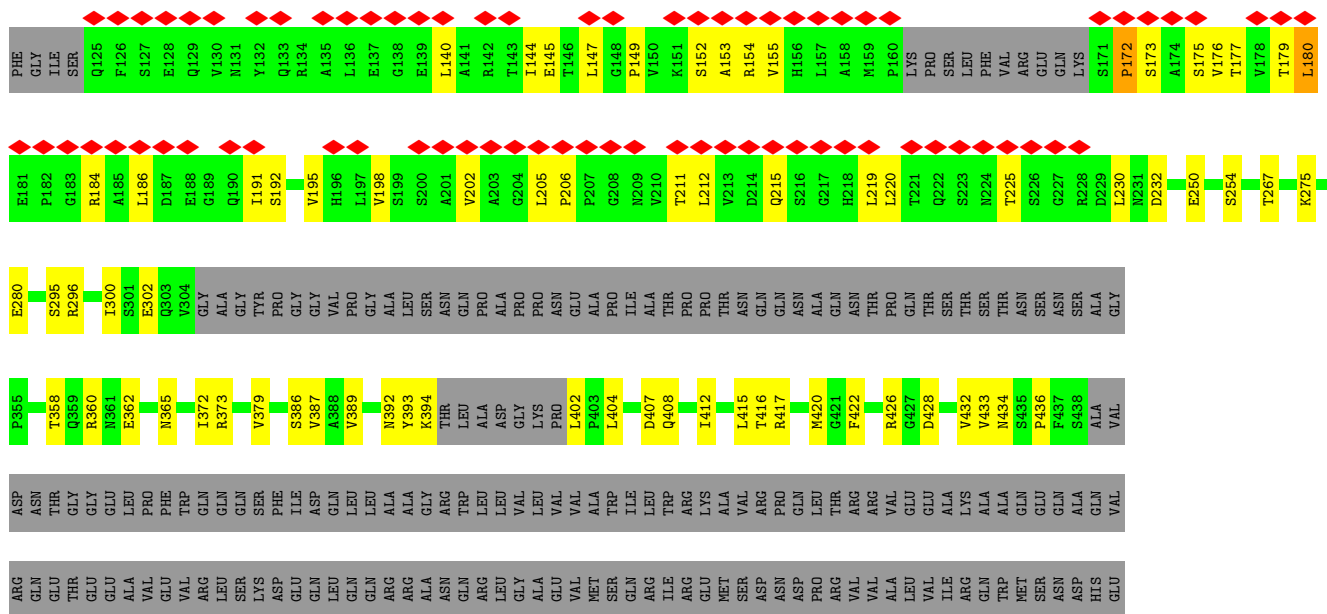


- Molecule 1: Flagellar M-ring protein

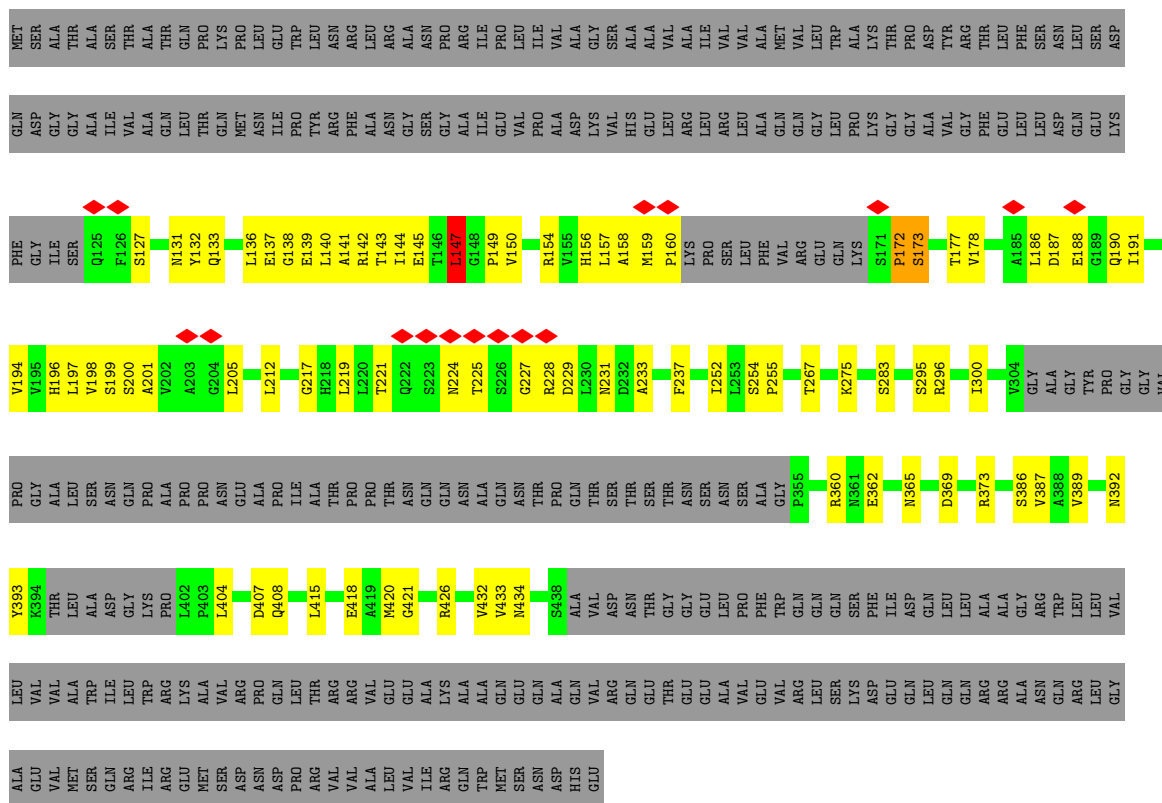


- Molecule 1: Flagellar M-ring protein

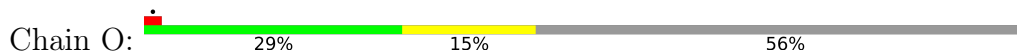


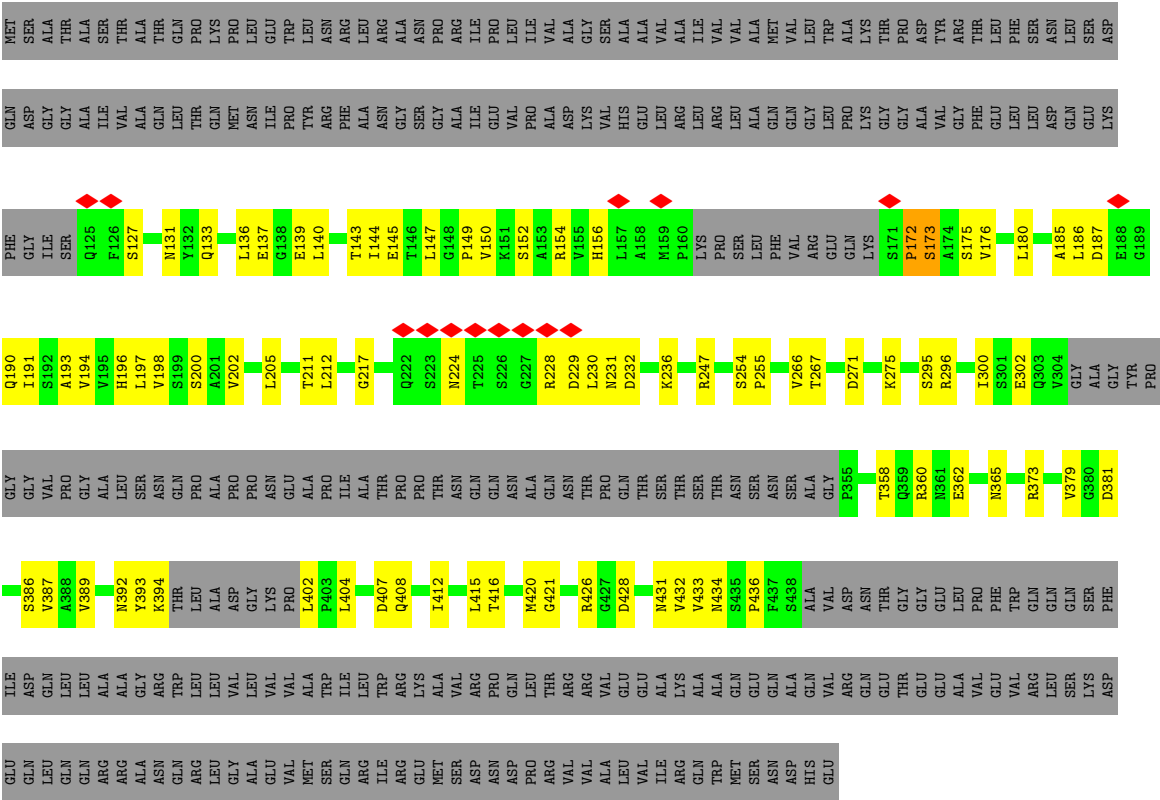


- Molecule 1: Flagellar M-ring protein

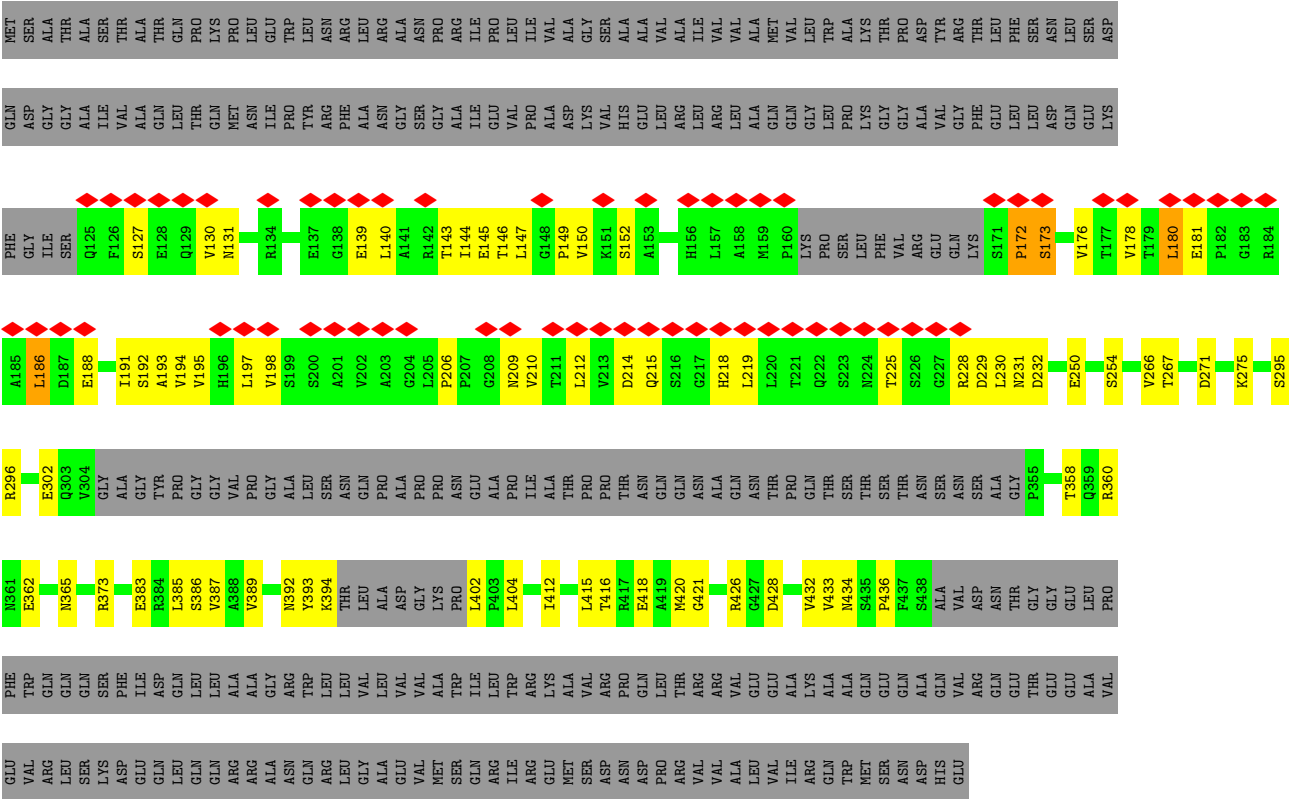


- Molecule 1: Flagellar M-ring protein



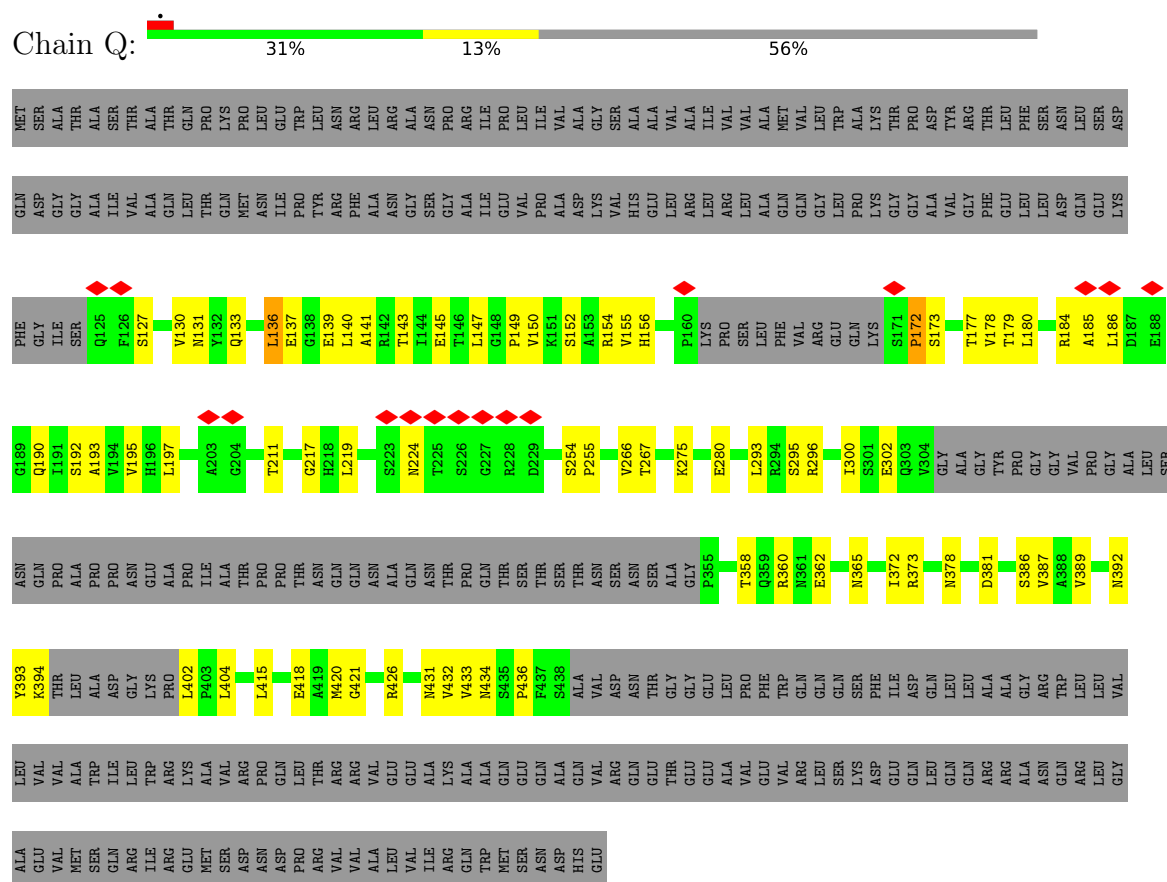


● Molecule 1: Flagellar M-ring protein



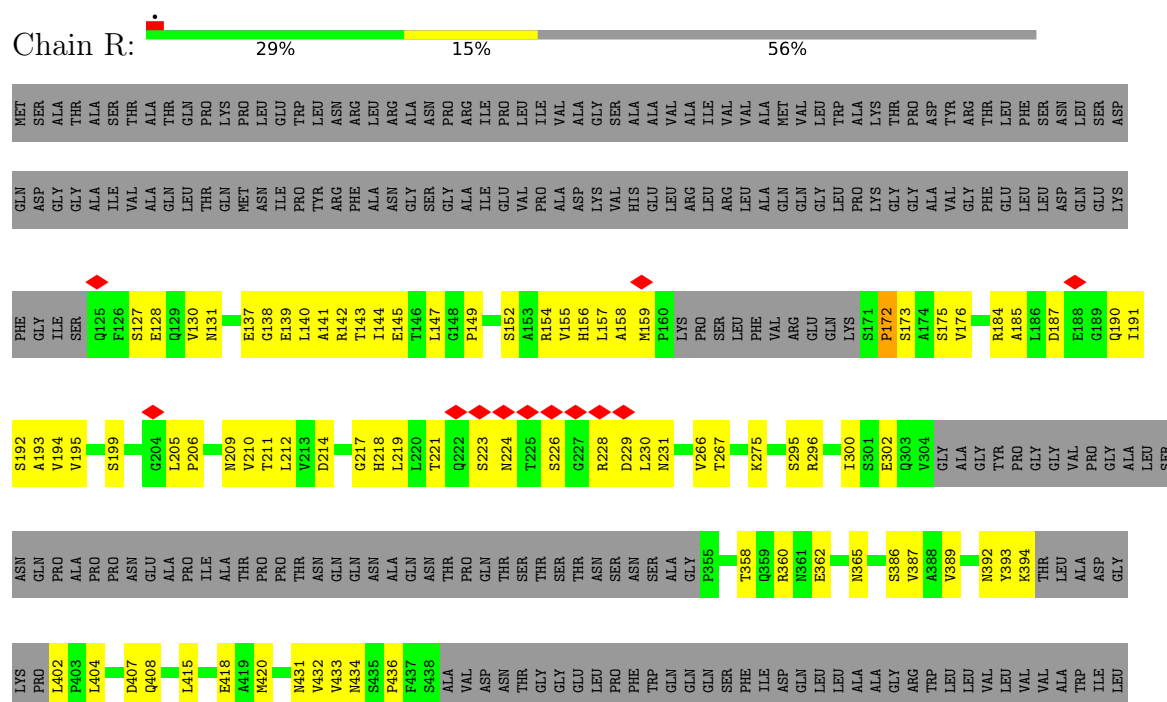
• Molecule 1: Flagellar M-ring protein

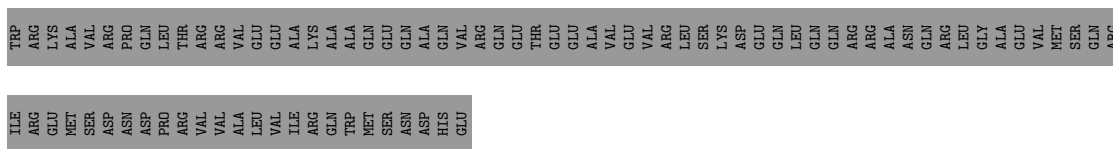
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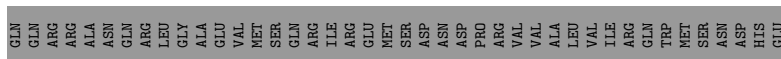
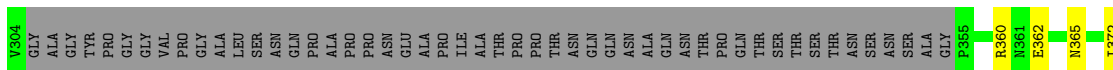
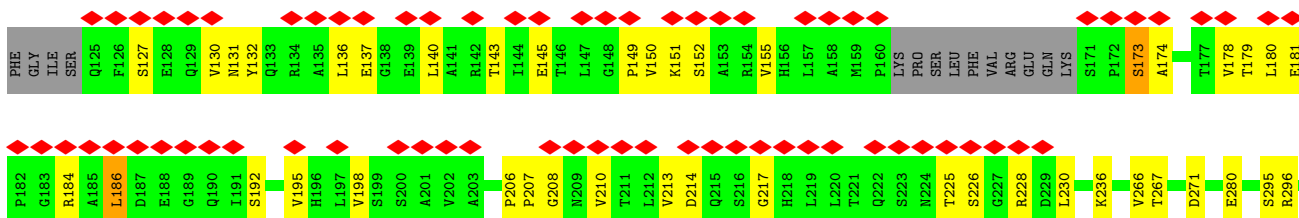
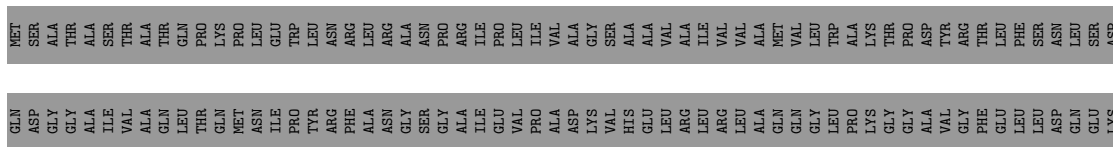
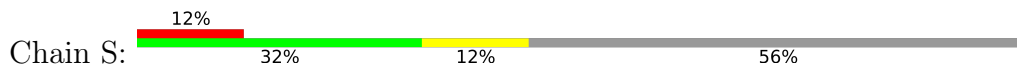
• Molecule 1: Flagellar M-ring protein

Chain R:

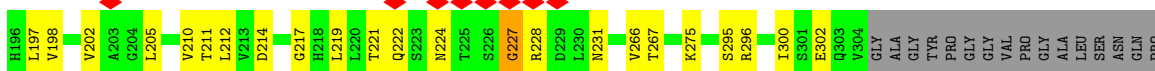
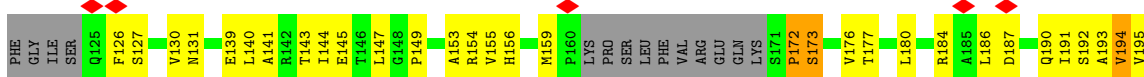
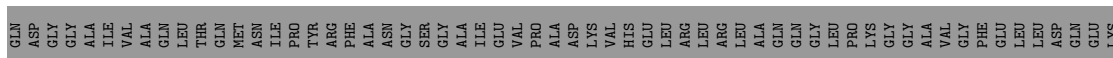
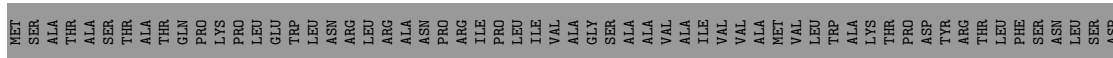


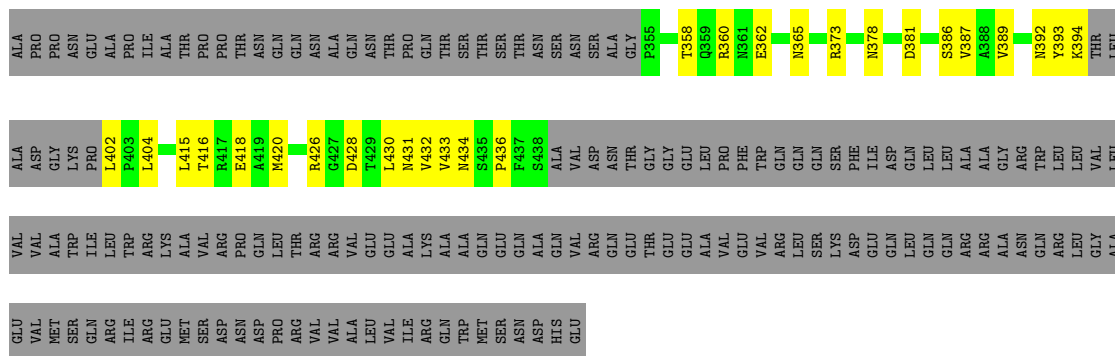


- Molecule 1: Flagellar M-ring protein

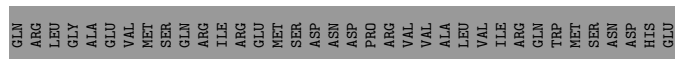
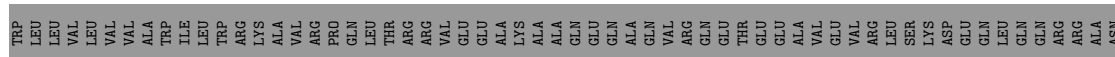
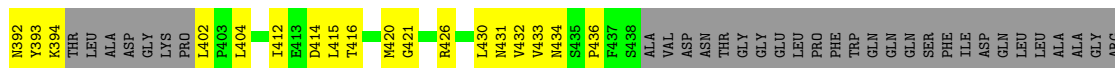
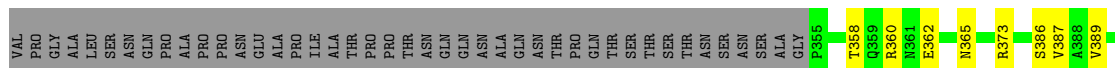
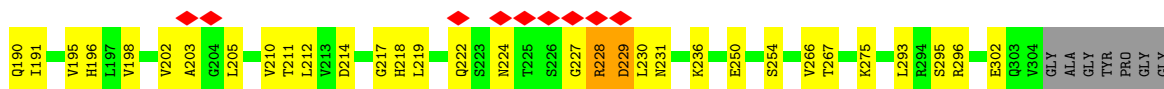
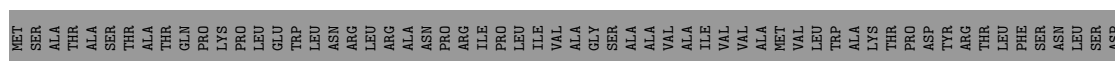


- Molecule 1: Flagellar M-ring protein

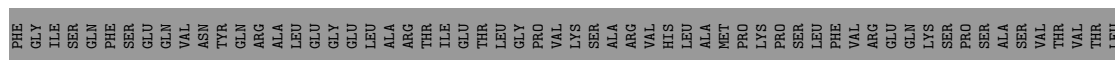
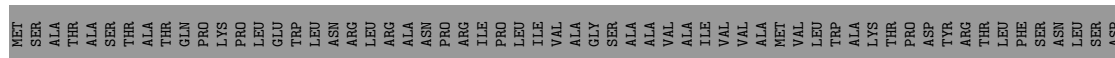


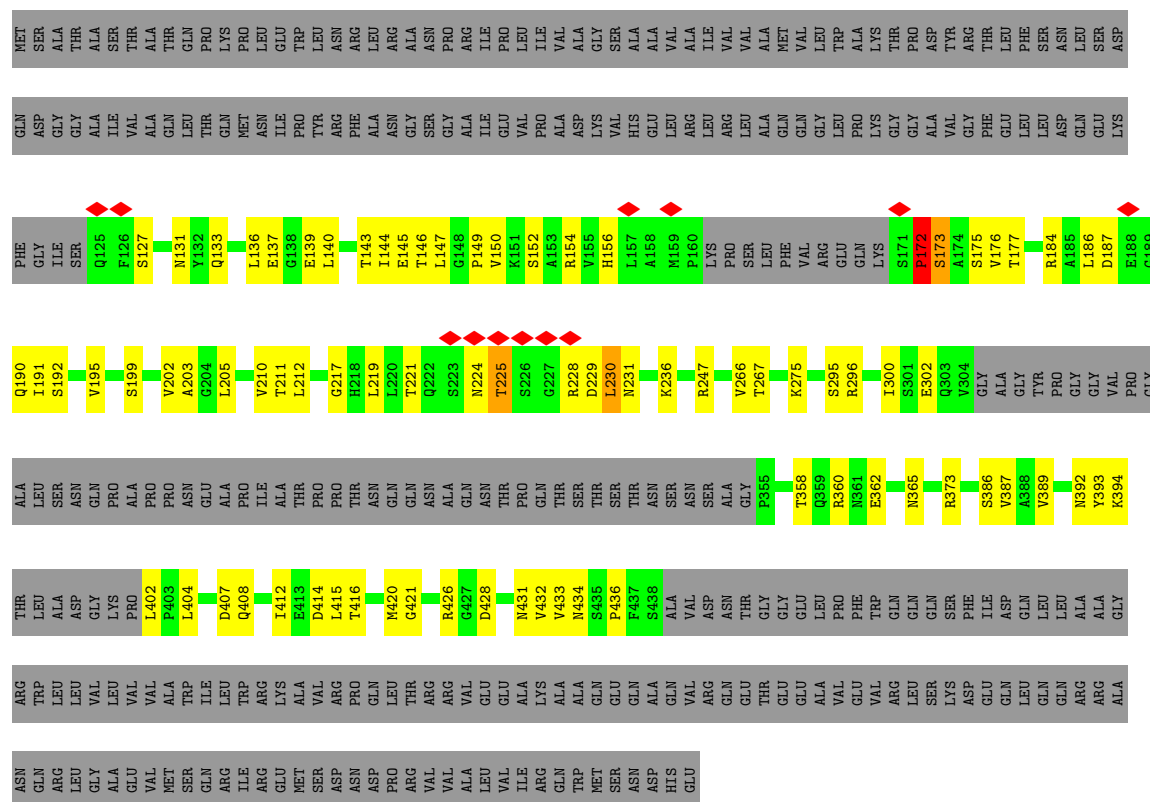


- Molecule 1: Flagellar M-ring protein

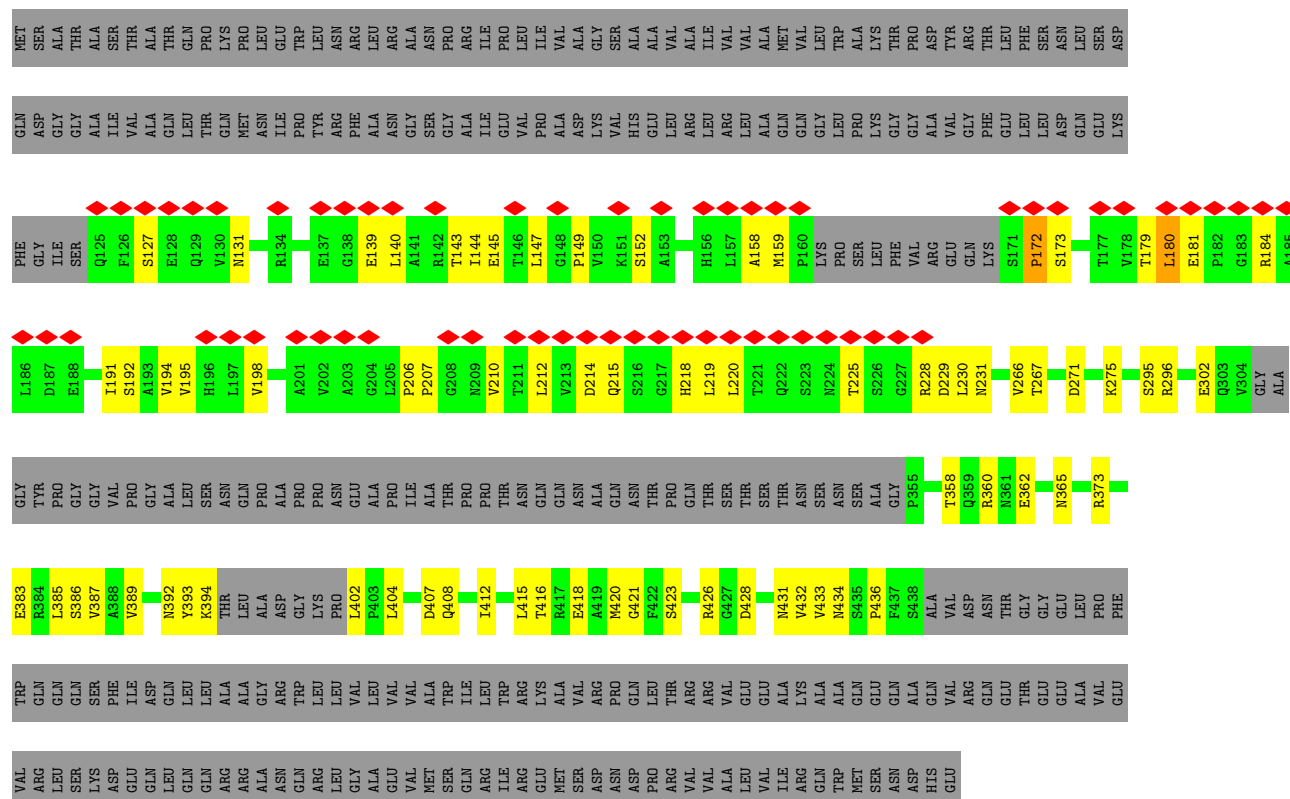
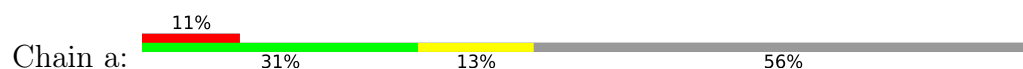


- Molecule 1: Flagellar M-ring protein

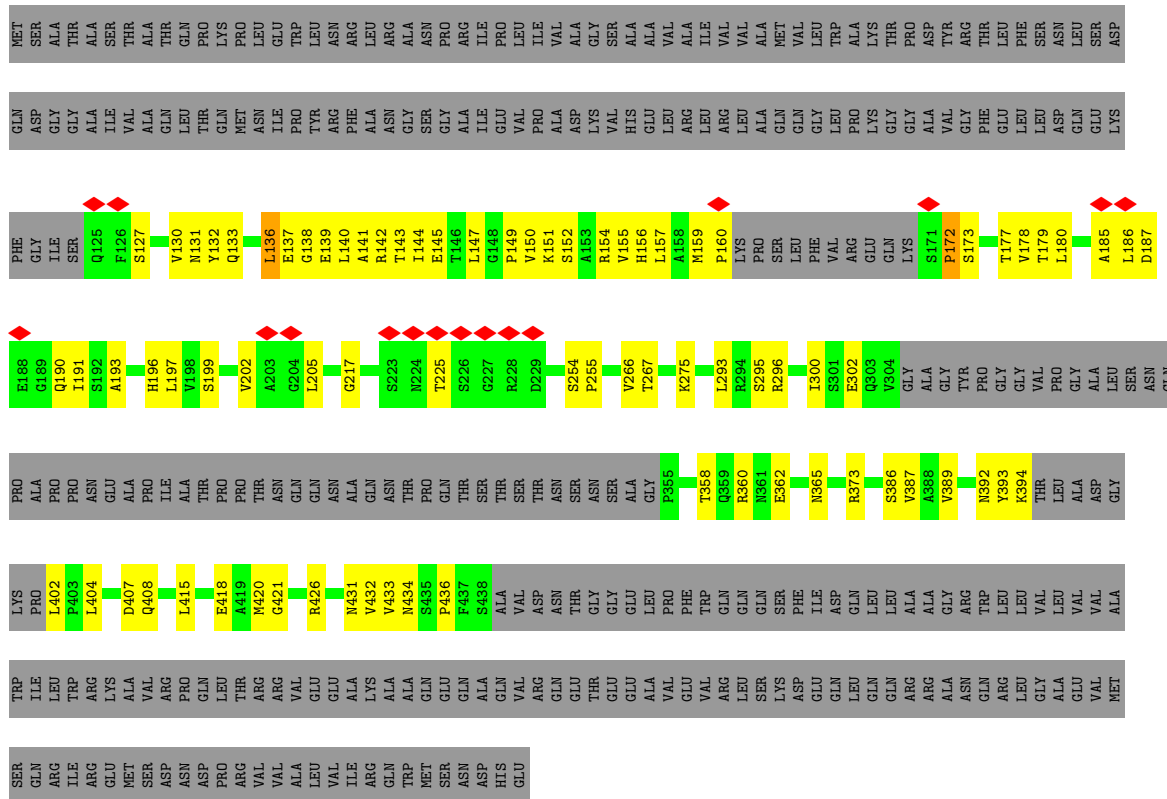




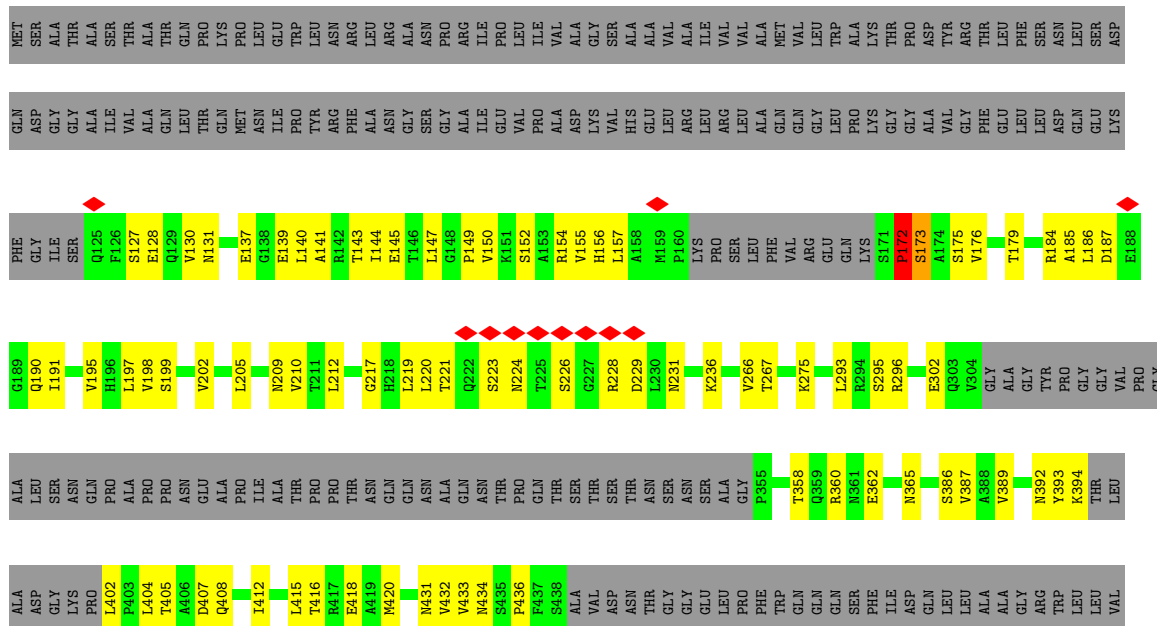
• Molecule 1: Flagellar M-ring protein



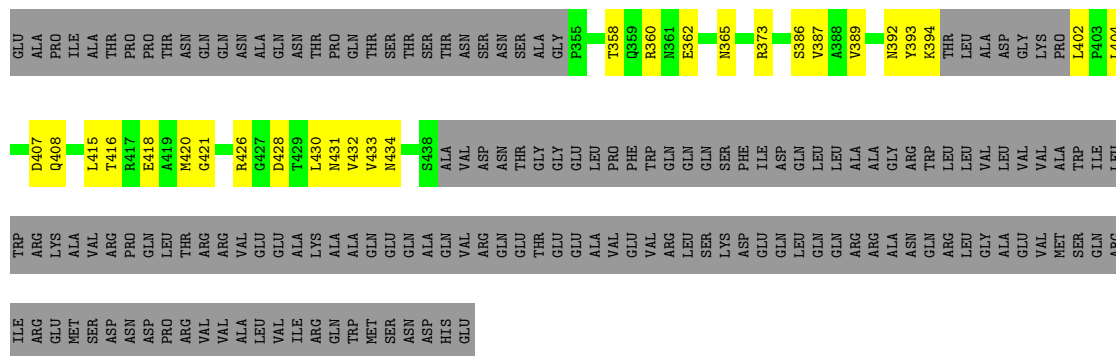
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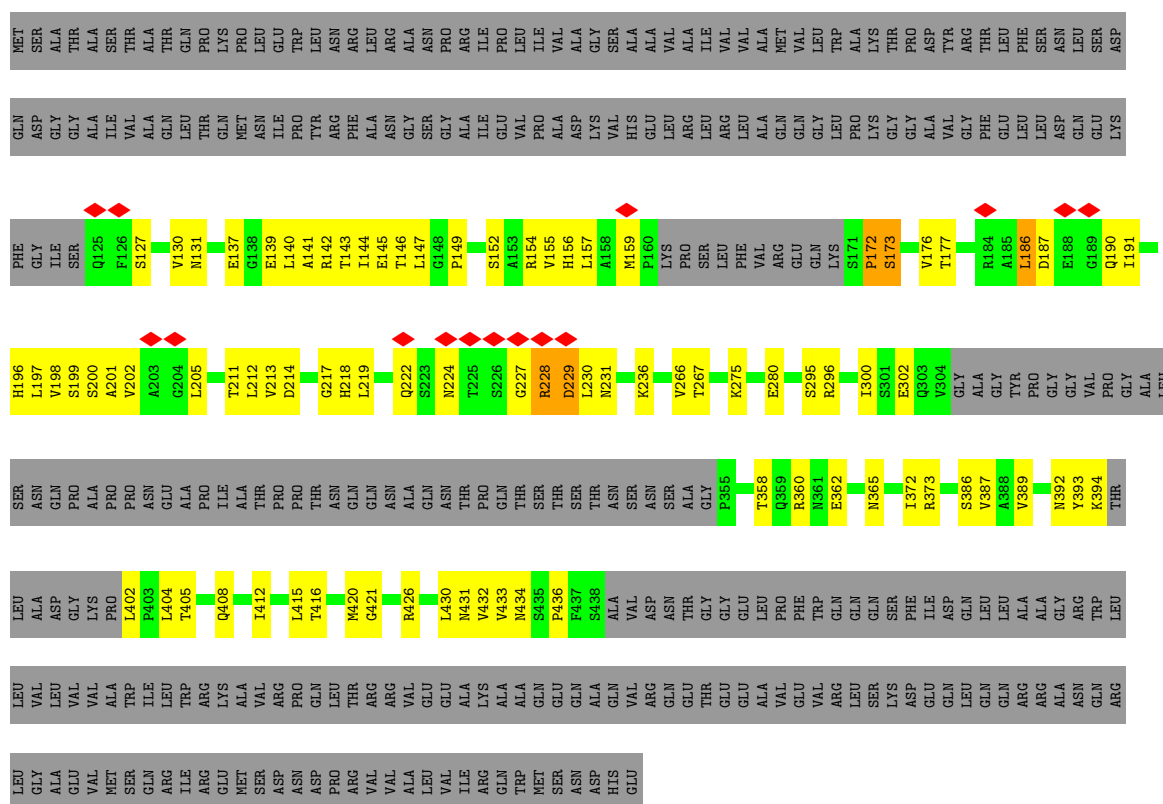
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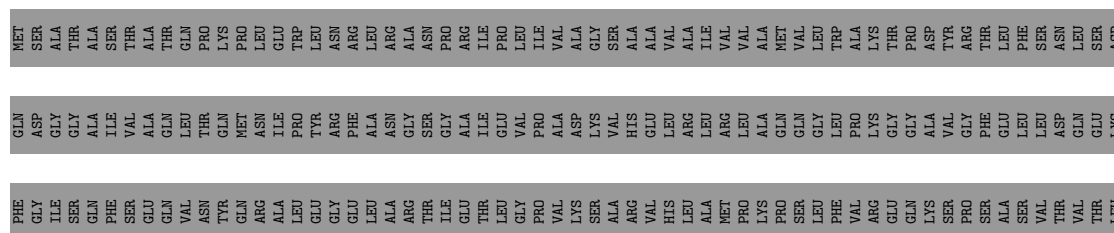


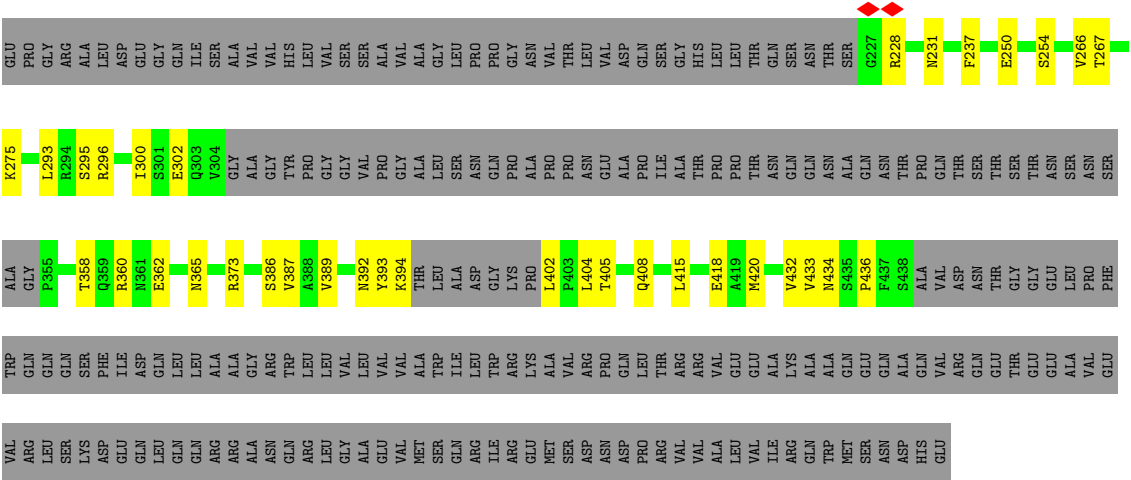


• Molecule 1: Flagellar M-ring protein



• Molecule 1: Flagellar M-ring protein





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C3	Depositor
Number of particles used	175233	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	48	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 QUANTUM (4k x 4k)	Depositor
Maximum map value	0.036	Depositor
Minimum map value	-0.009	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.002	Depositor
Recommended contour level	0.005	Depositor
Map size (Å)	355.104, 355.104, 355.104	wwPDB
Map dimensions	432, 432, 432	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.822, 0.822, 0.822	Depositor

5 Model quality

5.1 Standard geometry

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	A	0.31	0/1919	0.51	0/2598
1	B	0.30	0/1919	0.47	0/2598
1	C	0.31	0/1919	0.51	0/2598
1	D	0.31	0/1919	0.49	0/2598
1	E	0.30	0/1919	0.47	0/2598
1	F	0.31	0/1919	0.51	0/2598
1	G	0.31	0/1919	0.51	1/2598 (0.0%)
1	H	0.30	0/1919	0.48	0/2598
1	I	0.31	0/1919	0.50	0/2598
1	J	0.30	0/1919	0.48	0/2598
1	K	0.34	0/1236	0.44	0/1665
1	L	0.31	0/1919	0.52	0/2598
1	M	0.31	0/1919	0.50	0/2598
1	N	0.31	0/1919	0.52	1/2598 (0.0%)
1	O	0.32	0/1919	0.50	0/2598
1	P	0.30	0/1919	0.47	0/2598
1	Q	0.31	0/1919	0.50	0/2598
1	R	0.31	0/1919	0.48	0/2598
1	S	0.30	0/1919	0.48	0/2598
1	T	0.31	0/1919	0.49	0/2598
1	U	0.30	0/1919	0.48	0/2598
1	V	0.35	0/1236	0.43	0/1665
1	W	0.31	0/1919	0.53	0/2598
1	X	0.30	0/1919	0.50	0/2598
1	Y	0.31	0/1919	0.49	0/2598
1	Z	0.31	0/1919	0.52	1/2598 (0.0%)
1	a	0.30	0/1919	0.47	0/2598
1	b	0.31	0/1919	0.50	0/2598
1	c	0.31	0/1919	0.50	0/2598
1	d	0.30	0/1919	0.48	0/2598
1	e	0.31	0/1919	0.48	0/2598
1	f	0.30	0/1919	0.48	0/2598
1	g	0.34	0/1236	0.44	0/1665
All	All	0.31	0/61278	0.49	3/82935 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	I	0	1
1	T	0	1
All	All	0	2

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	Z	230	LEU	N-CA-C	-9.18	102.91	114.56
1	G	230	LEU	N-CA-C	-5.52	107.55	114.56
1	N	147	LEU	CA-CB-CG	5.44	135.36	116.30

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	I	227	GLY	Peptide
1	T	227	GLY	Peptide

5.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1897	0	1880	75	0
1	B	1897	0	1880	43	0
1	C	1897	0	1880	60	0
1	D	1897	0	1880	70	0
1	E	1897	0	1880	61	0
1	F	1897	0	1880	71	0
1	G	1897	0	1880	83	0
1	H	1897	0	1880	53	0
1	I	1897	0	1880	59	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	J	1897	0	1880	67	0
1	K	1224	0	1204	24	0
1	L	1897	0	1880	67	0
1	M	1897	0	1880	55	0
1	N	1897	0	1880	71	0
1	O	1897	0	1880	76	0
1	P	1897	0	1880	58	0
1	Q	1897	0	1880	58	0
1	R	1897	0	1880	68	0
1	S	1897	0	1880	49	0
1	T	1897	0	1880	68	0
1	U	1897	0	1880	67	0
1	V	1224	0	1204	27	0
1	W	1897	0	1880	68	0
1	X	1897	0	1880	53	0
1	Y	1897	0	1880	60	0
1	Z	1897	0	1880	77	0
1	a	1897	0	1880	57	0
1	b	1897	0	1880	63	0
1	c	1897	0	1880	76	0
1	d	1897	0	1880	53	0
1	e	1897	0	1880	67	0
1	f	1897	0	1880	72	0
1	g	1224	0	1204	25	0
All	All	60582	0	60012	1721	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 14.

All (1721) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:137:GLU:HG2	1:G:157:LEU:HD13	1.51	0.92
1:R:137:GLU:HG2	1:R:157:LEU:HD13	1.52	0.91
1:H:140:LEU:HD11	1:H:155:VAL:HG21	1.53	0.90
1:N:225:THR:HG22	1:N:227:GLY:H	1.42	0.85
1:c:190:GLN:HG3	1:e:217:GLY:HA3	1.56	0.85
1:F:190:GLN:HG3	1:G:217:GLY:HA3	1.59	0.84
1:F:379:VAL:HG13	1:G:231:ASN:HD21	1.41	0.83
1:Y:137:GLU:HG2	1:Y:157:LEU:HD23	1.59	0.83
1:c:221:THR:OG1	1:c:224:ASN:ND2	2.11	0.82

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:e:186:LEU:HD23	1:e:191:ILE:HD13	1.62	0.82
1:B:145:GLU:HG2	1:B:152:SER:HA	1.61	0.82
1:I:191:ILE:HG23	1:I:212:LEU:HD21	1.62	0.82
1:Y:212:LEU:HB2	1:Y:221:THR:HG23	1.63	0.81
1:L:191:ILE:HG23	1:L:212:LEU:HD21	1.63	0.80
1:C:144:ILE:HD11	1:C:197:LEU:HD11	1.60	0.80
1:c:137:GLU:HG2	1:c:157:LEU:HD13	1.62	0.80
1:Z:228:ARG:HE	1:Z:231:ASN:HB2	1.47	0.80
1:f:137:GLU:HG2	1:f:157:LEU:HD13	1.65	0.79
1:Z:192:SER:HA	1:Z:195:VAL:HG12	1.64	0.79
1:G:221:THR:OG1	1:G:224:ASN:ND2	2.16	0.79
1:T:186:LEU:HD23	1:T:191:ILE:HD13	1.65	0.78
1:E:225:THR:HG22	1:E:227:GLY:H	1.47	0.78
1:H:405:THR:OG1	1:H:407:ASP:OD1	2.04	0.76
1:X:145:GLU:HG2	1:X:152:SER:HA	1.67	0.76
1:O:186:LEU:HD23	1:O:191:ILE:HD13	1.67	0.76
1:J:197:LEU:HD11	1:L:213:VAL:HG21	1.68	0.75
1:F:379:VAL:O	1:G:231:ASN:ND2	2.20	0.75
1:c:228:ARG:HD2	1:c:231:ASN:HB2	1.66	0.74
1:M:145:GLU:HG2	1:M:152:SER:HA	1.67	0.74
1:Q:190:GLN:HG3	1:R:217:GLY:HA3	1.69	0.74
1:O:407:ASP:OD1	1:O:408:GLN:N	2.21	0.74
1:c:407:ASP:OD1	1:c:408:GLN:N	2.21	0.74
1:B:407:ASP:OD1	1:B:408:GLN:N	2.21	0.74
1:Z:407:ASP:OD1	1:Z:408:GLN:N	2.21	0.74
1:Q:180:LEU:HD21	1:Q:185:ALA:HA	1.69	0.73
1:D:192:SER:HA	1:D:195:VAL:HG12	1.69	0.73
1:d:140:LEU:HD11	1:d:155:VAL:HG21	1.69	0.73
1:V:405:THR:HG23	1:V:408:GLN:H	1.53	0.73
1:f:222:GLN:OE1	1:f:236:LYS:NZ	2.21	0.73
1:G:190:GLN:HG3	1:I:217:GLY:HA3	1.70	0.73
1:R:407:ASP:OD1	1:R:408:GLN:N	2.21	0.73
1:S:225:THR:HG22	1:S:226:SER:H	1.54	0.73
1:L:143:THR:HG21	1:N:156:HIS:NE2	2.04	0.73
1:M:176:VAL:HB	1:M:212:LEU:HD12	1.71	0.72
1:G:407:ASP:OD1	1:G:408:GLN:N	2.21	0.72
1:N:212:LEU:HB2	1:N:221:THR:HG23	1.70	0.72
1:b:190:GLN:HG3	1:c:217:GLY:HA3	1.71	0.72
1:A:143:THR:HG21	1:C:156:HIS:NE2	2.04	0.72
1:H:407:ASP:OD1	1:H:408:GLN:N	2.21	0.72
1:Y:225:THR:HG22	1:Y:227:GLY:H	1.54	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:222:GLN:O	1:D:225:THR:OG1	2.08	0.72
1:g:405:THR:HG23	1:g:408:GLN:H	1.52	0.72
1:K:405:THR:HG23	1:K:408:GLN:H	1.53	0.72
1:R:228:ARG:HD3	1:R:231:ASN:HB2	1.72	0.72
1:D:127:SER:O	1:D:131:ASN:ND2	2.23	0.71
1:H:145:GLU:HG2	1:H:152:SER:HA	1.71	0.71
1:C:190:GLN:HG3	1:D:217:GLY:HA3	1.71	0.71
1:W:190:GLN:HG3	1:Y:217:GLY:HA3	1.72	0.71
1:M:140:LEU:HD22	1:M:155:VAL:HG21	1.72	0.71
1:e:127:SER:O	1:e:131:ASN:ND2	2.23	0.71
1:C:194:VAL:HA	1:C:197:LEU:HG	1.73	0.71
1:J:186:LEU:HD23	1:J:191:ILE:HD13	1.73	0.71
1:O:127:SER:O	1:O:131:ASN:ND2	2.24	0.71
1:c:226:SER:HA	1:c:229:ASP:HB2	1.71	0.71
1:F:192:SER:HA	1:F:195:VAL:HG12	1.73	0.70
1:O:145:GLU:HG2	1:O:152:SER:HA	1.73	0.70
1:Z:127:SER:O	1:Z:131:ASN:ND2	2.24	0.70
1:L:145:GLU:HG2	1:L:152:SER:HA	1.74	0.70
1:a:127:SER:O	1:a:131:ASN:ND2	2.25	0.70
1:X:407:ASP:OD1	1:X:408:GLN:N	2.24	0.70
1:B:140:LEU:HD21	1:B:198:VAL:HG12	1.74	0.70
1:G:221:THR:O	1:G:224:ASN:ND2	2.25	0.69
1:T:154:ARG:HB3	1:T:177:THR:HG23	1.74	0.69
1:T:127:SER:O	1:T:131:ASN:ND2	2.25	0.69
1:I:186:LEU:HD23	1:I:191:ILE:HD13	1.74	0.69
1:P:127:SER:O	1:P:131:ASN:ND2	2.24	0.69
1:X:154:ARG:NH1	1:X:177:THR:O	2.25	0.69
1:C:225:THR:HG22	1:C:227:GLY:H	1.57	0.69
1:N:127:SER:O	1:N:131:ASN:ND2	2.26	0.69
1:N:194:VAL:HA	1:N:197:LEU:HG	1.73	0.69
1:Q:141:ALA:HB2	1:Q:155:VAL:HG12	1.75	0.69
1:C:127:SER:O	1:C:131:ASN:ND2	2.25	0.69
1:b:133:GLN:HA	1:b:136:LEU:HG	1.75	0.69
1:I:127:SER:O	1:I:131:ASN:ND2	2.24	0.69
1:R:128:GLU:N	1:R:128:GLU:OE1	2.26	0.69
1:T:180:LEU:HD12	1:T:180:LEU:H	1.58	0.69
1:Q:154:ARG:HB3	1:Q:177:THR:HB	1.74	0.68
1:E:127:SER:O	1:E:131:ASN:ND2	2.25	0.68
1:M:154:ARG:NH1	1:M:177:THR:O	2.26	0.68
1:W:199:SER:OG	1:W:205:LEU:O	2.11	0.68
1:U:186:LEU:HD23	1:U:191:ILE:HD13	1.75	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:W:127:SER:O	1:W:131:ASN:ND2	2.25	0.68
1:O:180:LEU:HD21	1:O:185:ALA:HA	1.74	0.68
1:G:128:GLU:N	1:G:128:GLU:OE1	2.26	0.68
1:c:145:GLU:HG2	1:c:152:SER:HA	1.75	0.68
1:F:141:ALA:HB2	1:F:155:VAL:HG12	1.75	0.68
1:J:137:GLU:HG2	1:J:157:LEU:HD23	1.76	0.68
1:Q:133:GLN:HA	1:Q:136:LEU:HG	1.76	0.68
1:Y:127:SER:O	1:Y:131:ASN:ND2	2.26	0.68
1:A:127:SER:O	1:A:131:ASN:ND2	2.26	0.68
1:R:219:LEU:HD21	1:R:224:ASN:HB2	1.74	0.68
1:b:141:ALA:HB2	1:b:155:VAL:HG12	1.76	0.67
1:f:227:GLY:O	1:f:228:ARG:HD3	1.94	0.67
1:D:186:LEU:HD23	1:D:191:ILE:HD13	1.76	0.67
1:E:407:ASP:OD2	1:E:408:GLN:N	2.28	0.67
1:L:187:ASP:O	1:L:191:ILE:HG12	1.94	0.67
1:c:128:GLU:OE1	1:c:128:GLU:N	2.26	0.67
1:Q:192:SER:HA	1:Q:195:VAL:HG12	1.77	0.67
1:A:145:GLU:HG2	1:A:152:SER:HA	1.76	0.67
1:N:190:GLN:HG3	1:O:217:GLY:HA3	1.75	0.67
1:U:137:GLU:HG2	1:U:157:LEU:HD23	1.75	0.67
1:P:228:ARG:HG3	1:P:231:ASN:HB2	1.77	0.67
1:F:133:GLN:HA	1:F:136:LEU:HG	1.75	0.66
1:W:192:SER:HA	1:W:195:VAL:HG22	1.77	0.66
1:H:140:LEU:O	1:H:144:ILE:HD12	1.96	0.66
1:L:127:SER:O	1:L:131:ASN:ND2	2.28	0.66
1:G:228:ARG:HH21	1:G:231:ASN:HB2	1.60	0.66
1:a:407:ASP:OD2	1:a:408:GLN:N	2.28	0.66
1:c:127:SER:O	1:c:131:ASN:ND2	2.27	0.66
1:A:192:SER:HA	1:A:195:VAL:HG22	1.78	0.66
1:I:202:VAL:HG11	1:I:205:LEU:HD23	1.77	0.66
1:c:219:LEU:HD21	1:c:224:ASN:HB2	1.77	0.66
1:N:137:GLU:HG2	1:N:157:LEU:HD13	1.76	0.66
1:H:296:ARG:NH2	1:H:362:GLU:OE2	2.28	0.66
1:R:211:THR:OG1	1:R:224:ASN:ND2	2.29	0.66
1:H:151:LYS:NZ	1:H:180:LEU:O	2.28	0.66
1:D:296:ARG:NH2	1:D:362:GLU:OE2	2.29	0.66
1:G:219:LEU:HD21	1:G:224:ASN:HB2	1.77	0.66
1:L:191:ILE:HD12	1:L:212:LEU:HD11	1.78	0.66
1:Q:197:LEU:HD12	1:R:175:SER:HB3	1.77	0.66
1:Z:176:VAL:HB	1:Z:212:LEU:HD12	1.77	0.66
1:Z:296:ARG:NH2	1:Z:362:GLU:OE2	2.28	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Z:133:GLN:HA	1:Z:136:LEU:HG	1.78	0.65
1:G:296:ARG:NH2	1:G:362:GLU:OE2	2.29	0.65
1:J:227:GLY:O	1:J:228:ARG:HD3	1.96	0.65
1:R:221:THR:OG1	1:R:224:ASN:OD1	2.13	0.65
1:D:143:THR:HG21	1:F:156:HIS:CE1	2.32	0.65
1:O:197:LEU:HD12	1:O:198:VAL:HG23	1.78	0.65
1:Y:296:ARG:NH2	1:Y:362:GLU:OE2	2.29	0.65
1:b:407:ASP:OD2	1:b:408:GLN:N	2.30	0.65
1:c:143:THR:HG21	1:e:156:HIS:NE2	2.11	0.65
1:A:199:SER:OG	1:A:205:LEU:O	2.15	0.65
1:M:202:VAL:HG11	1:M:205:LEU:HD23	1.78	0.65
1:U:227:GLY:O	1:U:228:ARG:HD3	1.96	0.65
1:O:296:ARG:NH2	1:O:362:GLU:OE2	2.28	0.65
1:P:180:LEU:H	1:P:180:LEU:HD12	1.62	0.65
1:M:230:LEU:HA	1:N:225:THR:HG23	1.78	0.65
1:M:407:ASP:OD2	1:M:408:GLN:N	2.29	0.65
1:E:180:LEU:H	1:E:180:LEU:HD12	1.62	0.65
1:H:140:LEU:O	1:H:143:THR:HG22	1.97	0.65
1:Z:145:GLU:HG2	1:Z:152:SER:HA	1.78	0.65
1:N:407:ASP:OD2	1:N:408:GLN:N	2.29	0.64
1:Q:394:LYS:O	1:Q:402:LEU:N	2.30	0.64
1:U:127:SER:O	1:U:131:ASN:ND2	2.29	0.64
1:A:221:THR:O	1:A:224:ASN:ND2	2.30	0.64
1:d:228:ARG:HG2	1:d:230:LEU:HG	1.79	0.64
1:W:143:THR:HG21	1:Y:156:HIS:NE2	2.12	0.64
1:f:127:SER:O	1:f:131:ASN:ND2	2.30	0.64
1:L:221:THR:OG1	1:L:224:ASN:ND2	2.30	0.64
1:Z:143:THR:HG21	1:b:156:HIS:CE1	2.32	0.64
1:b:394:LYS:O	1:b:402:LEU:N	2.30	0.64
1:V:228:ARG:HG3	1:V:231:ASN:HB3	1.79	0.64
1:f:154:ARG:HB3	1:f:177:THR:HG23	1.79	0.64
1:A:191:ILE:HG23	1:A:212:LEU:HD22	1.80	0.64
1:E:140:LEU:HD11	1:E:198:VAL:HG22	1.79	0.64
1:B:202:VAL:HG11	1:B:205:LEU:HD23	1.78	0.64
1:A:190:GLN:HG3	1:C:217:GLY:HA3	1.79	0.64
1:D:133:GLN:HA	1:D:136:LEU:HG	1.78	0.64
1:E:394:LYS:O	1:E:402:LEU:N	2.31	0.64
1:J:190:GLN:HG3	1:L:217:GLY:HA3	1.80	0.64
1:Q:139:GLU:O	1:Q:143:THR:HG23	1.98	0.64
1:S:296:ARG:NH2	1:S:362:GLU:OE2	2.31	0.64
1:X:140:LEU:HD21	1:X:198:VAL:HG12	1.80	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:R:190:GLN:HG3	1:T:217:GLY:HA3	1.78	0.64
1:e:187:ASP:O	1:e:191:ILE:HG12	1.98	0.64
1:D:394:LYS:O	1:D:402:LEU:N	2.31	0.64
1:F:127:SER:O	1:F:131:ASN:ND2	2.31	0.64
1:J:127:SER:O	1:J:131:ASN:ND2	2.30	0.64
1:W:296:ARG:NH2	1:W:362:GLU:OE2	2.30	0.64
1:a:394:LYS:O	1:a:402:LEU:N	2.31	0.63
1:d:296:ARG:NH2	1:d:362:GLU:OE2	2.31	0.63
1:a:212:LEU:HD22	1:a:220:LEU:HD12	1.80	0.63
1:B:296:ARG:NH2	1:B:362:GLU:OE2	2.31	0.63
1:G:187:ASP:OD1	1:H:208:GLY:N	2.30	0.63
1:L:190:GLN:HG3	1:N:217:GLY:HA3	1.81	0.63
1:W:221:THR:OG1	1:W:224:ASN:ND2	2.32	0.63
1:c:296:ARG:NH2	1:c:362:GLU:OE2	2.31	0.63
1:G:127:SER:O	1:G:131:ASN:ND2	2.30	0.63
1:U:143:THR:HG21	1:W:156:HIS:NE2	2.12	0.63
1:Z:394:LYS:O	1:Z:402:LEU:N	2.31	0.63
1:C:197:LEU:HD12	1:C:198:VAL:HG13	1.80	0.63
1:M:179:THR:HG23	1:M:215:GLN:HE22	1.64	0.63
1:e:296:ARG:NH2	1:e:362:GLU:OE2	2.32	0.63
1:R:296:ARG:NH2	1:R:362:GLU:OE2	2.31	0.63
1:P:394:LYS:O	1:P:402:LEU:N	2.32	0.63
1:C:154:ARG:HB3	1:C:177:THR:HG23	1.79	0.63
1:O:394:LYS:O	1:O:402:LEU:N	2.32	0.63
1:Z:187:ASP:O	1:Z:191:ILE:HG12	1.99	0.63
1:F:394:LYS:O	1:F:402:LEU:N	2.32	0.62
1:g:228:ARG:HG3	1:g:231:ASN:HB3	1.80	0.62
1:X:127:SER:O	1:X:131:ASN:ND2	2.32	0.62
1:D:145:GLU:HG2	1:D:152:SER:HA	1.81	0.62
1:X:296:ARG:NH2	1:X:362:GLU:OE2	2.32	0.62
1:c:186:LEU:HG	1:c:191:ILE:HD13	1.80	0.62
1:I:407:ASP:OD2	1:I:408:GLN:N	2.31	0.62
1:M:140:LEU:O	1:M:144:ILE:HD12	1.99	0.62
1:O:133:GLN:HA	1:O:136:LEU:HG	1.81	0.62
1:e:143:THR:HG21	1:f:156:HIS:NE2	2.14	0.62
1:e:407:ASP:OD2	1:e:408:GLN:N	2.32	0.62
1:A:296:ARG:NH2	1:A:362:GLU:OE2	2.33	0.62
1:F:139:GLU:O	1:F:143:THR:HG23	1.98	0.62
1:U:296:ARG:NH2	1:U:362:GLU:OE2	2.33	0.62
1:W:143:THR:HG21	1:Y:156:HIS:CE1	2.34	0.62
1:F:150:VAL:HG23	1:F:178:VAL:HG13	1.80	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:187:ASP:O	1:I:191:ILE:HG12	2.00	0.62
1:U:203:ALA:HB1	1:W:160:PRO:HG3	1.81	0.62
1:D:195:VAL:HG23	1:D:210:VAL:HB	1.82	0.62
1:R:127:SER:O	1:R:131:ASN:ND2	2.33	0.62
1:S:394:LYS:O	1:S:402:LEU:N	2.32	0.62
1:Y:145:GLU:HG2	1:Y:152:SER:HA	1.81	0.62
1:f:405:THR:HG23	1:f:408:GLN:H	1.65	0.62
1:C:147:LEU:HB3	1:C:150:VAL:HG21	1.82	0.62
1:M:296:ARG:NH2	1:M:362:GLU:OE2	2.33	0.62
1:N:133:GLN:HA	1:N:136:LEU:HG	1.81	0.62
1:N:228:ARG:HB3	1:N:231:ASN:HB2	1.82	0.62
1:Z:219:LEU:HD11	1:Z:224:ASN:HD21	1.64	0.62
1:b:139:GLU:O	1:b:143:THR:HG23	1.99	0.62
1:T:202:VAL:HG11	1:T:205:LEU:HD23	1.81	0.61
1:e:202:VAL:HG11	1:e:205:LEU:HD23	1.82	0.61
1:F:202:VAL:HG21	1:F:205:LEU:HD23	1.80	0.61
1:F:202:VAL:HG23	1:F:205:LEU:HB3	1.82	0.61
1:A:228:ARG:HD2	1:A:231:ASN:HD22	1.66	0.61
1:G:139:GLU:O	1:G:143:THR:HG23	2.00	0.61
1:J:203:ALA:HB1	1:L:160:PRO:HG3	1.80	0.61
1:L:296:ARG:NH2	1:L:362:GLU:OE2	2.33	0.61
1:T:296:ARG:NH2	1:T:362:GLU:OE2	2.33	0.61
1:Y:143:THR:HG21	1:Z:156:HIS:NE2	2.16	0.61
1:Z:143:THR:HG21	1:b:156:HIS:NE2	2.15	0.61
1:O:194:VAL:HA	1:O:197:LEU:HG	1.83	0.61
1:G:173:SER:HB3	1:G:209:ASN:ND2	2.15	0.61
1:Q:127:SER:O	1:Q:131:ASN:ND2	2.34	0.61
1:T:191:ILE:HG23	1:T:212:LEU:HD13	1.82	0.61
1:f:296:ARG:NH2	1:f:362:GLU:OE2	2.33	0.61
1:N:197:LEU:HD12	1:N:198:VAL:HG13	1.83	0.61
1:U:187:ASP:O	1:U:191:ILE:HG12	2.00	0.61
1:U:190:GLN:HG3	1:W:217:GLY:HA3	1.82	0.61
1:A:221:THR:OG1	1:A:224:ASN:ND2	2.32	0.61
1:R:394:LYS:O	1:R:402:LEU:N	2.34	0.61
1:e:180:LEU:H	1:e:180:LEU:HD22	1.66	0.61
1:C:193:ALA:HA	1:D:219:LEU:HD13	1.83	0.61
1:C:296:ARG:NH2	1:C:362:GLU:OE2	2.33	0.61
1:F:197:LEU:HD12	1:G:175:SER:HB3	1.83	0.61
1:Y:190:GLN:HG3	1:Z:217:GLY:HA3	1.82	0.61
1:I:296:ARG:NH2	1:I:362:GLU:OE2	2.33	0.60
1:P:195:VAL:HG23	1:P:210:VAL:HB	1.84	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:X:153:ALA:O	1:X:154:ARG:HD3	2.01	0.60
1:Y:158:ALA:O	1:Y:159:MET:HE2	2.01	0.60
1:b:127:SER:O	1:b:131:ASN:ND2	2.32	0.60
1:b:197:LEU:HD12	1:c:175:SER:HB3	1.82	0.60
1:c:152:SER:OG	1:c:179:THR:OG1	2.13	0.60
1:A:228:ARG:HH12	1:g:237:PHE:HB2	1.66	0.60
1:C:143:THR:HG21	1:D:156:HIS:NE2	2.16	0.60
1:S:145:GLU:HG2	1:S:152:SER:HA	1.82	0.60
1:S:178:VAL:HG13	1:S:214:ASP:HA	1.83	0.60
1:W:157:LEU:HD11	1:W:202:VAL:HG21	1.83	0.60
1:b:302:GLU:HG3	1:b:358:THR:HG22	1.83	0.60
1:c:173:SER:HB3	1:c:209:ASN:ND2	2.16	0.60
1:N:296:ARG:NH2	1:N:362:GLU:OE2	2.35	0.60
1:Q:404:LEU:H	1:Q:434:ASN:HD21	1.50	0.60
1:R:212:LEU:HB2	1:R:221:THR:HG23	1.82	0.60
1:Y:379:VAL:O	1:Z:231:ASN:ND2	2.34	0.60
1:b:404:LEU:H	1:b:434:ASN:HD21	1.49	0.60
1:c:394:LYS:O	1:c:402:LEU:N	2.34	0.60
1:D:202:VAL:HG13	1:D:205:LEU:HB3	1.83	0.60
1:G:187:ASP:O	1:G:191:ILE:HG12	2.02	0.60
1:H:394:LYS:O	1:H:402:LEU:N	2.35	0.60
1:L:133:GLN:HA	1:L:136:LEU:HD12	1.83	0.60
1:X:212:LEU:HD22	1:X:220:LEU:HD12	1.83	0.60
1:b:296:ARG:NH2	1:b:362:GLU:OE2	2.33	0.60
1:J:187:ASP:O	1:J:191:ILE:HG12	2.02	0.60
1:M:179:THR:HG23	1:M:215:GLN:NE2	2.16	0.60
1:O:143:THR:HG21	1:Q:156:HIS:NE2	2.16	0.60
1:S:149:PRO:HA	1:S:181:GLU:HG2	1.84	0.60
1:a:140:LEU:HD11	1:a:198:VAL:HG22	1.82	0.60
1:O:139:GLU:O	1:O:143:THR:HG23	2.01	0.60
1:D:187:ASP:O	1:D:191:ILE:HG12	2.01	0.60
1:K:418:GLU:HG3	1:L:431:ASN:HB2	1.83	0.60
1:c:139:GLU:O	1:c:143:THR:HG23	2.02	0.60
1:d:145:GLU:HG2	1:d:152:SER:HA	1.84	0.60
1:D:176:VAL:HB	1:D:212:LEU:HD12	1.82	0.60
1:M:153:ALA:O	1:M:154:ARG:HD3	2.01	0.60
1:O:202:VAL:HG13	1:O:205:LEU:HB3	1.84	0.60
1:Y:193:ALA:HA	1:Z:219:LEU:HD13	1.83	0.60
1:F:296:ARG:NH2	1:F:362:GLU:OE2	2.35	0.60
1:Z:195:VAL:HG23	1:Z:210:VAL:HB	1.82	0.60
1:T:202:VAL:HG13	1:T:205:LEU:HB3	1.84	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Z:139:GLU:O	1:Z:143:THR:HG23	2.02	0.59
1:b:202:VAL:HG23	1:b:205:LEU:HB3	1.84	0.59
1:D:139:GLU:O	1:D:143:THR:HG23	2.01	0.59
1:E:195:VAL:HG23	1:E:210:VAL:HB	1.84	0.59
1:W:142:ARG:O	1:W:145:GLU:HG3	2.02	0.59
1:J:404:LEU:H	1:J:434:ASN:HD21	1.51	0.59
1:K:228:ARG:HG3	1:K:231:ASN:HB3	1.82	0.59
1:J:202:VAL:HG13	1:J:205:LEU:HB3	1.84	0.59
1:X:414:ASP:HB3	1:Y:431:ASN:ND2	2.18	0.59
1:Z:211:THR:HA	1:Z:221:THR:HG21	1.84	0.59
1:N:158:ALA:O	1:N:159:MET:HE2	2.02	0.59
1:T:394:LYS:O	1:T:402:LEU:N	2.36	0.59
1:c:236:LYS:NZ	1:d:226:SER:OG	2.32	0.59
1:e:127:SER:HA	1:e:130:VAL:HG22	1.85	0.59
1:D:197:LEU:HD21	1:F:213:VAL:HB	1.84	0.59
1:F:154:ARG:HB3	1:F:177:THR:HB	1.85	0.59
1:F:404:LEU:H	1:F:434:ASN:HD21	1.50	0.59
1:J:296:ARG:NH2	1:J:362:GLU:OE2	2.35	0.59
1:L:150:VAL:HG13	1:L:178:VAL:HG23	1.82	0.59
1:C:158:ALA:O	1:C:159:MET:HE2	2.03	0.59
1:A:187:ASP:O	1:A:191:ILE:HG12	2.03	0.59
1:C:145:GLU:HG2	1:C:152:SER:HA	1.85	0.59
1:I:141:ALA:HB2	1:I:155:VAL:HG12	1.85	0.59
1:I:143:THR:HG21	1:J:156:HIS:NE2	2.18	0.59
1:Z:202:VAL:HG11	1:Z:205:LEU:HD23	1.85	0.59
1:L:143:THR:HG21	1:N:156:HIS:CE1	2.38	0.58
1:Q:211:THR:HA	1:Q:224:ASN:HD21	1.68	0.58
1:A:175:SER:HB3	1:f:197:LEU:HD12	1.84	0.58
1:G:394:LYS:O	1:G:402:LEU:N	2.36	0.58
1:O:176:VAL:HB	1:O:212:LEU:HD12	1.85	0.58
1:R:187:ASP:O	1:R:191:ILE:HG12	2.02	0.58
1:X:222:GLN:NE2	1:X:223:SER:O	2.36	0.58
1:c:221:THR:O	1:c:224:ASN:ND2	2.36	0.58
1:U:404:LEU:H	1:U:434:ASN:HD21	1.50	0.58
1:a:180:LEU:H	1:a:180:LEU:HD12	1.68	0.58
1:T:143:THR:HG21	1:U:156:HIS:NE2	2.18	0.58
1:U:202:VAL:HG13	1:U:205:LEU:HB3	1.85	0.58
1:U:210:VAL:O	1:U:224:ASN:ND2	2.36	0.58
1:Z:202:VAL:HG13	1:Z:205:LEU:HB3	1.85	0.58
1:b:150:VAL:HG23	1:b:178:VAL:HG13	1.84	0.58
1:C:133:GLN:HA	1:C:136:LEU:HG	1.84	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:394:LYS:O	1:K:402:LEU:N	2.37	0.58
1:Q:150:VAL:HG13	1:Q:178:VAL:HG13	1.84	0.58
1:T:127:SER:HA	1:T:130:VAL:HG22	1.85	0.58
1:W:150:VAL:HG13	1:W:178:VAL:HG23	1.86	0.58
1:c:404:LEU:H	1:c:434:ASN:HD21	1.50	0.58
1:f:202:VAL:HG13	1:f:205:LEU:HB3	1.85	0.58
1:D:360:ARG:NH1	1:D:362:GLU:OE1	2.36	0.58
1:A:212:LEU:HB2	1:A:221:THR:HG23	1.86	0.58
1:D:143:THR:HG21	1:F:156:HIS:NE2	2.19	0.58
1:O:143:THR:HG21	1:Q:156:HIS:CE1	2.38	0.58
1:f:404:LEU:H	1:f:434:ASN:HD21	1.52	0.58
1:J:173:SER:HA	1:J:205:LEU:HD13	1.84	0.58
1:M:219:LEU:HD12	1:M:219:LEU:O	2.04	0.58
1:B:404:LEU:H	1:B:434:ASN:HD21	1.52	0.57
1:Q:302:GLU:HG3	1:Q:358:THR:HG22	1.85	0.57
1:d:198:VAL:HG11	1:d:210:VAL:HG11	1.86	0.57
1:D:149:PRO:HB3	1:D:184:ARG:HG2	1.84	0.57
1:E:228:ARG:HG3	1:E:231:ASN:HB2	1.86	0.57
1:c:187:ASP:O	1:c:191:ILE:HG12	2.04	0.57
1:e:202:VAL:HG13	1:e:205:LEU:HB3	1.86	0.57
1:I:127:SER:HA	1:I:130:VAL:HG22	1.87	0.57
1:P:176:VAL:HB	1:P:212:LEU:HD12	1.85	0.57
1:C:228:ARG:HB3	1:C:231:ASN:HB2	1.86	0.57
1:N:143:THR:HG21	1:O:156:HIS:CE1	2.39	0.57
1:Q:296:ARG:NH2	1:Q:362:GLU:OE2	2.36	0.57
1:R:141:ALA:HB2	1:R:155:VAL:HG12	1.86	0.57
1:M:404:LEU:H	1:M:434:ASN:HD21	1.52	0.57
1:V:394:LYS:O	1:V:402:LEU:N	2.37	0.57
1:W:360:ARG:NH1	1:W:362:GLU:OE1	2.38	0.57
1:e:394:LYS:O	1:e:402:LEU:N	2.37	0.57
1:G:195:VAL:HG13	1:G:210:VAL:HG21	1.87	0.57
1:G:223:SER:HA	1:G:229:ASP:OD2	2.04	0.57
1:I:394:LYS:O	1:I:402:LEU:N	2.37	0.57
1:G:404:LEU:H	1:G:434:ASN:HD21	1.53	0.57
1:I:202:VAL:HG13	1:I:205:LEU:HB3	1.87	0.57
1:M:155:VAL:HG12	1:M:176:VAL:HG22	1.87	0.57
1:d:149:PRO:HA	1:d:181:GLU:HG2	1.87	0.57
1:D:219:LEU:HD11	1:D:224:ASN:HD21	1.69	0.57
1:O:228:ARG:HG2	1:O:229:ASP:N	2.20	0.57
1:T:187:ASP:O	1:T:191:ILE:HG12	2.04	0.57
1:b:202:VAL:HG21	1:b:205:LEU:HD23	1.87	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:202:VAL:HG13	1:B:205:LEU:HB3	1.87	0.57
1:E:202:VAL:HG23	1:E:205:LEU:HB3	1.86	0.57
1:B:414:ASP:HB3	1:C:431:ASN:ND2	2.20	0.57
1:G:236:LYS:NZ	1:H:226:SER:OG	2.32	0.57
1:L:389:VAL:HB	1:L:432:VAL:HG22	1.87	0.57
1:X:267:THR:HG23	1:X:386:SER:HB2	1.87	0.57
1:a:267:THR:CG2	1:a:386:SER:HB2	2.35	0.57
1:R:143:THR:HG21	1:T:156:HIS:NE2	2.20	0.56
1:Y:144:ILE:HD11	1:Y:197:LEU:HD22	1.87	0.56
1:Y:404:LEU:H	1:Y:434:ASN:HD21	1.53	0.56
1:g:296:ARG:NH2	1:g:362:GLU:OE2	2.38	0.56
1:G:143:THR:HG21	1:I:156:HIS:NE2	2.20	0.56
1:f:176:VAL:HB	1:f:212:LEU:HD12	1.87	0.56
1:f:187:ASP:O	1:f:191:ILE:HG12	2.05	0.56
1:A:213:VAL:HG21	1:f:197:LEU:HD22	1.87	0.56
1:A:223:SER:O	1:A:226:SER:OG	2.22	0.56
1:D:404:LEU:H	1:D:434:ASN:HD21	1.54	0.56
1:E:296:ARG:NH2	1:E:362:GLU:OE2	2.38	0.56
1:G:140:LEU:HD11	1:G:155:VAL:HG11	1.86	0.56
1:N:404:LEU:H	1:N:434:ASN:HD21	1.53	0.56
1:P:296:ARG:NH2	1:P:362:GLU:OE2	2.38	0.56
1:Y:267:THR:OG1	1:Y:386:SER:HB2	2.05	0.56
1:c:149:PRO:HB3	1:c:184:ARG:HG2	1.87	0.56
1:f:127:SER:HA	1:f:130:VAL:HG12	1.87	0.56
1:W:228:ARG:HB3	1:W:231:ASN:HB2	1.88	0.56
1:f:227:GLY:C	1:f:229:ASP:H	2.14	0.56
1:M:202:VAL:HG13	1:M:205:LEU:HB3	1.88	0.56
1:a:229:ASP:OD1	1:b:225:THR:OG1	2.24	0.56
1:f:214:ASP:HB2	1:f:218:HIS:HB2	1.88	0.56
1:J:211:THR:HG22	1:J:224:ASN:HB3	1.87	0.56
1:P:140:LEU:HD11	1:P:198:VAL:HG22	1.86	0.56
1:R:404:LEU:H	1:R:434:ASN:HD21	1.52	0.56
1:Y:187:ASP:O	1:Y:191:ILE:HG12	2.06	0.56
1:d:394:LYS:O	1:d:402:LEU:N	2.38	0.56
1:A:156:HIS:NE2	1:f:143:THR:HG21	2.20	0.56
1:A:202:VAL:HG13	1:A:205:LEU:HB3	1.87	0.56
1:T:404:LEU:H	1:T:434:ASN:HD21	1.52	0.56
1:d:178:VAL:HG13	1:d:214:ASP:HA	1.88	0.56
1:e:228:ARG:NE	1:e:231:ASN:HB2	2.20	0.56
1:a:195:VAL:HG23	1:a:210:VAL:HB	1.88	0.56
1:f:139:GLU:O	1:f:143:THR:HG23	2.06	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:g:394:LYS:O	1:g:402:LEU:N	2.39	0.56
1:L:127:SER:HA	1:L:130:VAL:HG12	1.88	0.56
1:O:360:ARG:NH1	1:O:362:GLU:OE1	2.38	0.56
1:R:139:GLU:O	1:R:143:THR:HG23	2.04	0.56
1:D:379:VAL:O	1:E:231:ASN:ND2	2.38	0.56
1:P:127:SER:HA	1:P:130:VAL:HG12	1.88	0.56
1:e:219:LEU:HD21	1:e:224:ASN:HD21	1.71	0.56
1:D:228:ARG:C	1:D:230:LEU:H	2.14	0.55
1:E:229:ASP:OD2	1:E:230:LEU:N	2.39	0.55
1:J:227:GLY:C	1:J:229:ASP:H	2.14	0.55
1:L:360:ARG:NH1	1:L:362:GLU:OE1	2.38	0.55
1:T:228:ARG:NE	1:T:231:ASN:HB2	2.21	0.55
1:U:227:GLY:C	1:U:229:ASP:H	2.14	0.55
1:D:144:ILE:HA	1:D:147:LEU:HD23	1.88	0.55
1:O:187:ASP:O	1:O:191:ILE:HG12	2.06	0.55
1:P:267:THR:CG2	1:P:386:SER:HB2	2.35	0.55
1:T:211:THR:HA	1:T:221:THR:HG21	1.88	0.55
1:W:187:ASP:O	1:W:191:ILE:HG12	2.06	0.55
1:Z:186:LEU:HD23	1:Z:191:ILE:HD13	1.88	0.55
1:e:141:ALA:HB2	1:e:155:VAL:HG12	1.87	0.55
1:A:132:TYR:CZ	1:A:136:LEU:HD11	2.42	0.55
1:B:389:VAL:HB	1:B:432:VAL:HG22	1.89	0.55
1:J:143:THR:HG21	1:L:156:HIS:NE2	2.20	0.55
1:I:404:LEU:H	1:I:434:ASN:HD21	1.54	0.55
1:W:202:VAL:HG13	1:W:205:LEU:HB3	1.88	0.55
1:c:302:GLU:HG3	1:c:358:THR:HG22	1.89	0.55
1:G:196:HIS:HB3	1:I:211:THR:HG21	1.89	0.55
1:V:389:VAL:HB	1:V:432:VAL:HG22	1.88	0.55
1:X:154:ARG:NH1	1:X:179:THR:OG1	2.29	0.55
1:X:295:SER:HB2	1:X:365:ASN:HD22	1.72	0.55
1:Y:139:GLU:O	1:Y:143:THR:HG23	2.06	0.55
1:B:267:THR:HG23	1:B:386:SER:HB2	1.88	0.55
1:M:360:ARG:NH1	1:M:362:GLU:OE1	2.40	0.55
1:R:302:GLU:HG3	1:R:358:THR:HG22	1.87	0.55
1:U:214:ASP:HB2	1:U:218:HIS:HB2	1.87	0.55
1:U:228:ARG:HG3	1:U:231:ASN:CG	2.32	0.55
1:U:414:ASP:HB3	1:V:431:ASN:ND2	2.22	0.55
1:Z:149:PRO:HB3	1:Z:184:ARG:HG2	1.89	0.55
1:Z:360:ARG:NH1	1:Z:362:GLU:OE1	2.38	0.55
1:b:154:ARG:HB3	1:b:177:THR:HB	1.88	0.55
1:A:360:ARG:NH1	1:A:362:GLU:OE1	2.39	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M:179:THR:HA	1:M:215:GLN:HE21	1.70	0.55
1:f:373:ARG:NH2	1:g:275:LYS:HE2	2.22	0.55
1:B:250:GLU:O	1:B:254:SER:OG	2.23	0.55
1:H:404:LEU:H	1:H:434:ASN:HD21	1.55	0.55
1:I:139:GLU:O	1:I:143:THR:HG23	2.07	0.55
1:M:295:SER:HB2	1:M:365:ASN:HD22	1.72	0.55
1:N:144:ILE:O	1:N:147:LEU:HG	2.07	0.55
1:W:416:THR:HG23	1:W:430:LEU:HD21	1.88	0.55
1:S:236:LYS:NZ	1:T:222:GLN:OE1	2.40	0.55
1:g:267:THR:OG1	1:g:386:SER:HB2	2.06	0.55
1:N:150:VAL:HG23	1:N:178:VAL:HG13	1.88	0.54
1:N:295:SER:HB2	1:N:365:ASN:HD22	1.73	0.54
1:T:141:ALA:HB2	1:T:155:VAL:HG12	1.89	0.54
1:A:143:THR:HG21	1:C:156:HIS:CE1	2.42	0.54
1:B:360:ARG:NH1	1:B:362:GLU:OE1	2.39	0.54
1:G:149:PRO:HB3	1:G:184:ARG:HG2	1.88	0.54
1:M:389:VAL:HB	1:M:432:VAL:HG22	1.87	0.54
1:X:389:VAL:HB	1:X:432:VAL:HG22	1.88	0.54
1:Z:302:GLU:HG3	1:Z:358:THR:HG22	1.89	0.54
1:a:296:ARG:NH2	1:a:362:GLU:OE2	2.39	0.54
1:g:302:GLU:HG3	1:g:358:THR:HG22	1.89	0.54
1:E:267:THR:HG23	1:E:386:SER:HB2	1.89	0.54
1:O:404:LEU:H	1:O:434:ASN:HD21	1.53	0.54
1:Y:389:VAL:HB	1:Y:432:VAL:HG22	1.88	0.54
1:b:127:SER:HA	1:b:130:VAL:HG22	1.89	0.54
1:G:141:ALA:HB2	1:G:155:VAL:HG12	1.89	0.54
1:G:302:GLU:HG3	1:G:358:THR:HG22	1.89	0.54
1:S:404:LEU:H	1:S:434:ASN:HD21	1.54	0.54
1:W:223:SER:O	1:W:226:SER:OG	2.21	0.54
1:X:416:THR:HG23	1:X:430:LEU:HD21	1.89	0.54
1:g:389:VAL:HB	1:g:432:VAL:HG22	1.90	0.54
1:A:416:THR:HG23	1:A:430:LEU:HD21	1.88	0.54
1:C:137:GLU:HG2	1:C:157:LEU:HD13	1.90	0.54
1:H:137:GLU:HG2	1:H:157:LEU:HD12	1.90	0.54
1:O:236:LYS:HB3	1:P:225:THR:HG21	1.89	0.54
1:e:404:LEU:H	1:e:434:ASN:HD21	1.54	0.54
1:G:212:LEU:HB2	1:G:221:THR:HG23	1.88	0.54
1:R:195:VAL:HG13	1:R:210:VAL:HG21	1.89	0.54
1:B:198:VAL:HG21	1:B:210:VAL:HG21	1.89	0.54
1:C:139:GLU:O	1:C:143:THR:HG23	2.08	0.54
1:E:228:ARG:HG3	1:E:231:ASN:CB	2.38	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:230:LEU:HG	1:F:227:GLY:HA2	1.89	0.54
1:F:127:SER:HA	1:F:130:VAL:HG22	1.90	0.54
1:J:176:VAL:HB	1:J:212:LEU:HD12	1.89	0.54
1:M:180:LEU:HD11	1:M:186:LEU:HG	1.90	0.54
1:N:143:THR:HG21	1:O:156:HIS:NE2	2.22	0.54
1:U:145:GLU:HG2	1:U:152:SER:HA	1.90	0.54
1:K:389:VAL:HB	1:K:432:VAL:HG22	1.90	0.54
1:F:302:GLU:HG3	1:F:358:THR:HG22	1.90	0.54
1:U:176:VAL:HB	1:U:212:LEU:HD12	1.88	0.54
1:W:127:SER:HA	1:W:130:VAL:HG12	1.89	0.54
1:X:202:VAL:HG13	1:X:205:LEU:HB3	1.90	0.54
1:Z:190:GLN:HG3	1:b:217:GLY:HA3	1.90	0.54
1:f:389:VAL:HB	1:f:432:VAL:HG22	1.90	0.54
1:D:150:VAL:HG23	1:D:178:VAL:HG13	1.90	0.53
1:I:186:LEU:HG	1:I:190:GLN:HB3	1.91	0.53
1:J:214:ASP:HB2	1:J:218:HIS:HB2	1.88	0.53
1:A:128:GLU:HA	1:A:131:ASN:HD21	1.73	0.53
1:J:139:GLU:O	1:J:143:THR:HG23	2.08	0.53
1:S:198:VAL:HG11	1:S:210:VAL:HG11	1.89	0.53
1:X:149:PRO:HB3	1:X:184:ARG:HG2	1.91	0.53
1:f:416:THR:HG23	1:f:430:LEU:HD21	1.89	0.53
1:A:225:THR:HG23	1:f:196:HIS:NE2	2.23	0.53
1:D:228:ARG:HB2	1:D:231:ASN:HB2	1.91	0.53
1:G:193:ALA:HA	1:I:219:LEU:HB2	1.89	0.53
1:I:228:ARG:NE	1:I:231:ASN:HB2	2.23	0.53
1:M:267:THR:CG2	1:M:386:SER:HB2	2.38	0.53
1:N:139:GLU:O	1:N:143:THR:HG23	2.08	0.53
1:X:404:LEU:H	1:X:434:ASN:HD21	1.56	0.53
1:I:173:SER:HA	1:I:205:LEU:HD13	1.90	0.53
1:Q:127:SER:HA	1:Q:130:VAL:HG22	1.91	0.53
1:V:296:ARG:NH2	1:V:362:GLU:OE2	2.41	0.53
1:e:416:THR:HG23	1:e:430:LEU:HD21	1.91	0.53
1:C:418:GLU:HG3	1:D:431:ASN:HB2	1.90	0.53
1:S:132:TYR:CZ	1:S:136:LEU:HD11	2.43	0.53
1:Z:404:LEU:H	1:Z:434:ASN:HD21	1.55	0.53
1:b:136:LEU:HD12	1:b:137:GLU:N	2.24	0.53
1:e:173:SER:HA	1:e:205:LEU:HD13	1.90	0.53
1:D:202:VAL:HG11	1:D:205:LEU:HD23	1.91	0.53
1:I:389:VAL:HB	1:I:432:VAL:HG22	1.91	0.53
1:O:381:ASP:OD1	1:O:381:ASP:N	2.39	0.53
1:d:389:VAL:HB	1:d:432:VAL:HG22	1.91	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:156:HIS:CE1	1:f:143:THR:HG21	2.44	0.53
1:B:416:THR:HG23	1:B:430:LEU:HD21	1.91	0.53
1:I:295:SER:HB2	1:I:365:ASN:HD22	1.74	0.53
1:L:295:SER:HB2	1:L:365:ASN:HD22	1.74	0.53
1:P:144:ILE:HA	1:P:147:LEU:HD13	1.91	0.53
1:e:139:GLU:O	1:e:143:THR:HG23	2.08	0.53
1:F:152:SER:O	1:F:179:THR:N	2.39	0.53
1:H:127:SER:O	1:H:131:ASN:ND2	2.42	0.53
1:J:143:THR:HG21	1:L:156:HIS:CE1	2.44	0.53
1:N:228:ARG:HE	1:N:231:ASN:CG	2.16	0.53
1:S:140:LEU:HD21	1:S:155:VAL:HG21	1.89	0.53
1:W:128:GLU:HA	1:W:131:ASN:HD21	1.74	0.53
1:a:228:ARG:NH1	1:a:231:ASN:OD1	2.41	0.53
1:e:389:VAL:HB	1:e:432:VAL:HG22	1.90	0.53
1:f:211:THR:HG22	1:f:224:ASN:HB3	1.91	0.53
1:A:217:GLY:HA3	1:f:190:GLN:HG3	1.91	0.53
1:N:147:LEU:HG	1:N:150:VAL:HG11	1.90	0.53
1:T:192:SER:HA	1:T:195:VAL:HB	1.91	0.53
1:U:154:ARG:HB3	1:U:177:THR:HG23	1.91	0.53
1:U:373:ARG:NH2	1:V:275:LYS:HE2	2.23	0.53
1:A:203:ALA:HB1	1:C:160:PRO:HG3	1.92	0.52
1:A:389:VAL:HB	1:A:432:VAL:HG22	1.90	0.52
1:D:173:SER:HA	1:D:205:LEU:HD13	1.91	0.52
1:E:295:SER:HB2	1:E:365:ASN:HD22	1.75	0.52
1:F:136:LEU:HD12	1:F:137:GLU:N	2.24	0.52
1:J:373:ARG:NH2	1:K:275:LYS:HE2	2.23	0.52
1:S:140:LEU:O	1:S:143:THR:HG22	2.08	0.52
1:a:214:ASP:CG	1:a:215:GLN:H	2.16	0.52
1:E:212:LEU:HD22	1:E:220:LEU:HD12	1.91	0.52
1:F:212:LEU:HD12	1:F:220:LEU:HB2	1.90	0.52
1:O:173:SER:HA	1:O:205:LEU:HD13	1.90	0.52
1:c:195:VAL:HG13	1:c:210:VAL:HG21	1.90	0.52
1:d:137:GLU:HG2	1:d:157:LEU:HD23	1.92	0.52
1:A:187:ASP:OD1	1:A:190:GLN:N	2.43	0.52
1:C:187:ASP:O	1:C:191:ILE:HG12	2.08	0.52
1:H:266:VAL:HG22	1:H:387:VAL:HG22	1.92	0.52
1:c:223:SER:HA	1:c:229:ASP:OD1	2.10	0.52
1:c:228:ARG:HG3	1:c:229:ASP:H	1.74	0.52
1:C:228:ARG:NH1	1:C:231:ASN:OD1	2.43	0.52
1:F:143:THR:HG22	1:G:154:ARG:CZ	2.39	0.52
1:J:198:VAL:O	1:J:202:VAL:HG12	2.09	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M:250:GLU:O	1:M:254:SER:OG	2.25	0.52
1:N:187:ASP:O	1:N:191:ILE:HG12	2.08	0.52
1:T:139:GLU:O	1:T:143:THR:HG23	2.09	0.52
1:W:132:TYR:CZ	1:W:136:LEU:HD11	2.44	0.52
1:Y:143:THR:HG21	1:Z:156:HIS:CE1	2.44	0.52
1:a:192:SER:HA	1:a:195:VAL:HG12	1.92	0.52
1:e:140:LEU:O	1:e:144:ILE:HG12	2.09	0.52
1:A:127:SER:HA	1:A:130:VAL:HG12	1.90	0.52
1:E:267:THR:CG2	1:E:386:SER:HB2	2.39	0.52
1:M:302:GLU:HG3	1:M:358:THR:HG22	1.91	0.52
1:N:418:GLU:HG3	1:O:431:ASN:HB2	1.91	0.52
1:W:389:VAL:HB	1:W:432:VAL:HG22	1.90	0.52
1:f:387:VAL:HG21	1:f:420:MET:HG2	1.91	0.52
1:E:192:SER:HA	1:E:195:VAL:HG12	1.90	0.52
1:P:139:GLU:O	1:P:143:THR:HG23	2.10	0.52
1:Q:143:THR:HG22	1:R:154:ARG:CZ	2.39	0.52
1:T:145:GLU:HG2	1:T:153:ALA:H	1.75	0.52
1:U:173:SER:HA	1:U:205:LEU:HD13	1.92	0.52
1:B:267:THR:CG2	1:B:386:SER:HB2	2.39	0.52
1:Q:136:LEU:HD12	1:Q:137:GLU:N	2.25	0.52
1:R:155:VAL:HB	1:R:176:VAL:HG12	1.92	0.52
1:U:139:GLU:O	1:U:143:THR:HG23	2.09	0.52
1:C:404:LEU:H	1:C:434:ASN:HD21	1.57	0.52
1:E:214:ASP:OD1	1:E:215:GLN:N	2.40	0.52
1:L:132:TYR:CZ	1:L:136:LEU:HD11	2.45	0.52
1:M:149:PRO:HB3	1:M:184:ARG:HG2	1.92	0.52
1:O:271:ASP:HB3	1:O:381:ASP:OD1	2.10	0.52
1:S:266:VAL:HG22	1:S:387:VAL:HG22	1.92	0.52
1:Z:199:SER:OG	1:Z:205:LEU:O	2.25	0.52
1:K:296:ARG:NH2	1:K:362:GLU:OE2	2.42	0.52
1:K:302:GLU:HG3	1:K:358:THR:HG22	1.91	0.52
1:N:187:ASP:CG	1:N:188:GLU:H	2.18	0.52
1:O:228:ARG:HG3	1:O:231:ASN:CG	2.35	0.52
1:P:389:VAL:HB	1:P:432:VAL:HG22	1.91	0.52
1:d:266:VAL:HG22	1:d:387:VAL:HG22	1.92	0.52
1:d:404:LEU:H	1:d:434:ASN:HD21	1.57	0.52
1:J:389:VAL:HB	1:J:432:VAL:HG22	1.91	0.52
1:T:415:LEU:HD11	1:U:433:VAL:HG21	1.91	0.52
1:Z:144:ILE:HA	1:Z:147:LEU:HD23	1.91	0.52
1:b:157:LEU:HD21	1:b:159:MET:HB2	1.92	0.52
1:R:193:ALA:HA	1:T:219:LEU:HD13	1.91	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:S:415:LEU:HD11	1:T:433:VAL:HG21	1.90	0.51
1:U:389:VAL:HB	1:U:432:VAL:HG22	1.91	0.51
1:V:302:GLU:HG3	1:V:358:THR:HG22	1.92	0.51
1:X:202:VAL:HG11	1:X:205:LEU:HD22	1.92	0.51
1:d:174:ALA:HB3	1:d:210:VAL:HG13	1.91	0.51
1:e:415:LEU:HD11	1:f:433:VAL:HG21	1.92	0.51
1:G:152:SER:O	1:G:179:THR:N	2.31	0.51
1:J:145:GLU:HG2	1:J:152:SER:HA	1.92	0.51
1:O:302:GLU:HG3	1:O:358:THR:HG22	1.91	0.51
1:X:360:ARG:NH1	1:X:362:GLU:OE1	2.39	0.51
1:Z:192:SER:HA	1:Z:195:VAL:CG1	2.38	0.51
1:Z:414:ASP:HB3	1:a:431:ASN:ND2	2.25	0.51
1:a:389:VAL:HB	1:a:432:VAL:HG22	1.91	0.51
1:D:302:GLU:HG3	1:D:358:THR:HG22	1.92	0.51
1:E:404:LEU:H	1:E:434:ASN:ND2	2.09	0.51
1:E:404:LEU:H	1:E:434:ASN:HD21	1.56	0.51
1:J:154:ARG:HB3	1:J:177:THR:HG23	1.91	0.51
1:N:136:LEU:HD12	1:N:137:GLU:N	2.26	0.51
1:Q:180:LEU:HD11	1:Q:184:ARG:HB3	1.93	0.51
1:R:127:SER:HA	1:R:130:VAL:HG22	1.92	0.51
1:X:198:VAL:HG21	1:X:210:VAL:HG21	1.91	0.51
1:e:302:GLU:HG3	1:e:358:THR:HG22	1.92	0.51
1:H:267:THR:CG2	1:H:386:SER:HB2	2.41	0.51
1:U:416:THR:HG23	1:U:430:LEU:HD21	1.92	0.51
1:W:212:LEU:HB2	1:W:221:THR:HG23	1.91	0.51
1:g:404:LEU:H	1:g:434:ASN:HD21	1.58	0.51
1:W:247:ARG:NH2	1:X:219:LEU:HD13	2.25	0.51
1:W:404:LEU:H	1:W:434:ASN:HD21	1.57	0.51
1:X:267:THR:CG2	1:X:386:SER:HB2	2.40	0.51
1:O:202:VAL:HG11	1:O:205:LEU:HD23	1.92	0.51
1:R:206:PRO:HD2	1:R:209:ASN:HD21	1.76	0.51
1:Y:228:ARG:NH1	1:Y:231:ASN:OD1	2.43	0.51
1:A:150:VAL:HG13	1:A:178:VAL:HG23	1.93	0.51
1:L:404:LEU:H	1:L:434:ASN:HD21	1.56	0.51
1:N:389:VAL:HB	1:N:432:VAL:HG22	1.93	0.51
1:P:295:SER:HB2	1:P:365:ASN:HD22	1.75	0.51
1:U:127:SER:HA	1:U:130:VAL:HG22	1.93	0.51
1:a:387:VAL:HG21	1:a:420:MET:HG2	1.93	0.51
1:b:143:THR:HG22	1:c:154:ARG:CZ	2.40	0.51
1:d:414:ASP:HB3	1:e:431:ASN:ND2	2.26	0.51
1:A:295:SER:HB2	1:A:365:ASN:HD22	1.76	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:415:LEU:HD11	1:I:433:VAL:HG21	1.93	0.51
1:J:416:THR:HG23	1:J:430:LEU:HD21	1.93	0.51
1:K:404:LEU:H	1:K:434:ASN:HD21	1.59	0.51
1:S:418:GLU:HG3	1:T:431:ASN:HB2	1.92	0.51
1:Y:415:LEU:HD11	1:Z:433:VAL:HG21	1.93	0.51
1:f:144:ILE:HG22	1:f:197:LEU:HD23	1.93	0.51
1:I:267:THR:CG2	1:I:386:SER:HB2	2.41	0.51
1:J:228:ARG:HG3	1:J:231:ASN:CG	2.35	0.51
1:N:143:THR:HG22	1:O:154:ARG:CZ	2.41	0.51
1:R:187:ASP:OD1	1:S:208:GLY:N	2.43	0.51
1:T:295:SER:HB2	1:T:365:ASN:HD22	1.76	0.51
1:D:267:THR:CG2	1:D:386:SER:HB2	2.41	0.51
1:W:139:GLU:O	1:W:143:THR:HG23	2.11	0.51
1:a:404:LEU:H	1:a:434:ASN:HD21	1.58	0.51
1:d:267:THR:CG2	1:d:386:SER:HB2	2.41	0.51
1:A:193:ALA:HA	1:C:219:LEU:HD13	1.93	0.50
1:E:266:VAL:HG22	1:E:387:VAL:HG22	1.93	0.50
1:H:199:SER:HA	1:H:205:LEU:HD23	1.93	0.50
1:J:126:PHE:O	1:J:130:VAL:HG13	2.11	0.50
1:J:227:GLY:O	1:J:229:ASP:N	2.38	0.50
1:J:415:LEU:HD11	1:K:433:VAL:HG21	1.93	0.50
1:f:145:GLU:HG2	1:f:152:SER:HA	1.94	0.50
1:L:139:GLU:O	1:L:143:THR:HG23	2.12	0.50
1:L:404:LEU:H	1:L:434:ASN:ND2	2.09	0.50
1:X:387:VAL:HG21	1:X:420:MET:HG2	1.92	0.50
1:Z:147:LEU:O	1:Z:149:PRO:HD2	2.12	0.50
1:c:187:ASP:OD2	1:d:207:PRO:HG2	2.11	0.50
1:C:415:LEU:HD11	1:D:433:VAL:HG21	1.93	0.50
1:E:387:VAL:HG21	1:E:420:MET:HG2	1.93	0.50
1:W:250:GLU:O	1:W:254:SER:OG	2.23	0.50
1:X:128:GLU:HA	1:X:131:ASN:HD21	1.75	0.50
1:a:145:GLU:HG2	1:a:152:SER:HA	1.93	0.50
1:e:226:SER:O	1:e:226:SER:OG	2.30	0.50
1:f:198:VAL:O	1:f:202:VAL:HG12	2.12	0.50
1:c:266:VAL:HG22	1:c:387:VAL:HG22	1.94	0.50
1:f:267:THR:CG2	1:f:386:SER:HB2	2.42	0.50
1:A:202:VAL:HG11	1:A:205:LEU:HD23	1.94	0.50
1:C:267:THR:OG1	1:C:386:SER:HB2	2.12	0.50
1:E:139:GLU:O	1:E:143:THR:HG23	2.12	0.50
1:S:267:THR:CG2	1:S:386:SER:HB2	2.41	0.50
1:U:196:HIS:NE2	1:W:225:THR:HG23	2.27	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:f:173:SER:HA	1:f:205:LEU:HD13	1.93	0.50
1:f:228:ARG:HG3	1:f:231:ASN:CG	2.36	0.50
1:L:302:GLU:HG3	1:L:358:THR:HG22	1.93	0.50
1:R:223:SER:HA	1:R:229:ASP:OD2	2.12	0.50
1:Z:267:THR:CG2	1:Z:386:SER:HB2	2.41	0.50
1:F:186:LEU:HG	1:F:191:ILE:HD13	1.93	0.50
1:H:389:VAL:HB	1:H:432:VAL:HG22	1.94	0.50
1:I:155:VAL:HG23	1:I:176:VAL:HG22	1.92	0.50
1:M:154:ARG:NH1	1:M:179:THR:OG1	2.38	0.50
1:P:266:VAL:HG22	1:P:387:VAL:HG22	1.94	0.50
1:X:140:LEU:HD11	1:X:198:VAL:HA	1.93	0.50
1:Y:404:LEU:H	1:Y:434:ASN:ND2	2.09	0.50
1:a:139:GLU:O	1:a:143:THR:HG23	2.12	0.50
1:a:267:THR:HG23	1:a:386:SER:HB2	1.94	0.50
1:e:300:ILE:HG12	1:e:360:ARG:HG3	1.93	0.50
1:D:146:THR:O	1:D:147:LEU:HD22	2.12	0.50
1:J:267:THR:CG2	1:J:386:SER:HB2	2.42	0.50
1:N:404:LEU:H	1:N:434:ASN:ND2	2.09	0.50
1:R:418:GLU:HG3	1:S:431:ASN:HB2	1.93	0.50
1:e:295:SER:HB3	1:e:365:ASN:HD22	1.76	0.50
1:A:387:VAL:HG21	1:A:420:MET:HG2	1.94	0.50
1:B:302:GLU:HG3	1:B:358:THR:HG22	1.94	0.50
1:C:136:LEU:HD12	1:C:137:GLU:N	2.26	0.50
1:C:404:LEU:H	1:C:434:ASN:ND2	2.10	0.50
1:D:236:LYS:HE3	1:E:225:THR:HG23	1.93	0.50
1:I:415:LEU:HD11	1:J:433:VAL:HG21	1.94	0.50
1:T:267:THR:CG2	1:T:386:SER:HB2	2.42	0.50
1:a:302:GLU:HG3	1:a:358:THR:HG22	1.94	0.50
1:c:404:LEU:H	1:c:434:ASN:ND2	2.10	0.50
1:e:147:LEU:O	1:e:149:PRO:HD2	2.12	0.50
1:A:219:LEU:HD21	1:A:224:ASN:HB2	1.94	0.49
1:C:224:ASN:OD1	1:C:225:THR:N	2.45	0.49
1:P:404:LEU:H	1:P:434:ASN:HD21	1.59	0.49
1:T:173:SER:HA	1:T:205:LEU:HD13	1.94	0.49
1:T:416:THR:HG23	1:T:430:LEU:HD21	1.93	0.49
1:W:193:ALA:HA	1:Y:219:LEU:HD13	1.94	0.49
1:g:387:VAL:HG21	1:g:420:MET:HG2	1.94	0.49
1:C:295:SER:HB2	1:C:365:ASN:HD22	1.76	0.49
1:L:212:LEU:HG	1:L:221:THR:HG23	1.95	0.49
1:O:187:ASP:OD1	1:P:206:PRO:HB2	2.11	0.49
1:P:387:VAL:HG21	1:P:420:MET:HG2	1.92	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:U:415:LEU:HD11	1:V:433:VAL:HG21	1.94	0.49
1:Z:136:LEU:HD12	1:Z:137:GLU:N	2.28	0.49
1:c:141:ALA:HB2	1:c:155:VAL:HG12	1.93	0.49
1:c:197:LEU:HG	1:e:213:VAL:HG21	1.95	0.49
1:e:267:THR:HG23	1:e:386:SER:HB2	1.93	0.49
1:A:140:LEU:O	1:A:144:ILE:HG12	2.13	0.49
1:A:247:ARG:NH2	1:B:219:LEU:HD13	2.28	0.49
1:B:387:VAL:HG21	1:B:420:MET:HG2	1.93	0.49
1:G:266:VAL:HG22	1:G:387:VAL:HG22	1.95	0.49
1:G:418:GLU:HG3	1:H:431:ASN:HB2	1.94	0.49
1:O:267:THR:CG2	1:O:386:SER:HB2	2.41	0.49
1:V:404:LEU:H	1:V:434:ASN:HD21	1.59	0.49
1:c:176:VAL:HG23	1:c:212:LEU:HD12	1.92	0.49
1:B:295:SER:HB3	1:B:365:ASN:HD22	1.76	0.49
1:D:136:LEU:HD12	1:D:137:GLU:N	2.27	0.49
1:J:405:THR:HG23	1:J:408:GLN:H	1.77	0.49
1:L:199:SER:OG	1:L:205:LEU:O	2.24	0.49
1:L:387:VAL:HG21	1:L:420:MET:HG2	1.93	0.49
1:P:404:LEU:H	1:P:434:ASN:ND2	2.10	0.49
1:R:295:SER:HB2	1:R:365:ASN:HD22	1.78	0.49
1:S:295:SER:HB2	1:S:365:ASN:HD22	1.77	0.49
1:Z:146:THR:O	1:Z:147:LEU:HD22	2.12	0.49
1:b:295:SER:HB2	1:b:365:ASN:HD22	1.77	0.49
1:e:195:VAL:HG13	1:e:210:VAL:HG11	1.94	0.49
1:f:228:ARG:HG3	1:f:231:ASN:ND2	2.27	0.49
1:C:155:VAL:HG13	1:C:176:VAL:HG22	1.94	0.49
1:L:196:HIS:CD2	1:N:224:ASN:HD21	2.30	0.49
1:N:415:LEU:HD11	1:O:433:VAL:HG21	1.94	0.49
1:R:392:ASN:OD1	1:R:393:TYR:N	2.46	0.49
1:T:389:VAL:HB	1:T:432:VAL:HG22	1.93	0.49
1:W:219:LEU:HD11	1:W:224:ASN:ND2	2.27	0.49
1:b:267:THR:CG2	1:b:386:SER:HB2	2.42	0.49
1:c:127:SER:HA	1:c:130:VAL:HG22	1.94	0.49
1:c:199:SER:OG	1:c:205:LEU:O	2.26	0.49
1:c:267:THR:CG2	1:c:386:SER:HB2	2.43	0.49
1:A:147:LEU:O	1:A:149:PRO:HD2	2.13	0.49
1:D:415:LEU:HD11	1:E:433:VAL:HG21	1.94	0.49
1:D:418:GLU:HG3	1:E:431:ASN:HB2	1.94	0.49
1:F:267:THR:CG2	1:F:386:SER:HB2	2.42	0.49
1:G:267:THR:CG2	1:G:386:SER:HB2	2.43	0.49
1:L:128:GLU:HA	1:L:131:ASN:HD21	1.77	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Q:267:THR:CG2	1:Q:386:SER:HB2	2.42	0.49
1:R:266:VAL:HG22	1:R:387:VAL:HG22	1.94	0.49
1:T:147:LEU:O	1:T:149:PRO:HD2	2.13	0.49
1:U:159:MET:SD	1:U:172:PRO:HB3	2.53	0.49
1:V:373:ARG:NH2	1:W:275:LYS:HE2	2.28	0.49
1:W:191:ILE:HG23	1:W:212:LEU:HD13	1.94	0.49
1:a:266:VAL:HG22	1:a:387:VAL:HG22	1.95	0.49
1:b:152:SER:O	1:b:179:THR:N	2.37	0.49
1:G:221:THR:HG1	1:G:224:ASN:HD21	1.52	0.49
1:N:187:ASP:CG	1:N:188:GLU:N	2.71	0.49
1:O:143:THR:HG22	1:Q:154:ARG:CZ	2.42	0.49
1:R:267:THR:CG2	1:R:386:SER:HB2	2.43	0.49
1:W:194:VAL:HG23	1:W:212:LEU:HD11	1.95	0.49
1:W:236:LYS:HE3	1:X:225:THR:HG23	1.93	0.49
1:c:212:LEU:HD23	1:c:220:LEU:HB2	1.95	0.49
1:d:149:PRO:HB3	1:d:184:ARG:HG2	1.93	0.49
1:H:207:PRO:O	1:H:210:VAL:HG22	2.13	0.49
1:I:302:GLU:HG3	1:I:358:THR:HG22	1.95	0.49
1:Q:152:SER:O	1:Q:179:THR:N	2.39	0.49
1:S:180:LEU:HD11	1:S:186:LEU:HD22	1.94	0.49
1:W:392:ASN:OD1	1:W:393:TYR:N	2.46	0.49
1:X:415:LEU:HD11	1:Y:433:VAL:HG21	1.94	0.49
1:e:155:VAL:HG23	1:e:176:VAL:HG22	1.95	0.49
1:I:198:VAL:O	1:I:202:VAL:HG12	2.12	0.49
1:M:387:VAL:HG21	1:M:420:MET:HG2	1.94	0.49
1:P:250:GLU:O	1:P:254:SER:OG	2.27	0.49
1:R:415:LEU:HD11	1:S:433:VAL:HG21	1.95	0.49
1:S:360:ARG:NH1	1:S:362:GLU:OE1	2.46	0.49
1:a:179:THR:HG23	1:a:215:GLN:OE1	2.12	0.49
1:b:196:HIS:HA	1:b:199:SER:OG	2.12	0.49
1:d:405:THR:HG23	1:d:408:GLN:H	1.77	0.49
1:A:247:ARG:HE	1:B:219:LEU:HD22	1.78	0.49
1:E:421:GLY:O	1:E:426:ARG:NH2	2.46	0.49
1:F:143:THR:HG21	1:G:156:HIS:NE2	2.27	0.49
1:J:387:VAL:HG21	1:J:420:MET:HG2	1.95	0.49
1:L:147:LEU:O	1:L:149:PRO:HD2	2.12	0.49
1:N:196:HIS:O	1:N:200:SER:OG	2.27	0.49
1:a:295:SER:HB2	1:a:365:ASN:HD22	1.78	0.49
1:e:198:VAL:O	1:e:202:VAL:HG12	2.13	0.49
1:e:267:THR:CG2	1:e:386:SER:HB2	2.42	0.49
1:g:266:VAL:HG22	1:g:387:VAL:HG22	1.95	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:415:LEU:HD11	1:C:433:VAL:HG21	1.95	0.48
1:E:228:ARG:O	1:E:231:ASN:N	2.39	0.48
1:O:136:LEU:HD12	1:O:137:GLU:N	2.28	0.48
1:R:149:PRO:HB3	1:R:184:ARG:HG2	1.94	0.48
1:Y:228:ARG:HB3	1:Y:231:ASN:HB2	1.94	0.48
1:c:128:GLU:HB3	1:e:126:PHE:CD2	2.48	0.48
1:A:197:LEU:HD12	1:C:175:SER:HB2	1.96	0.48
1:C:405:THR:HG23	1:C:408:GLN:H	1.79	0.48
1:D:143:THR:HG22	1:F:154:ARG:CZ	2.43	0.48
1:G:140:LEU:CD1	1:G:155:VAL:HG11	2.42	0.48
1:J:228:ARG:HG3	1:J:231:ASN:ND2	2.28	0.48
1:Q:378:ASN:HB3	1:Q:381:ASP:OD1	2.13	0.48
1:T:221:THR:O	1:T:224:ASN:ND2	2.46	0.48
1:U:267:THR:CG2	1:U:386:SER:HB2	2.42	0.48
1:a:404:LEU:H	1:a:434:ASN:ND2	2.10	0.48
1:F:378:ASN:HB3	1:F:381:ASP:OD1	2.13	0.48
1:J:127:SER:HA	1:J:130:VAL:HG22	1.94	0.48
1:L:219:LEU:HD11	1:L:224:ASN:ND2	2.27	0.48
1:R:228:ARG:NH2	1:R:231:ASN:HD22	2.10	0.48
1:U:227:GLY:O	1:U:229:ASP:N	2.39	0.48
1:U:392:ASN:OD1	1:U:393:TYR:N	2.46	0.48
1:V:295:SER:HB2	1:V:365:ASN:HD22	1.79	0.48
1:Z:224:ASN:OD1	1:Z:225:THR:N	2.41	0.48
1:d:180:LEU:HD11	1:d:186:LEU:HD22	1.94	0.48
1:f:196:HIS:HA	1:f:199:SER:OG	2.13	0.48
1:g:295:SER:HB2	1:g:365:ASN:HD22	1.78	0.48
1:E:250:GLU:O	1:E:254:SER:OG	2.28	0.48
1:E:418:GLU:HG3	1:F:431:ASN:HB2	1.95	0.48
1:G:127:SER:HA	1:G:130:VAL:HG22	1.95	0.48
1:G:150:VAL:HA	1:G:180:LEU:HA	1.94	0.48
1:L:203:ALA:HB1	1:N:160:PRO:HG3	1.96	0.48
1:N:140:LEU:O	1:N:144:ILE:HG23	2.13	0.48
1:R:194:VAL:HG21	1:R:212:LEU:HD11	1.96	0.48
1:W:302:GLU:HG3	1:W:358:THR:HG22	1.94	0.48
1:C:200:SER:OG	1:D:175:SER:OG	2.21	0.48
1:D:228:ARG:O	1:D:230:LEU:N	2.46	0.48
1:D:387:VAL:HG21	1:D:420:MET:HG2	1.96	0.48
1:K:373:ARG:NH2	1:L:275:LYS:HE2	2.29	0.48
1:O:228:ARG:HG3	1:O:231:ASN:OD1	2.12	0.48
1:S:149:PRO:HB3	1:S:184:ARG:HG2	1.95	0.48
1:U:266:VAL:HG22	1:U:387:VAL:HG22	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:187:ASP:OD1	1:E:206:PRO:HB2	2.14	0.48
1:E:389:VAL:HB	1:E:432:VAL:HG22	1.96	0.48
1:G:392:ASN:OD1	1:G:393:TYR:N	2.46	0.48
1:J:266:VAL:HG22	1:J:387:VAL:HG22	1.96	0.48
1:Y:373:ARG:NH2	1:Z:275:LYS:HE2	2.28	0.48
1:Y:418:GLU:HG3	1:Z:431:ASN:HB2	1.95	0.48
1:Z:228:ARG:O	1:Z:230:LEU:N	2.47	0.48
1:b:404:LEU:H	1:b:434:ASN:ND2	2.12	0.48
1:e:360:ARG:NH1	1:e:362:GLU:OE1	2.46	0.48
1:f:141:ALA:HB2	1:f:155:VAL:HG12	1.94	0.48
1:O:404:LEU:H	1:O:434:ASN:ND2	2.12	0.48
1:Q:143:THR:HB	1:R:154:ARG:HG2	1.96	0.48
1:A:191:ILE:O	1:A:195:VAL:HG13	2.13	0.48
1:D:295:SER:HB2	1:D:365:ASN:HD22	1.78	0.48
1:O:421:GLY:O	1:O:426:ARG:NH2	2.47	0.48
1:R:140:LEU:HD11	1:R:155:VAL:HG11	1.95	0.48
1:T:149:PRO:HB3	1:T:184:ARG:HG2	1.96	0.48
1:b:151:LYS:N	1:b:179:THR:O	2.43	0.48
1:d:360:ARG:NH1	1:d:362:GLU:OE1	2.45	0.48
1:A:195:VAL:HG12	1:A:212:LEU:HD13	1.95	0.48
1:B:192:SER:HA	1:B:195:VAL:HG12	1.95	0.48
1:V:387:VAL:HG21	1:V:420:MET:HG2	1.95	0.48
1:c:221:THR:HG1	1:c:224:ASN:HD21	1.53	0.48
1:f:266:VAL:HG22	1:f:387:VAL:HG22	1.96	0.48
1:O:198:VAL:O	1:O:202:VAL:HG12	2.14	0.48
1:P:192:SER:HA	1:P:195:VAL:HG12	1.95	0.48
1:P:214:ASP:HB3	1:P:218:HIS:HB2	1.96	0.48
1:Z:266:VAL:HG22	1:Z:387:VAL:HG22	1.96	0.48
1:c:143:THR:HG22	1:e:154:ARG:CZ	2.44	0.48
1:d:418:GLU:HG3	1:e:431:ASN:HB2	1.95	0.48
1:A:224:ASN:HB3	1:f:196:HIS:CG	2.49	0.47
1:A:392:ASN:OD1	1:A:393:TYR:N	2.46	0.47
1:A:404:LEU:H	1:A:434:ASN:HD21	1.61	0.47
1:D:266:VAL:HG22	1:D:387:VAL:HG22	1.97	0.47
1:G:143:THR:HG22	1:I:154:ARG:CZ	2.44	0.47
1:G:185:ALA:HB3	1:H:206:PRO:HB3	1.95	0.47
1:U:393:TYR:CE2	1:U:436:PRO:HD3	2.49	0.47
1:X:140:LEU:HD22	1:X:155:VAL:HG21	1.95	0.47
1:D:147:LEU:O	1:D:149:PRO:HD2	2.14	0.47
1:E:178:VAL:O	1:E:215:GLN:NE2	2.44	0.47
1:H:418:GLU:HG3	1:I:431:ASN:HB2	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M:192:SER:HA	1:M:195:VAL:HG22	1.95	0.47
1:M:267:THR:HG22	1:M:386:SER:HB2	1.96	0.47
1:N:186:LEU:H	1:N:186:LEU:HD12	1.78	0.47
1:Q:143:THR:HG21	1:R:156:HIS:NE2	2.30	0.47
1:R:192:SER:HA	1:R:195:VAL:HB	1.95	0.47
1:U:198:VAL:O	1:U:202:VAL:HG12	2.14	0.47
1:W:404:LEU:H	1:W:434:ASN:ND2	2.12	0.47
1:b:360:ARG:NH1	1:b:362:GLU:OE1	2.47	0.47
1:c:143:THR:HG21	1:e:156:HIS:CE1	2.49	0.47
1:A:194:VAL:HG21	1:A:212:LEU:HD21	1.95	0.47
1:J:295:SER:HB2	1:J:365:ASN:HD22	1.80	0.47
1:O:266:VAL:HG22	1:O:387:VAL:HG22	1.95	0.47
1:P:392:ASN:OD1	1:P:393:TYR:N	2.48	0.47
1:U:373:ARG:HH21	1:V:275:LYS:HE2	1.79	0.47
1:Z:143:THR:HG22	1:b:154:ARG:CZ	2.43	0.47
1:f:415:LEU:HD11	1:g:433:VAL:HG21	1.95	0.47
1:E:423:SER:OG	1:E:426:ARG:NE	2.45	0.47
1:G:153:ALA:HA	1:G:178:VAL:HA	1.96	0.47
1:I:373:ARG:NH2	1:J:275:LYS:HE2	2.29	0.47
1:K:387:VAL:HG21	1:K:420:MET:HG2	1.95	0.47
1:L:140:LEU:O	1:L:144:ILE:HG12	2.14	0.47
1:L:394:LYS:O	1:L:402:LEU:N	2.48	0.47
1:S:389:VAL:HB	1:S:432:VAL:HG22	1.95	0.47
1:S:392:ASN:OD1	1:S:393:TYR:N	2.47	0.47
1:Z:295:SER:HB2	1:Z:365:ASN:HD22	1.80	0.47
1:B:379:VAL:O	1:C:231:ASN:ND2	2.48	0.47
1:N:267:THR:OG1	1:N:386:SER:HB2	2.15	0.47
1:P:421:GLY:O	1:P:426:ARG:NH2	2.47	0.47
1:Q:211:THR:OG1	1:Q:224:ASN:ND2	2.48	0.47
1:R:199:SER:HA	1:R:205:LEU:HG	1.97	0.47
1:U:387:VAL:HG21	1:U:420:MET:HG2	1.95	0.47
1:A:173:SER:HB2	1:f:200:SER:OG	2.14	0.47
1:L:141:ALA:O	1:L:145:GLU:HG3	2.13	0.47
1:L:392:ASN:OD1	1:L:393:TYR:N	2.47	0.47
1:P:267:THR:HG22	1:P:386:SER:HB2	1.96	0.47
1:U:126:PHE:O	1:U:130:VAL:HG13	2.13	0.47
1:U:157:LEU:HD13	1:U:174:ALA:HB2	1.95	0.47
1:W:147:LEU:O	1:W:149:PRO:HD2	2.15	0.47
1:W:373:ARG:NH2	1:X:275:LYS:HE2	2.29	0.47
1:Z:147:LEU:HB2	1:Z:150:VAL:HG21	1.96	0.47
1:Z:228:ARG:C	1:Z:230:LEU:H	2.22	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:b:193:ALA:HA	1:c:219:LEU:HB2	1.96	0.47
1:f:154:ARG:HB3	1:f:177:THR:CG2	2.45	0.47
1:B:426:ARG:NH2	1:B:428:ASP:OD2	2.48	0.47
1:F:389:VAL:HB	1:F:432:VAL:HG22	1.97	0.47
1:O:140:LEU:O	1:O:144:ILE:HG12	2.15	0.47
1:O:149:PRO:O	1:O:180:LEU:HD12	2.14	0.47
1:P:146:THR:O	1:P:147:LEU:HD12	2.14	0.47
1:Q:295:SER:HB2	1:Q:365:ASN:HD22	1.80	0.47
1:S:127:SER:O	1:S:131:ASN:ND2	2.48	0.47
1:T:300:ILE:HG12	1:T:360:ARG:HG3	1.96	0.47
1:T:302:GLU:HG3	1:T:358:THR:HG22	1.97	0.47
1:T:373:ARG:NH2	1:U:275:LYS:HE2	2.30	0.47
1:Y:405:THR:HG23	1:Y:408:GLN:H	1.79	0.47
1:Z:172:PRO:HG2	1:Z:205:LEU:HA	1.97	0.47
1:a:360:ARG:NH1	1:a:362:GLU:OE1	2.47	0.47
1:b:415:LEU:HD11	1:c:433:VAL:HG21	1.97	0.47
1:c:418:GLU:HG3	1:d:431:ASN:HB2	1.96	0.47
1:d:415:LEU:HD11	1:e:433:VAL:HG21	1.97	0.47
1:F:387:VAL:HG21	1:F:420:MET:HG2	1.97	0.47
1:G:404:LEU:H	1:G:434:ASN:ND2	2.13	0.47
1:H:392:ASN:OD1	1:H:393:TYR:N	2.47	0.47
1:T:227:GLY:C	1:T:228:ARG:HD2	2.39	0.47
1:T:426:ARG:NH2	1:T:428:ASP:OD2	2.48	0.47
1:Y:147:LEU:HB3	1:Y:150:VAL:HG11	1.97	0.47
1:Z:387:VAL:HG21	1:Z:420:MET:HG2	1.97	0.47
1:a:144:ILE:O	1:a:147:LEU:HB2	2.15	0.47
1:f:392:ASN:OD1	1:f:393:TYR:N	2.46	0.47
1:C:300:ILE:HG12	1:C:360:ARG:HG3	1.97	0.47
1:D:228:ARG:HG2	1:D:229:ASP:N	2.30	0.47
1:I:227:GLY:C	1:I:228:ARG:HD2	2.40	0.47
1:O:300:ILE:HG12	1:O:360:ARG:HG3	1.96	0.47
1:P:415:LEU:HD11	1:Q:433:VAL:HG21	1.97	0.47
1:Y:228:ARG:HD3	1:Y:231:ASN:CG	2.40	0.47
1:Y:387:VAL:HG21	1:Y:420:MET:HG2	1.97	0.47
1:a:192:SER:O	1:a:195:VAL:HG12	2.15	0.47
1:b:389:VAL:HB	1:b:432:VAL:HG22	1.96	0.47
1:c:387:VAL:HG21	1:c:420:MET:HG2	1.97	0.47
1:d:127:SER:HA	1:d:130:VAL:HG12	1.96	0.47
1:d:392:ASN:OD1	1:d:393:TYR:N	2.47	0.47
1:A:373:ARG:NH2	1:B:275:LYS:HE2	2.30	0.47
1:H:387:VAL:HG21	1:H:420:MET:HG2	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:N:392:ASN:OD1	1:N:393:TYR:N	2.48	0.47
1:O:193:ALA:HA	1:Q:219:LEU:HD13	1.97	0.47
1:P:214:ASP:CG	1:P:215:GLN:H	2.24	0.47
1:T:360:ARG:NH1	1:T:362:GLU:OE1	2.48	0.47
1:e:193:ALA:HA	1:f:219:LEU:HB2	1.97	0.47
1:A:431:ASN:HB2	1:g:418:GLU:HG3	1.97	0.46
1:C:143:THR:HG21	1:D:156:HIS:CE1	2.50	0.46
1:J:159:MET:SD	1:J:172:PRO:HB3	2.55	0.46
1:O:228:ARG:C	1:O:230:LEU:H	2.23	0.46
1:Q:147:LEU:O	1:Q:149:PRO:HD2	2.15	0.46
1:W:155:VAL:HB	1:W:176:VAL:HG12	1.96	0.46
1:X:192:SER:HA	1:X:195:VAL:HG22	1.97	0.46
1:Y:392:ASN:OD1	1:Y:393:TYR:N	2.48	0.46
1:a:418:GLU:HG3	1:b:431:ASN:HB2	1.96	0.46
1:b:387:VAL:HG21	1:b:420:MET:HG2	1.97	0.46
1:c:187:ASP:OD1	1:d:208:GLY:N	2.44	0.46
1:c:392:ASN:OD1	1:c:393:TYR:N	2.46	0.46
1:c:415:LEU:HD11	1:d:433:VAL:HG21	1.97	0.46
1:d:173:SER:OG	1:d:174:ALA:N	2.48	0.46
1:A:275:LYS:HE2	1:g:373:ARG:NH2	2.31	0.46
1:G:387:VAL:HG21	1:G:420:MET:HG2	1.97	0.46
1:J:392:ASN:OD1	1:J:393:TYR:N	2.47	0.46
1:M:404:LEU:H	1:M:434:ASN:ND2	2.13	0.46
1:O:415:LEU:HD11	1:P:433:VAL:HG21	1.97	0.46
1:P:418:GLU:HG3	1:Q:431:ASN:HB2	1.96	0.46
1:W:387:VAL:HG21	1:W:420:MET:HG2	1.96	0.46
1:Z:404:LEU:H	1:Z:434:ASN:ND2	2.13	0.46
1:d:295:SER:HB2	1:d:365:ASN:HD22	1.80	0.46
1:d:412:ILE:O	1:d:416:THR:HG23	2.15	0.46
1:e:266:VAL:HG22	1:e:387:VAL:HG22	1.98	0.46
1:f:373:ARG:HH21	1:g:275:LYS:HE2	1.79	0.46
1:C:392:ASN:OD1	1:C:393:TYR:N	2.48	0.46
1:F:137:GLU:HA	1:F:140:LEU:CD2	2.45	0.46
1:G:192:SER:HA	1:G:195:VAL:HB	1.97	0.46
1:K:295:SER:HB3	1:K:365:ASN:HD22	1.80	0.46
1:L:222:GLN:HB2	1:L:229:ASP:HB3	1.96	0.46
1:Q:193:ALA:HA	1:R:219:LEU:HD13	1.98	0.46
1:S:421:GLY:O	1:S:426:ARG:NH2	2.49	0.46
1:U:404:LEU:H	1:U:434:ASN:ND2	2.12	0.46
1:Z:393:TYR:CE2	1:Z:436:PRO:HD3	2.51	0.46
1:c:185:ALA:HB3	1:d:206:PRO:HB3	1.96	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:415:LEU:HD11	1:B:433:VAL:HG21	1.97	0.46
1:E:271:ASP:OD1	1:E:383:GLU:HB2	2.16	0.46
1:G:389:VAL:HB	1:G:432:VAL:HG22	1.96	0.46
1:Q:415:LEU:HD11	1:R:433:VAL:HG21	1.97	0.46
1:X:392:ASN:OD1	1:X:393:TYR:N	2.47	0.46
1:B:392:ASN:OD1	1:B:393:TYR:N	2.47	0.46
1:C:373:ARG:NH2	1:D:275:LYS:HE2	2.31	0.46
1:F:143:THR:HB	1:G:154:ARG:HG2	1.96	0.46
1:F:211:THR:OG1	1:F:224:ASN:ND2	2.49	0.46
1:M:191:ILE:HG13	1:M:192:SER:N	2.30	0.46
1:O:387:VAL:HG21	1:O:420:MET:HG2	1.96	0.46
1:P:150:VAL:HG13	1:P:178:VAL:HG23	1.97	0.46
1:R:404:LEU:H	1:R:434:ASN:ND2	2.12	0.46
1:T:404:LEU:H	1:T:434:ASN:ND2	2.14	0.46
1:X:302:GLU:HG3	1:X:358:THR:HG22	1.97	0.46
1:a:191:ILE:O	1:a:194:VAL:HG22	2.16	0.46
1:A:267:THR:HB	1:A:386:SER:OG	2.15	0.46
1:E:381:ASP:OD1	1:E:381:ASP:N	2.41	0.46
1:F:415:LEU:HD11	1:G:433:VAL:HG21	1.97	0.46
1:G:202:VAL:HG23	1:G:205:LEU:HB3	1.97	0.46
1:J:373:ARG:HH21	1:K:275:LYS:HE2	1.80	0.46
1:P:192:SER:O	1:P:195:VAL:HG12	2.15	0.46
1:Q:389:VAL:HB	1:Q:432:VAL:HG22	1.96	0.46
1:S:173:SER:OG	1:S:174:ALA:N	2.48	0.46
1:X:188:GLU:HG2	1:X:189:GLY:N	2.31	0.46
1:Z:219:LEU:HD11	1:Z:224:ASN:ND2	2.31	0.46
1:a:228:ARG:HG3	1:a:231:ASN:ND2	2.31	0.46
1:d:140:LEU:HD11	1:d:155:VAL:CG2	2.42	0.46
1:d:271:ASP:OD1	1:d:383:GLU:HB2	2.15	0.46
1:H:271:ASP:OD1	1:H:383:GLU:HB2	2.16	0.46
1:I:426:ARG:NH2	1:I:428:ASP:OD2	2.48	0.46
1:L:228:ARG:HH21	1:L:231:ASN:HB2	1.79	0.46
1:P:228:ARG:HG3	1:P:231:ASN:CB	2.43	0.46
1:W:394:LYS:O	1:W:402:LEU:N	2.49	0.46
1:X:414:ASP:HB3	1:Y:431:ASN:HD22	1.80	0.46
1:L:186:LEU:H	1:L:186:LEU:HD12	1.81	0.46
1:O:193:ALA:O	1:O:197:LEU:HG	2.16	0.46
1:O:393:TYR:CE2	1:O:436:PRO:HD3	2.51	0.46
1:W:415:LEU:HD11	1:X:433:VAL:HG21	1.97	0.46
1:X:426:ARG:NH2	1:X:428:ASP:OD2	2.49	0.46
1:a:158:ALA:O	1:a:159:MET:HE2	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:b:266:VAL:HG22	1:b:387:VAL:HG22	1.98	0.46
1:A:198:VAL:O	1:A:202:VAL:HG12	2.15	0.46
1:D:191:ILE:HD12	1:D:212:LEU:HD23	1.97	0.46
1:E:412:ILE:O	1:E:416:THR:HG23	2.16	0.46
1:K:237:PHE:HB2	1:L:228:ARG:HH12	1.80	0.46
1:L:267:THR:HB	1:L:386:SER:OG	2.16	0.46
1:L:373:ARG:NH2	1:M:275:LYS:HE2	2.31	0.46
1:M:153:ALA:C	1:M:154:ARG:HD3	2.41	0.46
1:M:412:ILE:O	1:M:416:THR:HG23	2.16	0.46
1:N:373:ARG:NH2	1:O:275:LYS:HE2	2.30	0.46
1:S:228:ARG:C	1:S:230:LEU:H	2.24	0.46
1:Z:373:ARG:NH2	1:a:275:LYS:HE2	2.31	0.46
1:Z:415:LEU:HD11	1:a:433:VAL:HG21	1.96	0.46
1:e:190:GLN:HG3	1:f:217:GLY:HA3	1.97	0.46
1:e:404:LEU:H	1:e:434:ASN:ND2	2.14	0.46
1:C:187:ASP:OD1	1:C:190:GLN:HB2	2.15	0.46
1:D:393:TYR:CE2	1:D:436:PRO:HD3	2.51	0.46
1:O:267:THR:HG22	1:O:386:SER:HB2	1.98	0.46
1:T:155:VAL:HG23	1:T:176:VAL:HG22	1.97	0.46
1:U:295:SER:HB2	1:U:365:ASN:HD22	1.81	0.46
1:Z:187:ASP:OD1	1:a:207:PRO:HD2	2.16	0.46
1:b:193:ALA:HA	1:c:219:LEU:HD13	1.98	0.46
1:d:224:ASN:HD21	1:d:236:LYS:HD3	1.80	0.46
1:e:228:ARG:HB3	1:e:231:ASN:HB3	1.98	0.46
1:f:393:TYR:CE2	1:f:436:PRO:HD3	2.51	0.46
1:D:392:ASN:OD1	1:D:393:TYR:N	2.48	0.45
1:E:392:ASN:OD1	1:E:393:TYR:N	2.48	0.45
1:F:295:SER:HB2	1:F:365:ASN:HD22	1.81	0.45
1:O:228:ARG:NH1	1:O:232:ASP:OD2	2.49	0.45
1:R:389:VAL:HB	1:R:432:VAL:HG22	1.96	0.45
1:U:211:THR:HG22	1:U:224:ASN:HB3	1.98	0.45
1:V:266:VAL:HG22	1:V:387:VAL:HG22	1.98	0.45
1:Z:300:ILE:HG12	1:Z:360:ARG:HG3	1.97	0.45
1:a:415:LEU:HD11	1:b:433:VAL:HG21	1.98	0.45
1:e:176:VAL:HB	1:e:212:LEU:HD23	1.98	0.45
1:B:188:GLU:O	1:B:191:ILE:HG12	2.16	0.45
1:C:149:PRO:HB3	1:C:184:ARG:HG2	1.99	0.45
1:E:144:ILE:O	1:E:147:LEU:HB2	2.17	0.45
1:I:404:LEU:H	1:I:434:ASN:ND2	2.14	0.45
1:K:266:VAL:HG22	1:K:387:VAL:HG22	1.98	0.45
1:U:135:ALA:O	1:U:139:GLU:HG3	2.14	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:c:198:VAL:O	1:c:202:VAL:HG22	2.16	0.45
1:H:180:LEU:HD11	1:H:186:LEU:HD22	1.98	0.45
1:O:144:ILE:O	1:O:150:VAL:HG11	2.16	0.45
1:Q:266:VAL:HG22	1:Q:387:VAL:HG22	1.97	0.45
1:R:393:TYR:CE2	1:R:436:PRO:HD3	2.51	0.45
1:S:404:LEU:H	1:S:434:ASN:ND2	2.15	0.45
1:U:172:PRO:HG2	1:U:205:LEU:HA	1.96	0.45
1:W:214:ASP:HB3	1:W:218:HIS:HB2	1.98	0.45
1:b:418:GLU:HG3	1:c:431:ASN:HB2	1.97	0.45
1:d:149:PRO:HA	1:d:181:GLU:CG	2.46	0.45
1:C:147:LEU:HD12	1:D:215:GLN:HA	1.98	0.45
1:D:412:ILE:O	1:D:416:THR:HG23	2.17	0.45
1:G:415:LEU:HD11	1:H:433:VAL:HG21	1.98	0.45
1:I:225:THR:HG23	1:I:227:GLY:H	1.82	0.45
1:I:300:ILE:HG12	1:I:360:ARG:HG3	1.98	0.45
1:N:233:ALA:HB1	1:O:228:ARG:HH21	1.82	0.45
1:T:387:VAL:HG21	1:T:420:MET:HG2	1.97	0.45
1:Z:392:ASN:OD1	1:Z:393:TYR:N	2.49	0.45
1:a:392:ASN:OD1	1:a:393:TYR:N	2.48	0.45
1:e:373:ARG:NH2	1:f:275:LYS:HE2	2.31	0.45
1:f:421:GLY:O	1:f:426:ARG:NH2	2.50	0.45
1:g:250:GLU:O	1:g:254:SER:OG	2.30	0.45
1:C:187:ASP:OD2	1:C:189:GLY:N	2.50	0.45
1:C:228:ARG:HD3	1:C:231:ASN:CG	2.40	0.45
1:E:373:ARG:NH2	1:F:275:LYS:HE2	2.32	0.45
1:H:404:LEU:H	1:H:434:ASN:ND2	2.14	0.45
1:I:360:ARG:NH1	1:I:362:GLU:OE1	2.48	0.45
1:M:379:VAL:O	1:N:231:ASN:ND2	2.49	0.45
1:N:145:GLU:O	1:N:150:VAL:HG13	2.16	0.45
1:N:147:LEU:O	1:N:149:PRO:HD2	2.17	0.45
1:P:360:ARG:NH1	1:P:362:GLU:OE1	2.48	0.45
1:S:174:ALA:HB3	1:S:210:VAL:HG13	1.97	0.45
1:S:280:GLU:HG3	1:S:372:ILE:HG12	1.98	0.45
1:T:195:VAL:HG13	1:T:210:VAL:HG11	1.99	0.45
1:X:149:PRO:O	1:X:180:LEU:HD13	2.16	0.45
1:E:360:ARG:NH1	1:E:362:GLU:OE1	2.46	0.45
1:I:180:LEU:HD11	1:I:215:GLN:HE22	1.81	0.45
1:J:140:LEU:O	1:J:144:ILE:HG12	2.17	0.45
1:L:193:ALA:HA	1:N:219:LEU:HD13	1.99	0.45
1:N:201:ALA:HB2	1:O:175:SER:OG	2.17	0.45
1:N:233:ALA:HB1	1:O:228:ARG:NH2	2.31	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:T:186:LEU:HD11	1:T:190:GLN:HG2	1.98	0.45
1:T:198:VAL:O	1:T:202:VAL:HG12	2.16	0.45
1:U:222:GLN:OE1	1:U:236:LYS:NZ	2.50	0.45
1:b:143:THR:HB	1:c:154:ARG:HG2	1.98	0.45
1:G:190:GLN:CG	1:I:217:GLY:HA3	2.45	0.45
1:T:197:LEU:HD12	1:U:175:SER:HB2	1.98	0.45
1:Z:412:ILE:O	1:Z:416:THR:HG23	2.17	0.45
1:c:393:TYR:CE2	1:c:436:PRO:HD3	2.52	0.45
1:e:211:THR:HA	1:e:221:THR:HG21	1.98	0.45
1:f:186:LEU:H	1:f:186:LEU:HD22	1.82	0.45
1:F:198:VAL:HG21	1:F:210:VAL:HG11	1.99	0.45
1:G:155:VAL:HA	1:G:176:VAL:HA	1.98	0.45
1:I:147:LEU:O	1:I:149:PRO:HD2	2.17	0.45
1:I:190:GLN:HG3	1:J:217:GLY:HA3	1.97	0.45
1:M:392:ASN:OD1	1:M:393:TYR:N	2.48	0.45
1:U:142:ARG:O	1:U:146:THR:HG23	2.16	0.45
1:Z:247:ARG:NH2	1:a:219:LEU:HD22	2.32	0.45
1:d:387:VAL:HG21	1:d:420:MET:HG2	1.99	0.45
1:e:221:THR:HG23	1:e:224:ASN:ND2	2.32	0.45
1:B:195:VAL:HG23	1:B:210:VAL:CG1	2.46	0.45
1:J:141:ALA:O	1:J:145:GLU:HG3	2.17	0.45
1:R:193:ALA:HA	1:T:219:LEU:HB2	1.98	0.45
1:R:228:ARG:HH21	1:R:231:ASN:CB	2.29	0.45
1:S:149:PRO:HA	1:S:181:GLU:CG	2.46	0.45
1:U:394:LYS:O	1:U:402:LEU:N	2.50	0.45
1:X:300:ILE:HG12	1:X:360:ARG:HG3	1.98	0.45
1:Y:229:ASP:OD1	1:Y:230:LEU:N	2.45	0.45
1:A:394:LYS:O	1:A:402:LEU:N	2.50	0.45
1:C:154:ARG:HB3	1:C:177:THR:CG2	2.47	0.45
1:C:186:LEU:H	1:C:186:LEU:HD12	1.82	0.45
1:F:266:VAL:HG22	1:F:387:VAL:HG22	1.99	0.45
1:G:144:ILE:O	1:G:147:LEU:HB2	2.16	0.45
1:G:393:TYR:CE2	1:G:436:PRO:HD3	2.52	0.45
1:I:421:GLY:O	1:I:426:ARG:NH2	2.50	0.45
1:M:149:PRO:O	1:M:180:LEU:HA	2.17	0.45
1:O:295:SER:HB2	1:O:365:ASN:HD22	1.82	0.45
1:O:373:ARG:HH21	1:P:275:LYS:NZ	2.15	0.45
1:Q:145:GLU:HG2	1:Q:152:SER:HA	1.99	0.45
1:a:393:TYR:CE2	1:a:436:PRO:HD3	2.52	0.45
1:c:202:VAL:HG23	1:c:205:LEU:HB3	1.99	0.45
1:c:389:VAL:HB	1:c:432:VAL:HG22	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:f:142:ARG:O	1:f:146:THR:HG23	2.17	0.45
1:E:302:GLU:HG3	1:E:358:THR:HG22	1.98	0.44
1:F:143:THR:HG21	1:G:156:HIS:CE1	2.52	0.44
1:F:392:ASN:OD1	1:F:393:TYR:N	2.49	0.44
1:H:360:ARG:NH1	1:H:362:GLU:OE1	2.47	0.44
1:P:228:ARG:NH1	1:P:230:LEU:HB3	2.32	0.44
1:P:271:ASP:OD1	1:P:383:GLU:HB2	2.16	0.44
1:S:174:ALA:HB3	1:S:210:VAL:HG22	1.98	0.44
1:W:198:VAL:O	1:W:202:VAL:HG12	2.17	0.44
1:a:271:ASP:OD1	1:a:383:GLU:HB2	2.18	0.44
1:c:412:ILE:O	1:c:416:THR:HG23	2.17	0.44
1:f:202:VAL:HG11	1:f:205:LEU:HD23	2.00	0.44
1:f:295:SER:HB2	1:f:365:ASN:HD22	1.82	0.44
1:D:192:SER:HA	1:D:195:VAL:CG1	2.41	0.44
1:F:200:SER:OG	1:G:173:SER:HB2	2.16	0.44
1:G:249:ILE:HG23	1:G:416:THR:HG22	1.99	0.44
1:H:155:VAL:HG12	1:H:176:VAL:HG13	1.99	0.44
1:N:387:VAL:HG21	1:N:420:MET:HG2	1.99	0.44
1:O:373:ARG:NH2	1:P:275:LYS:HE2	2.32	0.44
1:O:412:ILE:O	1:O:416:THR:HG23	2.17	0.44
1:a:412:ILE:O	1:a:416:THR:HG23	2.17	0.44
1:c:173:SER:HA	1:c:205:LEU:HD13	1.98	0.44
1:e:392:ASN:OD1	1:e:393:TYR:N	2.50	0.44
1:f:227:GLY:O	1:f:229:ASP:N	2.38	0.44
1:A:141:ALA:O	1:A:145:GLU:HG3	2.18	0.44
1:A:232:ASP:HB3	1:g:237:PHE:HD1	1.81	0.44
1:D:300:ILE:HG12	1:D:360:ARG:HG3	1.98	0.44
1:D:404:LEU:H	1:D:434:ASN:ND2	2.15	0.44
1:F:147:LEU:O	1:F:149:PRO:HD2	2.18	0.44
1:H:172:PRO:HG2	1:H:209:ASN:ND2	2.33	0.44
1:O:193:ALA:HA	1:Q:219:LEU:HB2	2.00	0.44
1:O:392:ASN:OD1	1:O:393:TYR:N	2.49	0.44
1:P:302:GLU:HG3	1:P:358:THR:HG22	1.98	0.44
1:Q:421:GLY:O	1:Q:426:ARG:NH2	2.50	0.44
1:U:202:VAL:HG11	1:U:205:LEU:HD23	2.00	0.44
1:V:418:GLU:HG3	1:W:431:ASN:HB2	1.99	0.44
1:X:212:LEU:CD2	1:X:220:LEU:HD12	2.47	0.44
1:Y:196:HIS:ND1	1:Z:224:ASN:HB2	2.32	0.44
1:Z:191:ILE:HD12	1:Z:212:LEU:HD23	1.99	0.44
1:Z:426:ARG:NH2	1:Z:428:ASP:OD2	2.51	0.44
1:a:421:GLY:O	1:a:426:ARG:NH2	2.51	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:173:SER:HA	1:G:205:LEU:HD13	1.99	0.44
1:G:198:VAL:O	1:G:202:VAL:HG22	2.17	0.44
1:O:247:ARG:NH2	1:P:219:LEU:HD22	2.33	0.44
1:S:387:VAL:HG21	1:S:420:MET:HG2	1.99	0.44
1:U:154:ARG:HB3	1:U:177:THR:CG2	2.47	0.44
1:W:267:THR:HB	1:W:386:SER:OG	2.17	0.44
1:X:250:GLU:O	1:X:254:SER:OG	2.27	0.44
1:f:228:ARG:O	1:f:230:LEU:N	2.51	0.44
1:A:393:TYR:CE2	1:A:436:PRO:HD3	2.53	0.44
1:E:415:LEU:HD11	1:F:433:VAL:HG21	1.98	0.44
1:G:214:ASP:HB3	1:G:218:HIS:HB2	1.99	0.44
1:K:300:ILE:HG12	1:K:360:ARG:HG3	1.99	0.44
1:M:140:LEU:HD21	1:M:198:VAL:HG12	1.99	0.44
1:O:379:VAL:O	1:P:231:ASN:ND2	2.50	0.44
1:R:185:ALA:HB3	1:S:206:PRO:HB3	1.98	0.44
1:T:191:ILE:O	1:T:194:VAL:HG22	2.17	0.44
1:V:393:TYR:CE2	1:V:436:PRO:HD3	2.53	0.44
1:Z:187:ASP:OD1	1:a:206:PRO:HB2	2.17	0.44
1:a:373:ARG:NH2	1:b:275:LYS:HE2	2.32	0.44
1:e:214:ASP:HB2	1:e:218:HIS:HB2	1.99	0.44
1:e:387:VAL:HG21	1:e:420:MET:HG2	1.99	0.44
1:B:151:LYS:HB3	1:B:181:GLU:OE1	2.17	0.44
1:I:392:ASN:OD1	1:I:393:TYR:N	2.50	0.44
1:K:393:TYR:CE2	1:K:436:PRO:HD3	2.53	0.44
1:L:142:ARG:O	1:L:146:THR:HG23	2.17	0.44
1:M:426:ARG:NH2	1:M:428:ASP:OD2	2.50	0.44
1:P:145:GLU:HG2	1:P:152:SER:HA	2.00	0.44
1:P:373:ARG:NH2	1:Q:275:LYS:HE2	2.32	0.44
1:Q:300:ILE:HG12	1:Q:360:ARG:HG3	1.98	0.44
1:Q:392:ASN:OD1	1:Q:393:TYR:N	2.49	0.44
1:R:128:GLU:HB3	1:T:126:PHE:CD2	2.53	0.44
1:U:195:VAL:HG13	1:U:210:VAL:HG11	1.99	0.44
1:V:415:LEU:HD11	1:W:433:VAL:HG21	1.99	0.44
1:Z:140:LEU:O	1:Z:144:ILE:HG12	2.18	0.44
1:b:143:THR:HG21	1:c:156:HIS:NE2	2.32	0.44
1:F:404:LEU:H	1:F:434:ASN:ND2	2.14	0.44
1:J:154:ARG:HB3	1:J:177:THR:CG2	2.48	0.44
1:J:202:VAL:HG11	1:J:205:LEU:HD23	1.99	0.44
1:W:228:ARG:O	1:W:230:LEU:HD23	2.18	0.44
1:X:205:LEU:HD23	1:X:205:LEU:O	2.18	0.44
1:Z:389:VAL:HB	1:Z:432:VAL:HG22	2.00	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:202:VAL:HG21	1:E:205:LEU:HD23	2.00	0.44
1:H:393:TYR:CE2	1:H:436:PRO:HD3	2.53	0.44
1:H:423:SER:OG	1:H:426:ARG:NE	2.46	0.44
1:I:418:GLU:HG3	1:J:431:ASN:HB2	1.99	0.44
1:J:393:TYR:CE2	1:J:436:PRO:HD3	2.52	0.44
1:Q:418:GLU:HG3	1:R:431:ASN:HB2	1.99	0.44
1:W:202:VAL:HG11	1:W:205:LEU:HD23	2.00	0.44
1:b:187:ASP:O	1:b:191:ILE:HG12	2.17	0.44
1:b:392:ASN:OD1	1:b:393:TYR:N	2.50	0.44
1:d:192:SER:HA	1:d:195:VAL:HB	2.00	0.44
1:d:404:LEU:H	1:d:434:ASN:ND2	2.15	0.44
1:B:414:ASP:HB3	1:C:431:ASN:HD22	1.81	0.44
1:D:198:VAL:O	1:D:202:VAL:HG12	2.17	0.44
1:E:228:ARG:HH12	1:E:230:LEU:HD22	1.83	0.44
1:L:247:ARG:HH21	1:M:219:LEU:HD22	1.82	0.44
1:R:140:LEU:CD1	1:R:155:VAL:HG11	2.48	0.44
1:S:151:LYS:HD3	1:S:179:THR:HG22	2.00	0.44
1:Y:414:ASP:HB3	1:Z:431:ASN:ND2	2.33	0.44
1:d:393:TYR:CE2	1:d:436:PRO:HD3	2.53	0.44
1:e:186:LEU:HG	1:e:190:GLN:HB3	2.00	0.44
1:B:149:PRO:HB3	1:B:184:ARG:HG2	1.99	0.43
1:D:187:ASP:OD1	1:E:207:PRO:HD2	2.18	0.43
1:D:267:THR:HG22	1:D:386:SER:HB2	1.98	0.43
1:J:404:LEU:H	1:J:434:ASN:ND2	2.13	0.43
1:N:141:ALA:O	1:N:145:GLU:HG3	2.18	0.43
1:N:196:HIS:CE1	1:O:224:ASN:HB3	2.53	0.43
1:V:283:SER:OG	1:V:369:ASP:HB2	2.18	0.43
1:W:187:ASP:OD1	1:W:190:GLN:HB2	2.18	0.43
1:X:153:ALA:C	1:X:154:ARG:HD3	2.42	0.43
1:c:186:LEU:HG	1:c:191:ILE:CD1	2.48	0.43
1:A:433:VAL:HG21	1:g:415:LEU:HD11	1.99	0.43
1:F:193:ALA:HA	1:G:219:LEU:HD13	2.01	0.43
1:F:300:ILE:HG12	1:F:360:ARG:HG3	1.99	0.43
1:H:173:SER:OG	1:H:174:ALA:N	2.51	0.43
1:S:192:SER:HA	1:S:195:VAL:HB	1.99	0.43
1:S:271:ASP:OD1	1:S:383:GLU:HB2	2.18	0.43
1:T:172:PRO:O	1:T:173:SER:OG	2.29	0.43
1:W:200:SER:HB2	1:Y:173:SER:OG	2.18	0.43
1:Z:228:ARG:HB3	1:Z:231:ASN:HB2	1.99	0.43
1:c:140:LEU:CD1	1:c:155:VAL:HG11	2.47	0.43
1:g:392:ASN:OD1	1:g:393:TYR:N	2.50	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:139:GLU:O	1:A:143:THR:HG23	2.18	0.43
1:A:225:THR:O	1:A:227:GLY:N	2.50	0.43
1:E:228:ARG:NH1	1:E:230:LEU:HB3	2.33	0.43
1:P:178:VAL:O	1:P:215:GLN:NE2	2.38	0.43
1:Q:360:ARG:NH1	1:Q:362:GLU:OE1	2.50	0.43
1:Q:387:VAL:HG21	1:Q:420:MET:HG2	1.99	0.43
1:T:193:ALA:HA	1:U:219:LEU:HB2	2.00	0.43
1:W:228:ARG:C	1:W:230:LEU:H	2.26	0.43
1:b:147:LEU:O	1:b:149:PRO:HD2	2.18	0.43
1:b:300:ILE:HG12	1:b:360:ARG:HG3	2.00	0.43
1:c:137:GLU:HG2	1:c:157:LEU:CD1	2.43	0.43
1:c:360:ARG:NH1	1:c:362:GLU:OE1	2.51	0.43
1:D:373:ARG:NH2	1:E:275:LYS:HE2	2.32	0.43
1:E:149:PRO:HB3	1:E:184:ARG:NH1	2.33	0.43
1:I:150:VAL:HA	1:I:180:LEU:HA	1.99	0.43
1:O:196:HIS:O	1:O:200:SER:OG	2.37	0.43
1:O:426:ARG:NH2	1:O:428:ASP:OD2	2.51	0.43
1:P:180:LEU:H	1:P:180:LEU:CD1	2.30	0.43
1:R:387:VAL:HG21	1:R:420:MET:HG2	1.99	0.43
1:T:392:ASN:OD1	1:T:393:TYR:N	2.50	0.43
1:U:141:ALA:O	1:U:145:GLU:HG3	2.18	0.43
1:W:295:SER:OG	1:W:365:ASN:ND2	2.34	0.43
1:X:187:ASP:O	1:X:191:ILE:HD12	2.18	0.43
1:Z:236:LYS:HB3	1:a:225:THR:HG21	2.00	0.43
1:b:180:LEU:HD12	1:b:185:ALA:HA	1.99	0.43
1:c:295:SER:HB2	1:c:365:ASN:HD22	1.83	0.43
1:d:280:GLU:HG3	1:d:372:ILE:HG12	1.99	0.43
1:e:426:ARG:NH2	1:e:428:ASP:OD2	2.50	0.43
1:D:389:VAL:HB	1:D:432:VAL:HG22	2.00	0.43
1:E:147:LEU:O	1:E:149:PRO:HD2	2.19	0.43
1:H:416:THR:HG23	1:H:430:LEU:HD21	2.00	0.43
1:L:393:TYR:CE2	1:L:436:PRO:HD3	2.54	0.43
1:N:154:ARG:HB3	1:N:177:THR:HG23	2.01	0.43
1:P:385:LEU:N	1:P:428:ASP:OD1	2.42	0.43
1:P:412:ILE:O	1:P:416:THR:HG23	2.18	0.43
1:T:266:VAL:HG22	1:T:387:VAL:HG22	2.00	0.43
1:X:186:LEU:HD12	1:X:186:LEU:H	1.84	0.43
1:A:302:GLU:HG3	1:A:358:THR:HG22	1.99	0.43
1:D:219:LEU:HD21	1:D:224:ASN:HD21	1.83	0.43
1:F:180:LEU:HD12	1:F:185:ALA:HA	1.99	0.43
1:G:187:ASP:OD2	1:H:207:PRO:HG2	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:373:ARG:NH2	1:I:275:LYS:HE2	2.34	0.43
1:I:141:ALA:O	1:I:145:GLU:HG3	2.18	0.43
1:S:373:ARG:NH2	1:T:275:LYS:HE2	2.34	0.43
1:S:393:TYR:CE2	1:S:436:PRO:HD3	2.54	0.43
1:T:141:ALA:O	1:T:145:GLU:HG3	2.19	0.43
1:U:412:ILE:O	1:U:416:THR:HG22	2.17	0.43
1:V:392:ASN:OD1	1:V:393:TYR:N	2.50	0.43
1:Z:154:ARG:HB3	1:Z:177:THR:OG1	2.19	0.43
1:a:385:LEU:N	1:a:428:ASP:OD1	2.42	0.43
1:b:143:THR:HG21	1:c:156:HIS:CE1	2.54	0.43
1:A:404:LEU:H	1:A:434:ASN:ND2	2.16	0.43
1:C:136:LEU:HD11	1:C:157:LEU:HD22	2.01	0.43
1:H:300:ILE:HG12	1:H:360:ARG:HG3	1.99	0.43
1:J:412:ILE:O	1:J:416:THR:HG22	2.19	0.43
1:K:237:PHE:HD1	1:L:232:ASP:HB3	1.83	0.43
1:L:160:PRO:HD2	1:L:171:SER:O	2.18	0.43
1:M:280:GLU:HG3	1:M:372:ILE:HG12	2.00	0.43
1:O:147:LEU:O	1:O:149:PRO:HD2	2.18	0.43
1:P:147:LEU:O	1:P:149:PRO:HD2	2.19	0.43
1:U:228:ARG:O	1:U:230:LEU:N	2.51	0.43
1:b:137:GLU:HA	1:b:140:LEU:CD2	2.48	0.43
1:c:172:PRO:O	1:c:209:ASN:ND2	2.52	0.43
1:e:192:SER:HA	1:e:195:VAL:HB	1.99	0.43
1:e:212:LEU:HD23	1:e:212:LEU:HA	1.83	0.43
1:B:280:GLU:HG3	1:B:372:ILE:HG12	2.00	0.43
1:F:228:ARG:HB2	1:F:231:ASN:ND2	2.34	0.43
1:G:360:ARG:NH1	1:G:362:GLU:OE1	2.50	0.43
1:I:145:GLU:HG2	1:I:153:ALA:H	1.84	0.43
1:O:211:THR:OG1	1:O:224:ASN:ND2	2.51	0.43
1:b:393:TYR:CE2	1:b:436:PRO:HD3	2.54	0.43
1:c:144:ILE:O	1:c:150:VAL:HG11	2.18	0.43
1:f:141:ALA:O	1:f:145:GLU:HG3	2.18	0.43
1:f:394:LYS:O	1:f:402:LEU:N	2.52	0.43
1:g:293:LEU:HD11	1:g:296:ARG:HH11	1.83	0.43
1:g:300:ILE:HG12	1:g:360:ARG:HG3	2.00	0.43
1:F:212:LEU:HG	1:F:221:THR:OG1	2.18	0.43
1:F:418:GLU:HG3	1:G:431:ASN:HB2	2.00	0.43
1:H:421:GLY:O	1:H:426:ARG:NH2	2.52	0.43
1:J:157:LEU:HD13	1:J:174:ALA:HB2	2.00	0.43
1:L:228:ARG:C	1:L:230:LEU:H	2.26	0.43
1:M:394:LYS:O	1:M:402:LEU:N	2.52	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:P:191:ILE:O	1:P:194:VAL:HG22	2.18	0.43
1:Q:137:GLU:HA	1:Q:140:LEU:CD2	2.48	0.43
1:R:158:ALA:O	1:R:159:MET:HE2	2.19	0.43
1:R:226:SER:HA	1:R:229:ASP:HB2	2.00	0.43
1:T:190:GLN:HG3	1:U:217:GLY:HA3	2.01	0.43
1:Z:373:ARG:HH21	1:a:275:LYS:NZ	2.17	0.43
1:e:149:PRO:HB3	1:e:184:ARG:HG2	2.01	0.43
1:f:412:ILE:O	1:f:416:THR:HG22	2.19	0.43
1:g:393:TYR:CE2	1:g:436:PRO:HD3	2.54	0.43
1:B:373:ARG:NH2	1:C:275:LYS:HE2	2.34	0.43
1:D:219:LEU:HD11	1:D:224:ASN:ND2	2.31	0.43
1:F:191:ILE:HG23	1:F:212:LEU:HD21	2.00	0.43
1:I:266:VAL:HG22	1:I:387:VAL:HG22	2.01	0.43
1:L:415:LEU:HD11	1:M:433:VAL:HG21	2.00	0.43
1:N:194:VAL:O	1:N:198:VAL:HG22	2.19	0.43
1:X:404:LEU:H	1:X:434:ASN:ND2	2.17	0.43
1:b:373:ARG:NH2	1:c:275:LYS:HE2	2.34	0.43
1:c:187:ASP:N	1:c:190:GLN:HB3	2.34	0.43
1:d:151:LYS:HE2	1:d:180:LEU:O	2.19	0.43
1:f:159:MET:SD	1:f:172:PRO:HB3	2.59	0.43
1:H:151:LYS:HG2	1:H:179:THR:O	2.19	0.42
1:J:143:THR:HG22	1:L:154:ARG:CZ	2.49	0.42
1:J:221:THR:HG23	1:J:224:ASN:HB2	2.01	0.42
1:N:136:LEU:HD11	1:N:157:LEU:HD22	2.01	0.42
1:R:214:ASP:HB3	1:R:218:HIS:HB2	2.01	0.42
1:T:154:ARG:HB3	1:T:177:THR:CG2	2.47	0.42
1:U:140:LEU:O	1:U:144:ILE:HG12	2.18	0.42
1:W:293:LEU:HD13	1:W:296:ARG:HD2	2.01	0.42
1:Y:196:HIS:HA	1:Y:199:SER:OG	2.19	0.42
1:Y:360:ARG:NH1	1:Y:362:GLU:OE1	2.50	0.42
1:c:212:LEU:HB3	1:c:221:THR:HG23	2.00	0.42
1:G:132:TYR:CZ	1:G:136:LEU:HD11	2.53	0.42
1:H:280:GLU:HG3	1:H:372:ILE:HG12	2.00	0.42
1:J:302:GLU:HG3	1:J:358:THR:HG22	2.00	0.42
1:N:132:TYR:CZ	1:N:136:LEU:HD23	2.54	0.42
1:N:196:HIS:HA	1:N:199:SER:OG	2.19	0.42
1:d:373:ARG:NH2	1:e:275:LYS:HE2	2.34	0.42
1:e:228:ARG:HB3	1:e:231:ASN:CB	2.48	0.42
1:f:172:PRO:HG2	1:f:205:LEU:HA	2.00	0.42
1:A:228:ARG:C	1:A:230:LEU:H	2.28	0.42
1:A:266:VAL:HG22	1:A:387:VAL:HG22	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:144:ILE:HD11	1:C:197:LEU:CD1	2.41	0.42
1:F:421:GLY:O	1:F:426:ARG:NH2	2.52	0.42
1:G:147:LEU:O	1:G:149:PRO:HD2	2.19	0.42
1:K:404:LEU:H	1:K:434:ASN:ND2	2.18	0.42
1:S:127:SER:HA	1:S:130:VAL:HG12	2.00	0.42
1:Y:147:LEU:O	1:Y:149:PRO:HD2	2.19	0.42
1:Y:295:SER:OG	1:Y:365:ASN:ND2	2.38	0.42
1:Z:421:GLY:O	1:Z:426:ARG:NH2	2.53	0.42
1:a:149:PRO:HB3	1:a:184:ARG:NH1	2.34	0.42
1:E:214:ASP:CG	1:E:215:GLN:H	2.24	0.42
1:K:392:ASN:OD1	1:K:393:TYR:N	2.50	0.42
1:L:157:LEU:HD23	1:L:158:ALA:N	2.33	0.42
1:R:145:GLU:HG2	1:R:152:SER:HA	2.01	0.42
1:V:373:ARG:HH21	1:W:275:LYS:HE2	1.84	0.42
1:X:266:VAL:HG22	1:X:387:VAL:HG22	2.02	0.42
1:Y:300:ILE:HG12	1:Y:360:ARG:HG3	2.01	0.42
1:a:228:ARG:NH1	1:a:230:LEU:HB3	2.34	0.42
1:a:423:SER:OG	1:a:426:ARG:NE	2.48	0.42
1:b:254:SER:OG	1:b:255:PRO:HD3	2.19	0.42
1:c:140:LEU:HD11	1:c:155:VAL:HG11	2.00	0.42
1:C:138:GLY:O	1:C:142:ARG:HG3	2.20	0.42
1:F:136:LEU:HD11	1:F:157:LEU:HD13	2.02	0.42
1:P:173:SER:HA	1:P:209:ASN:HB3	2.01	0.42
1:P:229:ASP:HA	1:P:232:ASP:OD1	2.18	0.42
1:R:228:ARG:C	1:R:230:LEU:H	2.26	0.42
1:W:197:LEU:HD12	1:Y:175:SER:HB2	2.01	0.42
1:X:140:LEU:O	1:X:144:ILE:HG12	2.20	0.42
1:Y:133:GLN:O	1:Y:137:GLU:HG3	2.20	0.42
1:C:144:ILE:O	1:C:150:VAL:HG21	2.20	0.42
1:E:393:TYR:CE2	1:E:436:PRO:HD3	2.55	0.42
1:F:191:ILE:HG23	1:F:212:LEU:HD11	2.01	0.42
1:G:128:GLU:HB3	1:I:126:PHE:CD2	2.54	0.42
1:G:143:THR:HG21	1:I:156:HIS:CE1	2.53	0.42
1:G:158:ALA:O	1:G:159:MET:HE2	2.20	0.42
1:L:143:THR:HG22	1:N:154:ARG:CZ	2.49	0.42
1:Q:254:SER:OG	1:Q:255:PRO:HD3	2.20	0.42
1:S:150:VAL:HG22	1:S:178:VAL:HG23	2.01	0.42
1:U:250:GLU:O	1:U:254:SER:OG	2.28	0.42
1:a:426:ARG:NH2	1:a:428:ASP:OD2	2.53	0.42
1:c:147:LEU:O	1:c:149:PRO:HD2	2.19	0.42
1:g:404:LEU:H	1:g:434:ASN:ND2	2.17	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:187:ASP:O	1:F:191:ILE:HG12	2.19	0.42
1:F:360:ARG:NH1	1:F:362:GLU:OE1	2.49	0.42
1:G:421:GLY:O	1:G:426:ARG:NH2	2.52	0.42
1:J:198:VAL:HG21	1:J:210:VAL:HG21	2.01	0.42
1:J:228:ARG:O	1:J:230:LEU:N	2.52	0.42
1:K:415:LEU:HD11	1:L:433:VAL:HG21	2.01	0.42
1:b:141:ALA:O	1:b:145:GLU:HG3	2.19	0.42
1:b:293:LEU:HD13	1:b:296:ARG:HD2	2.02	0.42
1:c:405:THR:OG1	1:c:407:ASP:OD1	2.30	0.42
1:A:228:ARG:CZ	1:A:228:ARG:HB2	2.50	0.42
1:C:387:VAL:HG21	1:C:420:MET:HG2	2.01	0.42
1:D:373:ARG:HH21	1:E:275:LYS:NZ	2.17	0.42
1:F:141:ALA:O	1:F:145:GLU:HG3	2.19	0.42
1:F:151:LYS:N	1:F:179:THR:O	2.42	0.42
1:G:172:PRO:O	1:G:209:ASN:ND2	2.52	0.42
1:H:149:PRO:HB3	1:H:184:ARG:HG2	2.01	0.42
1:H:199:SER:HA	1:H:205:LEU:CD2	2.50	0.42
1:H:426:ARG:NH2	1:H:428:ASP:OD2	2.52	0.42
1:M:300:ILE:HG12	1:M:360:ARG:HG3	2.01	0.42
1:R:147:LEU:O	1:R:149:PRO:HD2	2.20	0.42
1:V:293:LEU:HD13	1:V:296:ARG:HD2	2.02	0.42
1:Y:149:PRO:HB3	1:Y:184:ARG:HG2	2.02	0.42
1:Y:186:LEU:H	1:Y:186:LEU:HD12	1.85	0.42
1:Z:267:THR:HG22	1:Z:386:SER:HB2	2.01	0.42
1:D:140:LEU:O	1:D:144:ILE:HG12	2.20	0.42
1:G:300:ILE:HG12	1:G:360:ARG:HG3	2.00	0.42
1:J:136:LEU:HD12	1:J:140:LEU:HD23	2.02	0.42
1:J:142:ARG:O	1:J:146:THR:HG23	2.20	0.42
1:J:421:GLY:O	1:J:426:ARG:NH2	2.53	0.42
1:K:293:LEU:HD13	1:K:296:ARG:HD2	2.02	0.42
1:L:237:PHE:CD1	1:M:232:ASP:HB3	2.55	0.42
1:Q:393:TYR:CE2	1:Q:436:PRO:HD3	2.55	0.42
1:T:418:GLU:HG3	1:U:431:ASN:HB2	2.02	0.42
1:W:145:GLU:HA	1:W:150:VAL:HG12	2.02	0.42
1:W:203:ALA:HB1	1:Y:160:PRO:HG3	2.02	0.42
1:W:300:ILE:HG12	1:W:360:ARG:HG3	2.01	0.42
1:Y:191:ILE:O	1:Y:194:VAL:HG22	2.20	0.42
1:b:186:LEU:HG	1:b:191:ILE:HD13	2.01	0.42
1:d:213:VAL:HG13	1:d:217:GLY:O	2.20	0.42
1:f:159:MET:HE3	1:f:159:MET:HA	2.01	0.42
1:f:302:GLU:HG3	1:f:358:THR:HG22	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:154:ARG:CZ	1:f:143:THR:HG22	2.50	0.42
1:B:404:LEU:H	1:B:434:ASN:ND2	2.14	0.42
1:D:250:GLU:O	1:D:254:SER:OG	2.31	0.42
1:L:266:VAL:HG22	1:L:387:VAL:HG22	2.01	0.42
1:M:212:LEU:HD23	1:M:220:LEU:HB2	2.02	0.42
1:N:237:PHE:HD1	1:O:232:ASP:HB3	1.85	0.42
1:O:147:LEU:HB3	1:O:150:VAL:HG11	2.01	0.42
1:Q:267:THR:HG23	1:Q:386:SER:HB2	2.02	0.42
1:W:143:THR:HG22	1:Y:154:ARG:CZ	2.49	0.42
1:X:202:VAL:CG1	1:X:205:LEU:HD22	2.50	0.42
1:a:214:ASP:HB3	1:a:218:HIS:HB2	2.02	0.42
1:b:421:GLY:O	1:b:426:ARG:NH2	2.53	0.42
1:e:172:PRO:HG2	1:e:205:LEU:HA	2.02	0.42
1:e:180:LEU:HD21	1:e:214:ASP:OD1	2.19	0.42
1:C:147:LEU:O	1:C:149:PRO:HD2	2.20	0.41
1:G:155:VAL:HG23	1:G:176:VAL:HG22	2.02	0.41
1:G:293:LEU:HD13	1:G:296:ARG:HD2	2.02	0.41
1:H:179:THR:HA	1:H:215:GLN:HB3	2.02	0.41
1:O:190:GLN:HG3	1:Q:217:GLY:HA3	2.02	0.41
1:R:360:ARG:NH1	1:R:362:GLU:OE1	2.52	0.41
1:S:228:ARG:HG2	1:S:230:LEU:HB3	2.02	0.41
1:F:144:ILE:O	1:F:150:VAL:HG11	2.20	0.41
1:F:254:SER:OG	1:F:255:PRO:HD3	2.19	0.41
1:H:127:SER:O	1:H:130:VAL:HG12	2.19	0.41
1:J:360:ARG:NH1	1:J:362:GLU:OE1	2.52	0.41
1:L:212:LEU:HD12	1:L:220:LEU:HB2	2.00	0.41
1:R:191:ILE:HG23	1:R:212:LEU:HG	2.02	0.41
1:T:140:LEU:O	1:T:144:ILE:HG12	2.21	0.41
1:U:302:GLU:HG3	1:U:358:THR:HG22	2.02	0.41
1:V:300:ILE:HG12	1:V:360:ARG:HG3	2.01	0.41
1:e:145:GLU:HG2	1:e:153:ALA:H	1.85	0.41
1:F:373:ARG:NH2	1:G:275:LYS:HE2	2.35	0.41
1:I:211:THR:HA	1:I:221:THR:HG21	2.02	0.41
1:L:300:ILE:HG12	1:L:360:ARG:HG3	2.02	0.41
1:M:417:ARG:HG3	1:M:422:PHE:CB	2.51	0.41
1:V:237:PHE:HD1	1:W:232:ASP:HB3	1.85	0.41
1:W:266:VAL:HG22	1:W:387:VAL:HG22	2.02	0.41
1:X:373:ARG:NH2	1:Y:275:LYS:HE2	2.34	0.41
1:b:144:ILE:O	1:b:150:VAL:HG11	2.20	0.41
1:d:159:MET:HA	1:d:160:PRO:HD3	1.86	0.41
1:F:132:TYR:CZ	1:F:136:LEU:HD23	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:186:LEU:HG	1:F:191:ILE:CD1	2.50	0.41
1:G:141:ALA:HA	1:G:144:ILE:HG12	2.02	0.41
1:G:145:GLU:O	1:G:150:VAL:HG13	2.20	0.41
1:J:177:THR:HA	1:J:213:VAL:O	2.21	0.41
1:P:186:LEU:H	1:P:186:LEU:HD22	1.84	0.41
1:P:393:TYR:CE2	1:P:436:PRO:HD3	2.55	0.41
1:V:293:LEU:HD11	1:V:296:ARG:HH11	1.84	0.41
1:X:219:LEU:O	1:X:219:LEU:HG	2.20	0.41
1:a:147:LEU:HD21	1:a:194:VAL:HG12	2.01	0.41
1:b:132:TYR:CZ	1:b:136:LEU:HD23	2.55	0.41
1:f:177:THR:HA	1:f:213:VAL:O	2.20	0.41
1:f:404:LEU:H	1:f:434:ASN:ND2	2.16	0.41
1:B:300:ILE:HG12	1:B:360:ARG:HG3	2.01	0.41
1:D:144:ILE:O	1:D:150:VAL:HG11	2.20	0.41
1:E:198:VAL:O	1:E:202:VAL:HG22	2.20	0.41
1:H:423:SER:HG	1:H:426:ARG:HE	1.68	0.41
1:J:211:THR:HG22	1:J:224:ASN:CB	2.51	0.41
1:J:211:THR:HA	1:J:221:THR:HG21	2.03	0.41
1:J:227:GLY:C	1:J:228:ARG:HD3	2.45	0.41
1:K:293:LEU:HD11	1:K:296:ARG:HH11	1.85	0.41
1:L:250:GLU:O	1:L:254:SER:OG	2.25	0.41
1:M:373:ARG:NH2	1:N:275:LYS:HE2	2.35	0.41
1:N:300:ILE:HG12	1:N:360:ARG:HG3	2.01	0.41
1:P:188:GLU:O	1:P:191:ILE:HG12	2.21	0.41
1:Q:373:ARG:NH2	1:R:275:LYS:HE2	2.35	0.41
1:Q:404:LEU:H	1:Q:434:ASN:ND2	2.15	0.41
1:U:421:GLY:O	1:U:426:ARG:NH2	2.53	0.41
1:Z:373:ARG:HH21	1:a:275:LYS:HE2	1.85	0.41
1:c:293:LEU:HD13	1:c:296:ARG:HD2	2.02	0.41
1:d:206:PRO:HD2	1:d:209:ASN:HD21	1.86	0.41
1:f:280:GLU:HG3	1:f:372:ILE:HG12	2.03	0.41
1:B:192:SER:O	1:B:195:VAL:HG12	2.21	0.41
1:C:271:ASP:OD1	1:C:383:GLU:HB2	2.20	0.41
1:E:155:VAL:HA	1:E:175:SER:O	2.21	0.41
1:F:393:TYR:CE2	1:F:436:PRO:HD3	2.56	0.41
1:T:186:LEU:HG	1:T:190:GLN:HB3	2.03	0.41
1:T:393:TYR:CE2	1:T:436:PRO:HD3	2.56	0.41
1:f:300:ILE:HG12	1:f:360:ARG:HG3	2.02	0.41
1:A:228:ARG:HH21	1:A:231:ASN:HB2	1.85	0.41
1:A:293:LEU:HD13	1:A:296:ARG:HD2	2.03	0.41
1:H:172:PRO:O	1:H:173:SER:HB2	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:140:LEU:O	1:I:144:ILE:HG12	2.21	0.41
1:L:247:ARG:HH21	1:M:219:LEU:CD2	2.34	0.41
1:M:415:LEU:HD11	1:N:433:VAL:HG21	2.02	0.41
1:T:145:GLU:HG2	1:T:153:ALA:N	2.35	0.41
1:T:180:LEU:HD11	1:T:214:ASP:OD1	2.21	0.41
1:U:227:GLY:C	1:U:228:ARG:HD3	2.46	0.41
1:X:141:ALA:O	1:X:145:GLU:HG3	2.21	0.41
1:Y:154:ARG:HB3	1:Y:177:THR:CG2	2.50	0.41
1:E:145:GLU:HG2	1:E:152:SER:HA	2.03	0.41
1:N:229:ASP:OD1	1:N:229:ASP:N	2.52	0.41
1:N:283:SER:HB2	1:N:369:ASP:HB2	2.03	0.41
1:R:138:GLY:O	1:R:142:ARG:HG3	2.21	0.41
1:V:404:LEU:H	1:V:434:ASN:ND2	2.19	0.41
1:X:179:THR:HA	1:X:215:GLN:CG	2.51	0.41
1:Y:144:ILE:O	1:Y:150:VAL:HG11	2.21	0.41
1:Z:203:ALA:HB1	1:b:160:PRO:HG3	2.03	0.41
1:e:141:ALA:O	1:e:145:GLU:HG3	2.21	0.41
1:A:175:SER:HB2	1:f:201:ALA:HB2	2.03	0.41
1:B:266:VAL:HG22	1:B:387:VAL:HG22	2.03	0.41
1:E:192:SER:O	1:E:195:VAL:HG12	2.20	0.41
1:H:293:LEU:HD13	1:H:296:ARG:HD2	2.02	0.41
1:I:193:ALA:HA	1:J:219:LEU:HB2	2.02	0.41
1:I:387:VAL:HG21	1:I:420:MET:HG2	2.01	0.41
1:J:172:PRO:HG2	1:J:205:LEU:HA	2.02	0.41
1:N:138:GLY:O	1:N:142:ARG:HG3	2.21	0.41
1:N:154:ARG:HB3	1:N:177:THR:CG2	2.50	0.41
1:P:149:PRO:HA	1:P:181:GLU:CD	2.46	0.41
1:Q:143:THR:HG21	1:R:156:HIS:CE1	2.56	0.41
1:R:187:ASP:OD2	1:S:207:PRO:HG2	2.20	0.41
1:T:267:THR:HG23	1:T:386:SER:HB2	2.03	0.41
1:T:378:ASN:ND2	1:T:381:ASP:OD2	2.54	0.41
1:U:147:LEU:O	1:U:149:PRO:HD2	2.21	0.41
1:U:360:ARG:NH1	1:U:362:GLU:OE1	2.52	0.41
1:W:393:TYR:CE2	1:W:436:PRO:HD3	2.56	0.41
1:Z:173:SER:HA	1:Z:205:LEU:HD13	2.02	0.41
1:a:147:LEU:O	1:a:149:PRO:HD2	2.21	0.41
1:a:149:PRO:HA	1:a:181:GLU:CD	2.46	0.41
1:a:214:ASP:CG	1:a:215:GLN:N	2.79	0.41
1:b:145:GLU:O	1:b:150:VAL:HG13	2.21	0.41
1:e:176:VAL:HB	1:e:212:LEU:CD2	2.51	0.41
1:e:418:GLU:HG3	1:f:431:ASN:HB2	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:f:227:GLY:C	1:f:228:ARG:HD3	2.46	0.41
1:A:125:GLN:CD	1:A:126:PHE:N	2.79	0.41
1:G:373:ARG:HH21	1:H:275:LYS:NZ	2.19	0.41
1:H:283:SER:HB2	1:H:369:ASP:HB2	2.03	0.41
1:I:142:ARG:O	1:I:146:THR:HG23	2.21	0.41
1:O:389:VAL:HB	1:O:432:VAL:HG22	2.02	0.41
1:Q:293:LEU:HD13	1:Q:296:ARG:HD2	2.03	0.41
1:T:159:MET:HE3	1:T:159:MET:HB3	1.96	0.41
1:W:125:GLN:CD	1:W:126:PHE:N	2.78	0.41
1:Y:154:ARG:HB3	1:Y:177:THR:HG23	2.03	0.41
1:d:149:PRO:O	1:d:180:LEU:HD13	2.21	0.41
1:f:140:LEU:O	1:f:144:ILE:HG12	2.19	0.41
1:A:228:ARG:O	1:A:230:LEU:HD23	2.21	0.40
1:B:140:LEU:O	1:B:144:ILE:HG12	2.21	0.40
1:C:229:ASP:OD1	1:C:229:ASP:N	2.54	0.40
1:D:247:ARG:NH2	1:E:219:LEU:HD22	2.36	0.40
1:L:228:ARG:HB3	1:L:231:ASN:CG	2.46	0.40
1:N:421:GLY:O	1:N:426:ARG:NH2	2.54	0.40
1:Q:141:ALA:O	1:Q:145:GLU:HG3	2.20	0.40
1:T:180:LEU:H	1:T:180:LEU:CD1	2.32	0.40
1:b:186:LEU:HG	1:b:191:ILE:CD1	2.51	0.40
1:e:421:GLY:O	1:e:426:ARG:NH2	2.54	0.40
1:A:142:ARG:O	1:A:146:THR:HG23	2.20	0.40
1:B:155:VAL:HG22	1:B:176:VAL:HG22	2.02	0.40
1:B:393:TYR:CE2	1:B:436:PRO:HD3	2.56	0.40
1:L:236:LYS:HE3	1:M:225:THR:HG23	2.03	0.40
1:M:393:TYR:CE2	1:M:436:PRO:HD3	2.56	0.40
1:N:144:ILE:O	1:N:150:VAL:HG11	2.20	0.40
1:N:173:SER:HA	1:N:205:LEU:HD13	2.04	0.40
1:O:373:ARG:HH21	1:P:275:LYS:HE2	1.87	0.40
1:S:137:GLU:HA	1:S:140:LEU:CD2	2.52	0.40
1:B:141:ALA:O	1:B:145:GLU:HG3	2.21	0.40
1:F:280:GLU:HG3	1:F:372:ILE:HG12	2.02	0.40
1:I:172:PRO:HG2	1:I:205:LEU:HA	2.03	0.40
1:I:228:ARG:HB3	1:I:231:ASN:CB	2.52	0.40
1:L:185:ALA:O	1:M:206:PRO:HB3	2.22	0.40
1:N:254:SER:OG	1:N:255:PRO:HD3	2.22	0.40
1:S:178:VAL:HG22	1:S:180:LEU:HD22	2.03	0.40
1:U:293:LEU:HD13	1:U:296:ARG:HD2	2.04	0.40
1:W:172:PRO:HG2	1:W:205:LEU:HA	2.03	0.40
1:Y:150:VAL:HA	1:Y:180:LEU:HA	2.04	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Y:293:LEU:HD13	1:Y:296:ARG:HD2	2.02	0.40
1:Z:186:LEU:HD12	1:Z:186:LEU:HA	1.87	0.40
1:d:149:PRO:O	1:d:180:LEU:HA	2.22	0.40
1:d:267:THR:HG23	1:d:386:SER:HB2	2.04	0.40
1:A:219:LEU:HD21	1:A:224:ASN:CB	2.52	0.40
1:F:293:LEU:HD13	1:F:296:ARG:HD2	2.03	0.40
1:M:175:SER:HA	1:M:211:THR:O	2.20	0.40
1:P:193:ALA:O	1:P:197:LEU:HD13	2.22	0.40
1:Q:280:GLU:HG3	1:Q:372:ILE:HG12	2.03	0.40
1:R:140:LEU:O	1:R:144:ILE:HG12	2.21	0.40
1:R:300:ILE:HG12	1:R:360:ARG:HG3	2.03	0.40
1:S:186:LEU:HD22	1:S:186:LEU:H	1.85	0.40
1:b:138:GLY:O	1:b:142:ARG:HG3	2.22	0.40
1:d:186:LEU:HD22	1:d:186:LEU:H	1.86	0.40
1:d:228:ARG:HD3	1:d:231:ASN:ND2	2.36	0.40
1:f:147:LEU:O	1:f:149:PRO:HD2	2.21	0.40
1:B:186:LEU:HD12	1:B:186:LEU:H	1.86	0.40
1:E:188:GLU:O	1:E:191:ILE:HG12	2.21	0.40
1:F:373:ARG:HH21	1:G:275:LYS:NZ	2.20	0.40
1:G:138:GLY:O	1:G:142:ARG:HG3	2.22	0.40
1:H:213:VAL:HG13	1:H:217:GLY:O	2.22	0.40
1:M:147:LEU:O	1:M:149:PRO:HD2	2.21	0.40
1:N:252:ILE:HD12	1:N:252:ILE:HA	1.96	0.40
1:O:254:SER:OG	1:O:255:PRO:HD3	2.21	0.40
1:Q:192:SER:HA	1:Q:195:VAL:CG1	2.50	0.40
1:S:213:VAL:HG13	1:S:217:GLY:O	2.22	0.40
1:V:254:SER:OG	1:V:255:PRO:HD3	2.22	0.40
1:Y:201:ALA:HB2	1:Z:175:SER:HB2	2.02	0.40
1:Y:284:PRO:O	1:Y:290:LYS:HE2	2.21	0.40
1:d:127:SER:O	1:d:131:ASN:ND2	2.55	0.40
1:d:212:LEU:HD22	1:d:220:LEU:HD12	2.04	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	239/560 (43%)	222 (93%)	15 (6%)	2 (1%)	16	47
1	B	239/560 (43%)	225 (94%)	12 (5%)	2 (1%)	16	47
1	C	239/560 (43%)	227 (95%)	11 (5%)	1 (0%)	30	61
1	D	239/560 (43%)	224 (94%)	12 (5%)	3 (1%)	9	35
1	E	239/560 (43%)	225 (94%)	12 (5%)	2 (1%)	16	47
1	F	239/560 (43%)	224 (94%)	13 (5%)	2 (1%)	16	47
1	G	239/560 (43%)	223 (93%)	14 (6%)	2 (1%)	16	47
1	H	239/560 (43%)	224 (94%)	13 (5%)	2 (1%)	16	47
1	I	239/560 (43%)	226 (95%)	12 (5%)	1 (0%)	30	61
1	J	239/560 (43%)	224 (94%)	12 (5%)	3 (1%)	9	35
1	K	149/560 (27%)	148 (99%)	1 (1%)	0	100	100
1	L	239/560 (43%)	222 (93%)	15 (6%)	2 (1%)	16	47
1	M	239/560 (43%)	226 (95%)	11 (5%)	2 (1%)	16	47
1	N	239/560 (43%)	225 (94%)	12 (5%)	2 (1%)	16	47
1	O	239/560 (43%)	223 (93%)	14 (6%)	2 (1%)	16	47
1	P	239/560 (43%)	225 (94%)	12 (5%)	2 (1%)	16	47
1	Q	239/560 (43%)	226 (95%)	11 (5%)	2 (1%)	16	47
1	R	239/560 (43%)	224 (94%)	13 (5%)	2 (1%)	16	47
1	S	239/560 (43%)	224 (94%)	14 (6%)	1 (0%)	30	61
1	T	239/560 (43%)	226 (95%)	12 (5%)	1 (0%)	30	61
1	U	239/560 (43%)	224 (94%)	12 (5%)	3 (1%)	9	35
1	V	149/560 (27%)	148 (99%)	1 (1%)	0	100	100
1	W	239/560 (43%)	221 (92%)	15 (6%)	3 (1%)	9	35
1	X	239/560 (43%)	227 (95%)	10 (4%)	2 (1%)	16	47
1	Y	239/560 (43%)	227 (95%)	11 (5%)	1 (0%)	30	61
1	Z	239/560 (43%)	226 (95%)	10 (4%)	3 (1%)	9	35
1	a	239/560 (43%)	225 (94%)	12 (5%)	2 (1%)	16	47
1	b	239/560 (43%)	226 (95%)	11 (5%)	2 (1%)	16	47
1	c	239/560 (43%)	225 (94%)	12 (5%)	2 (1%)	16	47
1	d	239/560 (43%)	224 (94%)	13 (5%)	2 (1%)	16	47

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	e	239/560 (43%)	227 (95%)	11 (5%)	1 (0%)	30	61
1	f	239/560 (43%)	224 (94%)	12 (5%)	3 (1%)	9	35
1	g	149/560 (27%)	148 (99%)	1 (1%)	0	100	100
All	All	7617/18480 (41%)	7185 (94%)	372 (5%)	60 (1%)	18	47

All (60) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	172	PRO
1	B	172	PRO
1	D	172	PRO
1	E	172	PRO
1	F	172	PRO
1	G	172	PRO
1	H	172	PRO
1	L	172	PRO
1	M	172	PRO
1	N	172	PRO
1	O	172	PRO
1	P	172	PRO
1	Q	172	PRO
1	R	172	PRO
1	W	172	PRO
1	X	172	PRO
1	Z	172	PRO
1	a	172	PRO
1	b	172	PRO
1	c	172	PRO
1	d	172	PRO
1	D	229	ASP
1	B	173	SER
1	E	173	SER
1	H	173	SER
1	J	228	ARG
1	M	173	SER
1	P	173	SER
1	S	173	SER
1	U	228	ARG
1	X	173	SER
1	a	173	SER
1	d	173	SER

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Mol	Chain	Res	Type
1	f	228	ARG
1	G	173	SER
1	R	173	SER
1	U	229	ASP
1	Y	173	SER
1	Z	229	ASP
1	c	173	SER
1	A	173	SER
1	C	173	SER
1	D	173	SER
1	F	173	SER
1	I	173	SER
1	J	173	SER
1	J	229	ASP
1	L	173	SER
1	N	173	SER
1	O	173	SER
1	Q	173	SER
1	T	173	SER
1	U	173	SER
1	W	173	SER
1	W	229	ASP
1	Z	173	SER
1	b	173	SER
1	e	173	SER
1	f	173	SER
1	f	229	ASP

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	213/467 (46%)	212 (100%)	1 (0%)	81	85
1	B	213/467 (46%)	211 (99%)	2 (1%)	70	80
1	C	213/467 (46%)	210 (99%)	3 (1%)	59	76

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	D	213/467 (46%)	211 (99%)	2 (1%)	70	80
1	E	213/467 (46%)	210 (99%)	3 (1%)	59	76
1	F	213/467 (46%)	211 (99%)	2 (1%)	70	80
1	G	213/467 (46%)	212 (100%)	1 (0%)	81	85
1	H	213/467 (46%)	211 (99%)	2 (1%)	70	80
1	I	213/467 (46%)	212 (100%)	1 (0%)	81	85
1	J	213/467 (46%)	212 (100%)	1 (0%)	81	85
1	K	137/467 (29%)	137 (100%)	0	100	100
1	L	213/467 (46%)	210 (99%)	3 (1%)	59	76
1	M	213/467 (46%)	211 (99%)	2 (1%)	70	80
1	N	213/467 (46%)	211 (99%)	2 (1%)	70	80
1	O	213/467 (46%)	212 (100%)	1 (0%)	81	85
1	P	213/467 (46%)	210 (99%)	3 (1%)	59	76
1	Q	213/467 (46%)	210 (99%)	3 (1%)	59	76
1	R	213/467 (46%)	212 (100%)	1 (0%)	81	85
1	S	213/467 (46%)	212 (100%)	1 (0%)	81	85
1	T	213/467 (46%)	211 (99%)	2 (1%)	70	80
1	U	213/467 (46%)	211 (99%)	2 (1%)	70	80
1	V	137/467 (29%)	137 (100%)	0	100	100
1	W	213/467 (46%)	212 (100%)	1 (0%)	81	85
1	X	213/467 (46%)	211 (99%)	2 (1%)	70	80
1	Y	213/467 (46%)	211 (99%)	2 (1%)	70	80
1	Z	213/467 (46%)	211 (99%)	2 (1%)	70	80
1	a	213/467 (46%)	211 (99%)	2 (1%)	70	80
1	b	213/467 (46%)	211 (99%)	2 (1%)	70	80
1	c	213/467 (46%)	212 (100%)	1 (0%)	81	85
1	d	213/467 (46%)	211 (99%)	2 (1%)	70	80
1	e	213/467 (46%)	211 (99%)	2 (1%)	70	80
1	f	213/467 (46%)	211 (99%)	2 (1%)	70	80
1	g	137/467 (29%)	137 (100%)	0	100	100
All	All	6801/15411 (44%)	6745 (99%)	56 (1%)	70	81

All (56) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	172	PRO
1	B	172	PRO
1	B	405	THR
1	C	172	PRO
1	C	177	THR
1	C	197	LEU
1	D	172	PRO
1	D	225	THR
1	E	172	PRO
1	E	180	LEU
1	E	186	LEU
1	F	136	LEU
1	F	172	PRO
1	G	172	PRO
1	H	172	PRO
1	H	186	LEU
1	I	172	PRO
1	J	172	PRO
1	L	159	MET
1	L	172	PRO
1	L	194	VAL
1	M	172	PRO
1	M	180	LEU
1	N	147	LEU
1	N	172	PRO
1	O	172	PRO
1	P	172	PRO
1	P	180	LEU
1	P	186	LEU
1	Q	136	LEU
1	Q	172	PRO
1	Q	186	LEU
1	R	172	PRO
1	S	186	LEU
1	T	172	PRO
1	T	194	VAL
1	U	136	LEU
1	U	172	PRO
1	W	172	PRO
1	X	172	PRO
1	X	405	THR
1	Y	172	PRO

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Mol	Chain	Res	Type
1	Y	186	LEU
1	Z	172	PRO
1	Z	225	THR
1	a	172	PRO
1	a	180	LEU
1	b	136	LEU
1	b	172	PRO
1	c	172	PRO
1	d	172	PRO
1	d	186	LEU
1	e	172	PRO
1	e	180	LEU
1	f	172	PRO
1	f	186	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (274) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	131	ASN
1	A	133	GLN
1	A	196	HIS
1	A	231	ASN
1	A	274	ASN
1	A	281	HIS
1	A	365	ASN
1	A	431	ASN
1	A	434	ASN
1	B	125	GLN
1	B	222	GLN
1	B	224	ASN
1	B	231	ASN
1	B	281	HIS
1	B	299	ASN
1	B	365	ASN
1	B	431	ASN
1	B	434	ASN
1	C	125	GLN
1	C	133	GLN
1	C	274	ASN
1	C	277	GLN
1	C	281	HIS
1	C	361	ASN

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Mol	Chain	Res	Type
1	C	365	ASN
1	C	378	ASN
1	C	434	ASN
1	D	125	GLN
1	D	133	GLN
1	D	224	ASN
1	D	234	GLN
1	D	274	ASN
1	D	281	HIS
1	D	365	ASN
1	D	434	ASN
1	E	125	GLN
1	E	133	GLN
1	E	209	ASN
1	E	224	ASN
1	E	299	ASN
1	E	365	ASN
1	E	431	ASN
1	E	434	ASN
1	F	133	GLN
1	F	196	HIS
1	F	224	ASN
1	F	277	GLN
1	F	361	ASN
1	F	365	ASN
1	F	378	ASN
1	F	431	ASN
1	F	434	ASN
1	G	125	GLN
1	G	133	GLN
1	G	196	HIS
1	G	224	ASN
1	G	234	GLN
1	G	281	HIS
1	G	361	ASN
1	G	365	ASN
1	G	431	ASN
1	G	434	ASN
1	H	125	GLN
1	H	133	GLN
1	H	196	HIS
1	H	222	GLN

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Mol	Chain	Res	Type
1	H	224	ASN
1	H	299	ASN
1	H	378	ASN
1	H	431	ASN
1	H	434	ASN
1	I	125	GLN
1	I	133	GLN
1	I	222	GLN
1	I	234	GLN
1	I	281	HIS
1	I	299	ASN
1	I	361	ASN
1	I	365	ASN
1	I	378	ASN
1	I	431	ASN
1	I	434	ASN
1	J	131	ASN
1	J	133	GLN
1	J	218	HIS
1	J	234	GLN
1	J	299	ASN
1	J	365	ASN
1	J	431	ASN
1	J	434	ASN
1	K	274	ASN
1	K	281	HIS
1	K	361	ASN
1	K	365	ASN
1	K	431	ASN
1	K	434	ASN
1	L	131	ASN
1	L	133	GLN
1	L	196	HIS
1	L	224	ASN
1	L	274	ASN
1	L	365	ASN
1	L	434	ASN
1	M	125	GLN
1	M	133	GLN
1	M	196	HIS
1	M	215	GLN
1	M	281	HIS

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Mol	Chain	Res	Type
1	M	299	ASN
1	M	365	ASN
1	M	431	ASN
1	M	434	ASN
1	N	125	GLN
1	N	133	GLN
1	N	222	GLN
1	N	277	GLN
1	N	281	HIS
1	N	365	ASN
1	N	378	ASN
1	N	434	ASN
1	O	125	GLN
1	O	133	GLN
1	O	234	GLN
1	O	281	HIS
1	O	365	ASN
1	O	434	ASN
1	P	125	GLN
1	P	133	GLN
1	P	156	HIS
1	P	209	ASN
1	P	281	HIS
1	P	299	ASN
1	P	361	ASN
1	P	365	ASN
1	P	431	ASN
1	P	434	ASN
1	Q	133	GLN
1	Q	156	HIS
1	Q	224	ASN
1	Q	281	HIS
1	Q	365	ASN
1	Q	378	ASN
1	Q	431	ASN
1	Q	434	ASN
1	R	125	GLN
1	R	133	GLN
1	R	231	ASN
1	R	234	GLN
1	R	281	HIS
1	R	299	ASN

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Mol	Chain	Res	Type
1	R	365	ASN
1	R	378	ASN
1	R	431	ASN
1	R	434	ASN
1	S	125	GLN
1	S	133	GLN
1	S	196	HIS
1	S	234	GLN
1	S	277	GLN
1	S	281	HIS
1	S	299	ASN
1	S	365	ASN
1	S	431	ASN
1	S	434	ASN
1	T	133	GLN
1	T	224	ASN
1	T	281	HIS
1	T	299	ASN
1	T	365	ASN
1	T	431	ASN
1	T	434	ASN
1	U	133	GLN
1	U	218	HIS
1	U	224	ASN
1	U	231	ASN
1	U	365	ASN
1	U	431	ASN
1	U	434	ASN
1	V	274	ASN
1	V	281	HIS
1	V	299	ASN
1	V	361	ASN
1	V	365	ASN
1	V	434	ASN
1	W	131	ASN
1	W	133	GLN
1	W	196	HIS
1	W	224	ASN
1	W	281	HIS
1	W	299	ASN
1	W	378	ASN
1	W	431	ASN

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Mol	Chain	Res	Type
1	W	434	ASN
1	X	125	GLN
1	X	131	ASN
1	X	133	GLN
1	X	215	GLN
1	X	231	ASN
1	X	234	GLN
1	X	281	HIS
1	X	299	ASN
1	X	365	ASN
1	X	431	ASN
1	X	434	ASN
1	Y	125	GLN
1	Y	133	GLN
1	Y	274	ASN
1	Y	277	GLN
1	Y	281	HIS
1	Y	434	ASN
1	Z	125	GLN
1	Z	133	GLN
1	Z	281	HIS
1	Z	365	ASN
1	Z	434	ASN
1	a	125	GLN
1	a	131	ASN
1	a	209	ASN
1	a	281	HIS
1	a	299	ASN
1	a	361	ASN
1	a	365	ASN
1	a	434	ASN
1	b	133	GLN
1	b	224	ASN
1	b	277	GLN
1	b	281	HIS
1	b	365	ASN
1	b	378	ASN
1	b	431	ASN
1	b	434	ASN
1	c	125	GLN
1	c	133	GLN
1	c	224	ASN

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Mol	Chain	Res	Type
1	c	234	GLN
1	c	274	ASN
1	c	281	HIS
1	c	299	ASN
1	c	361	ASN
1	c	365	ASN
1	c	431	ASN
1	c	434	ASN
1	d	125	GLN
1	d	133	GLN
1	d	196	HIS
1	d	222	GLN
1	d	224	ASN
1	d	281	HIS
1	d	299	ASN
1	d	365	ASN
1	d	431	ASN
1	d	434	ASN
1	e	125	GLN
1	e	133	GLN
1	e	281	HIS
1	e	299	ASN
1	e	361	ASN
1	e	365	ASN
1	e	431	ASN
1	e	434	ASN
1	f	131	ASN
1	f	133	GLN
1	f	218	HIS
1	f	299	ASN
1	f	365	ASN
1	f	431	ASN
1	f	434	ASN
1	g	274	ASN
1	g	281	HIS
1	g	299	ASN
1	g	361	ASN
1	g	365	ASN
1	g	431	ASN
1	g	434	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

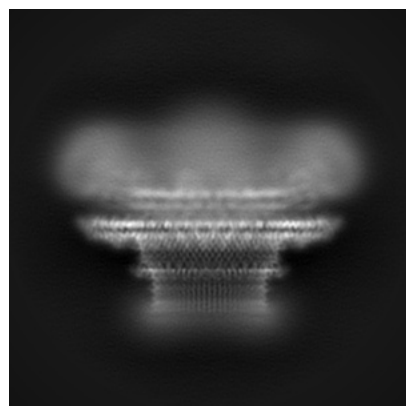
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-10143. These allow visual inspection of the internal detail of the map and identification of artifacts.

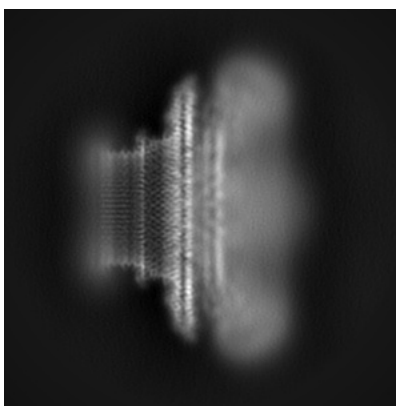
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

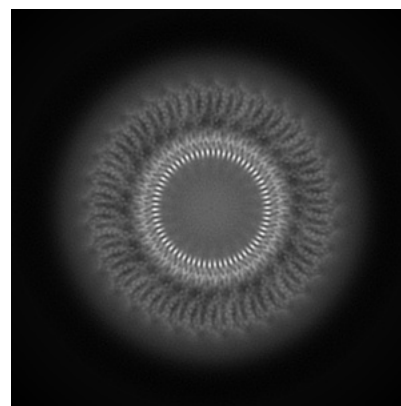
6.1.1 Primary map



X

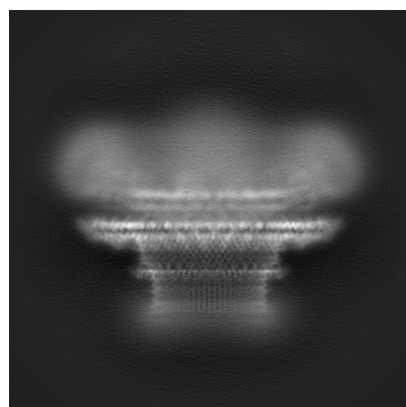


Y

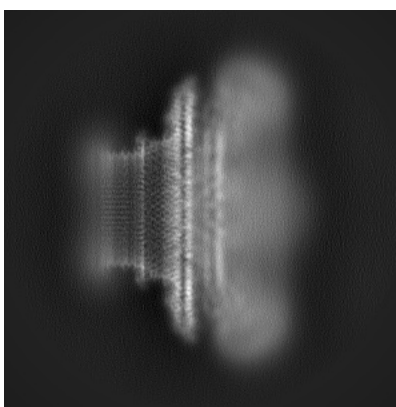


Z

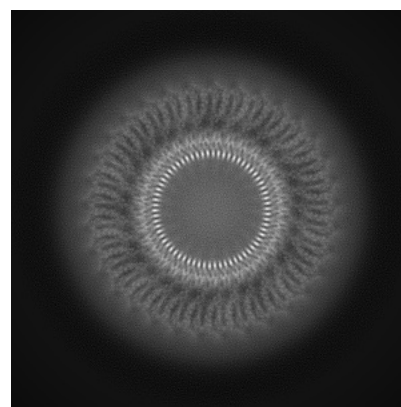
6.1.2 Raw map



X



Y

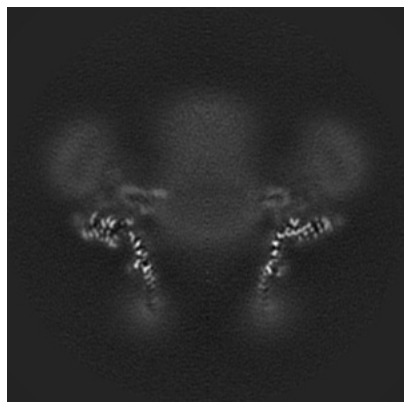


Z

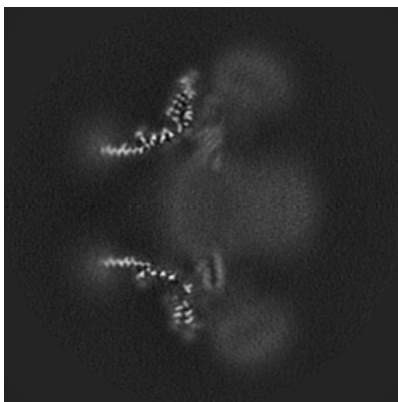
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

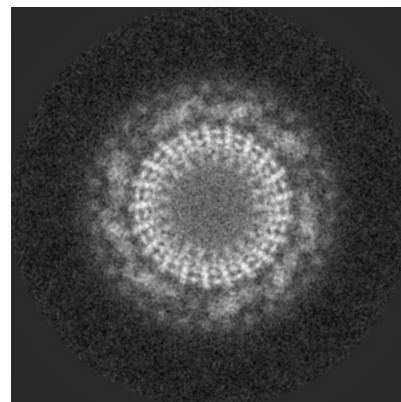
6.2.1 Primary map



X Index: 216

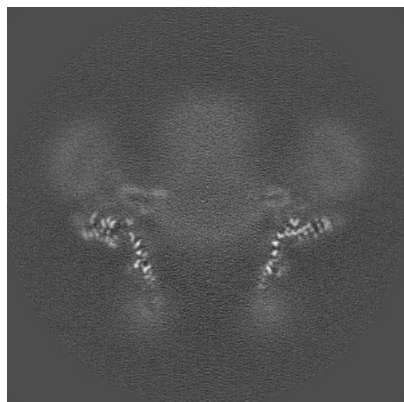


Y Index: 216

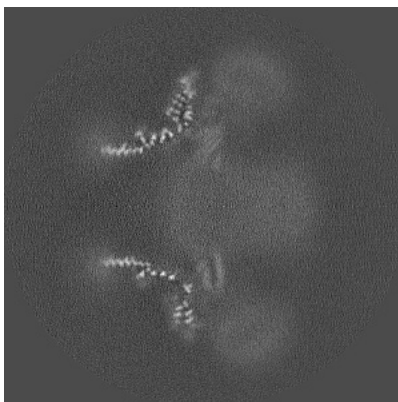


Z Index: 216

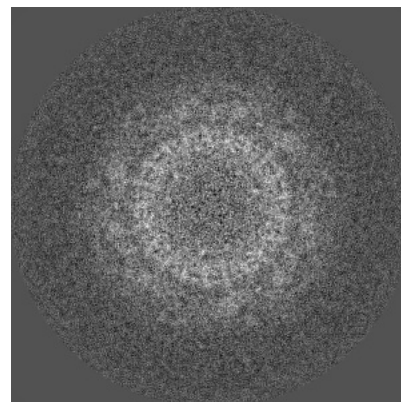
6.2.2 Raw map



X Index: 216



Y Index: 216

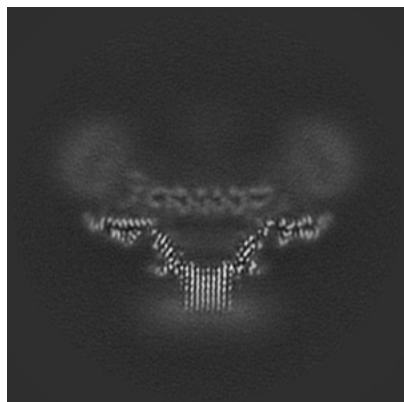


Z Index: 216

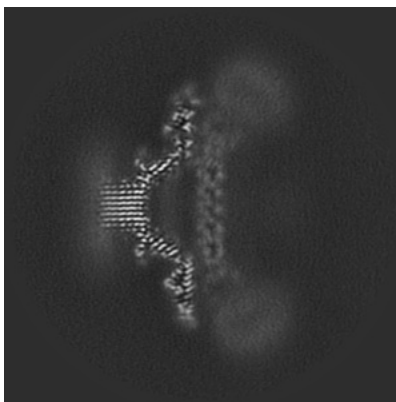
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

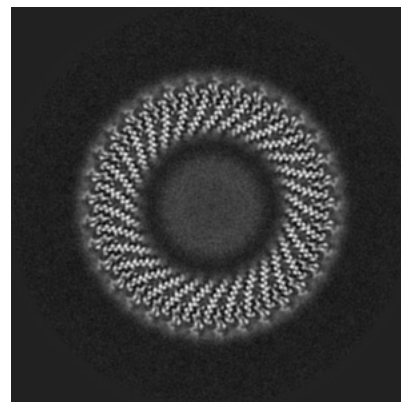
6.3.1 Primary map



X Index: 275

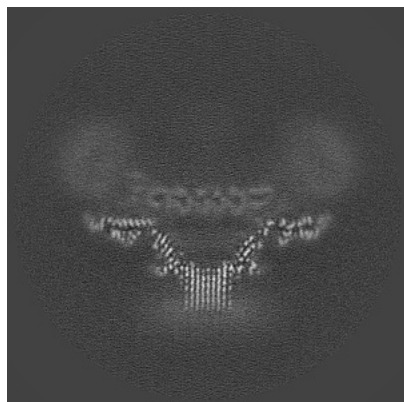


Y Index: 156

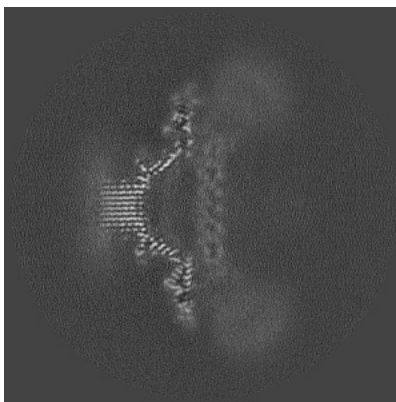


Z Index: 199

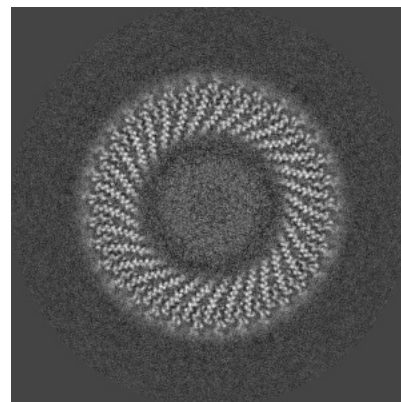
6.3.2 Raw map



X Index: 275



Y Index: 157

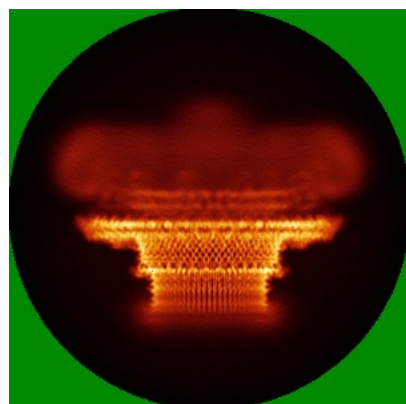


Z Index: 199

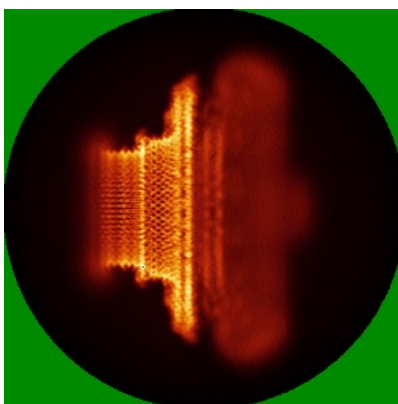
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) [i](#)

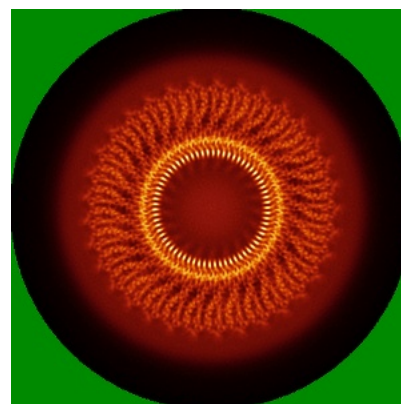
6.4.1 Primary map



X

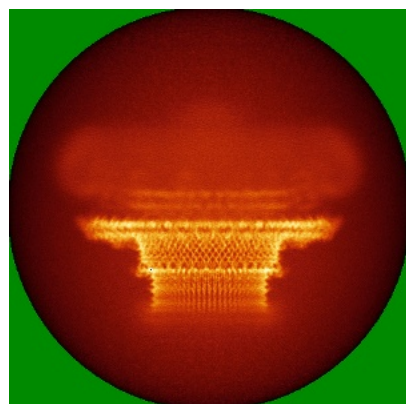


Y

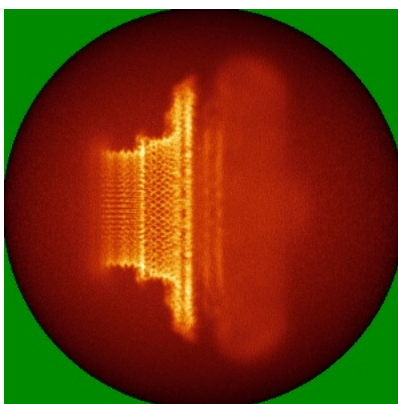


Z

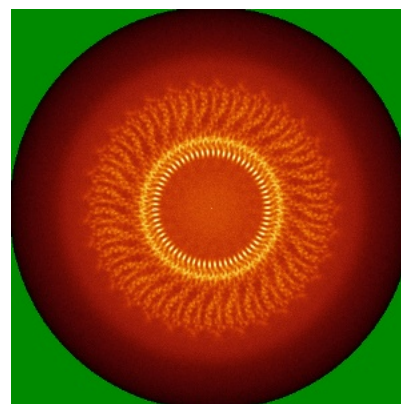
6.4.2 Raw map



X



Y

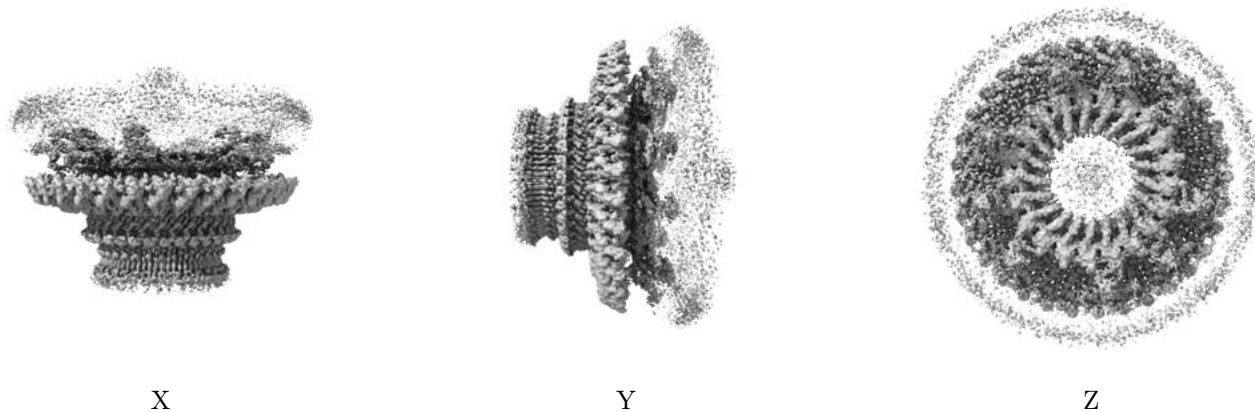


Z

The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

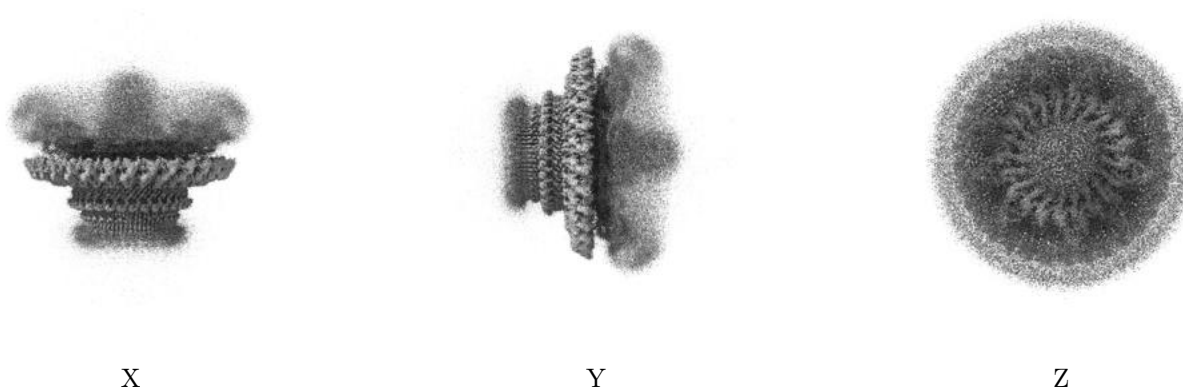
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.005. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

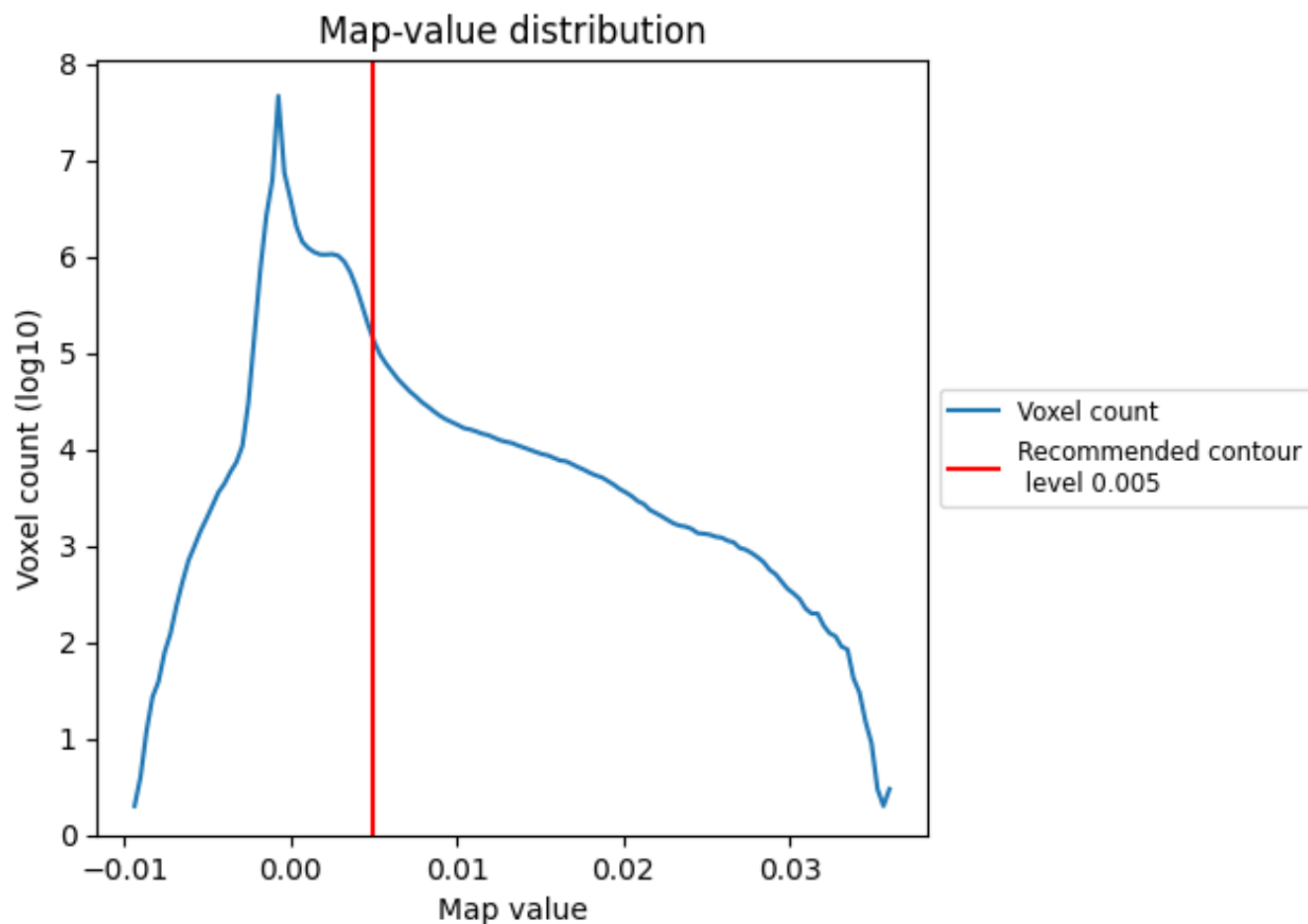
6.6 Mask visualisation [i](#)

This section was not generated. No masks/segmentation were deposited.

7 Map analysis [i](#)

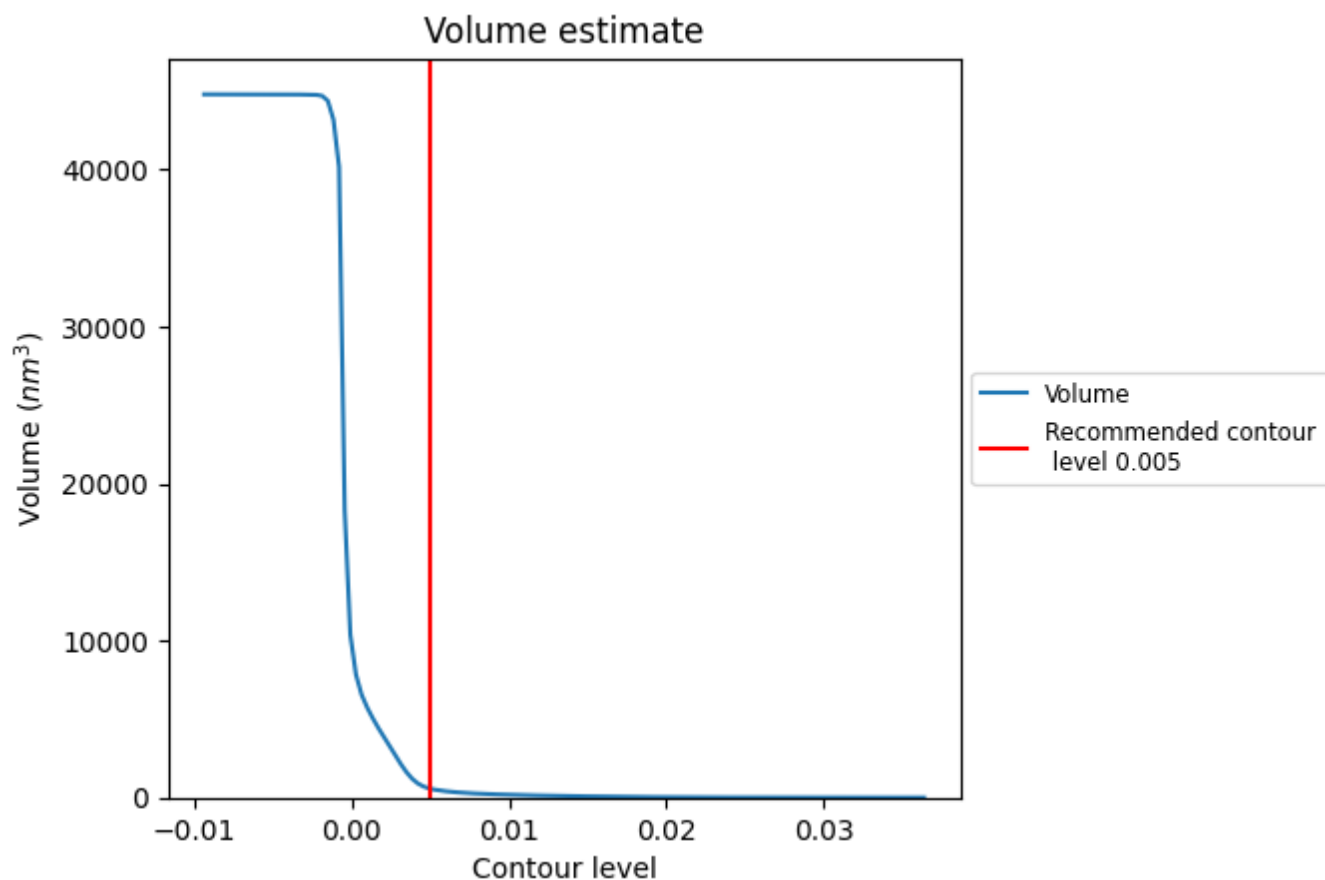
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

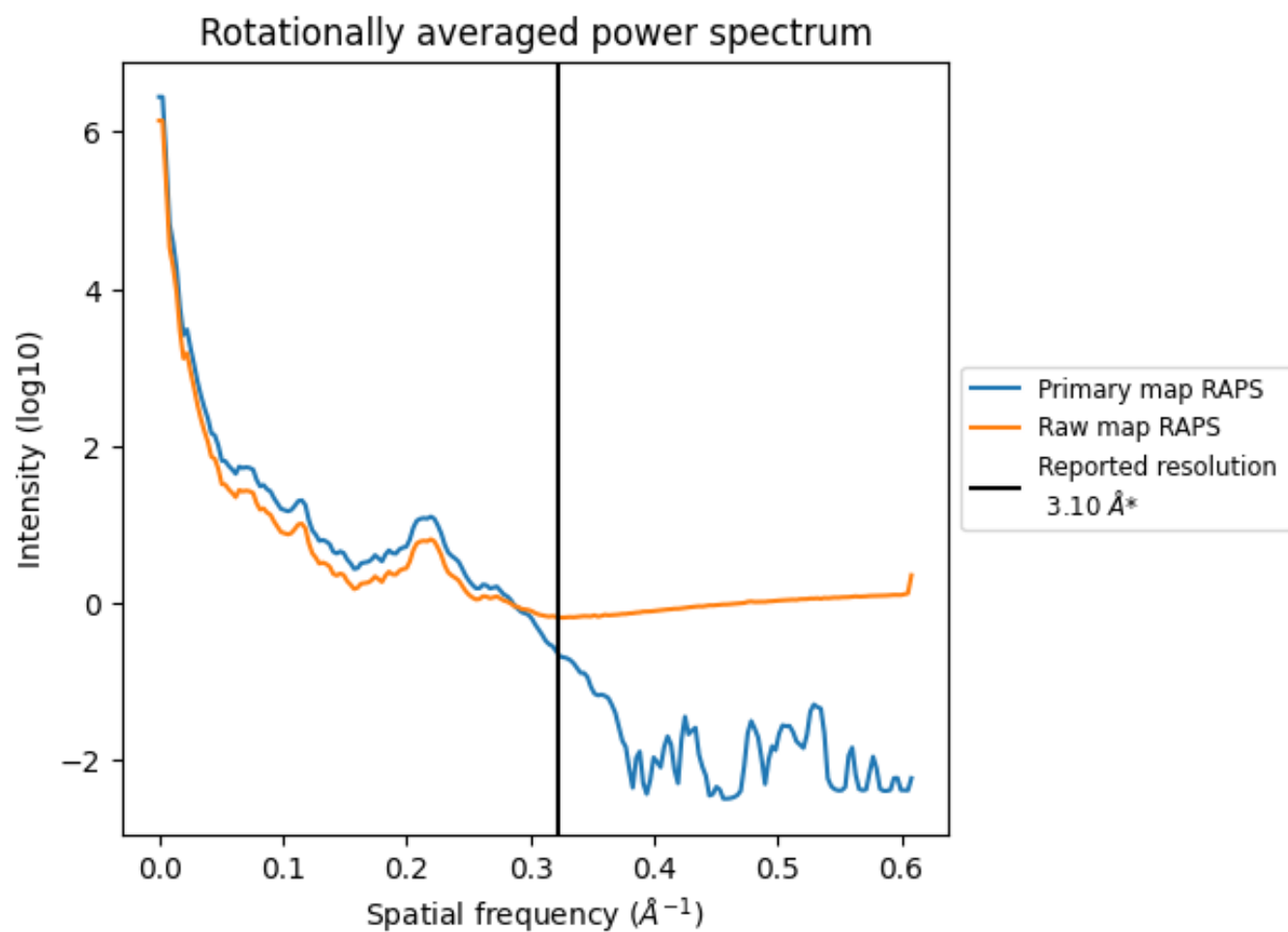
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 565 nm³; this corresponds to an approximate mass of 510 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum ⓘ

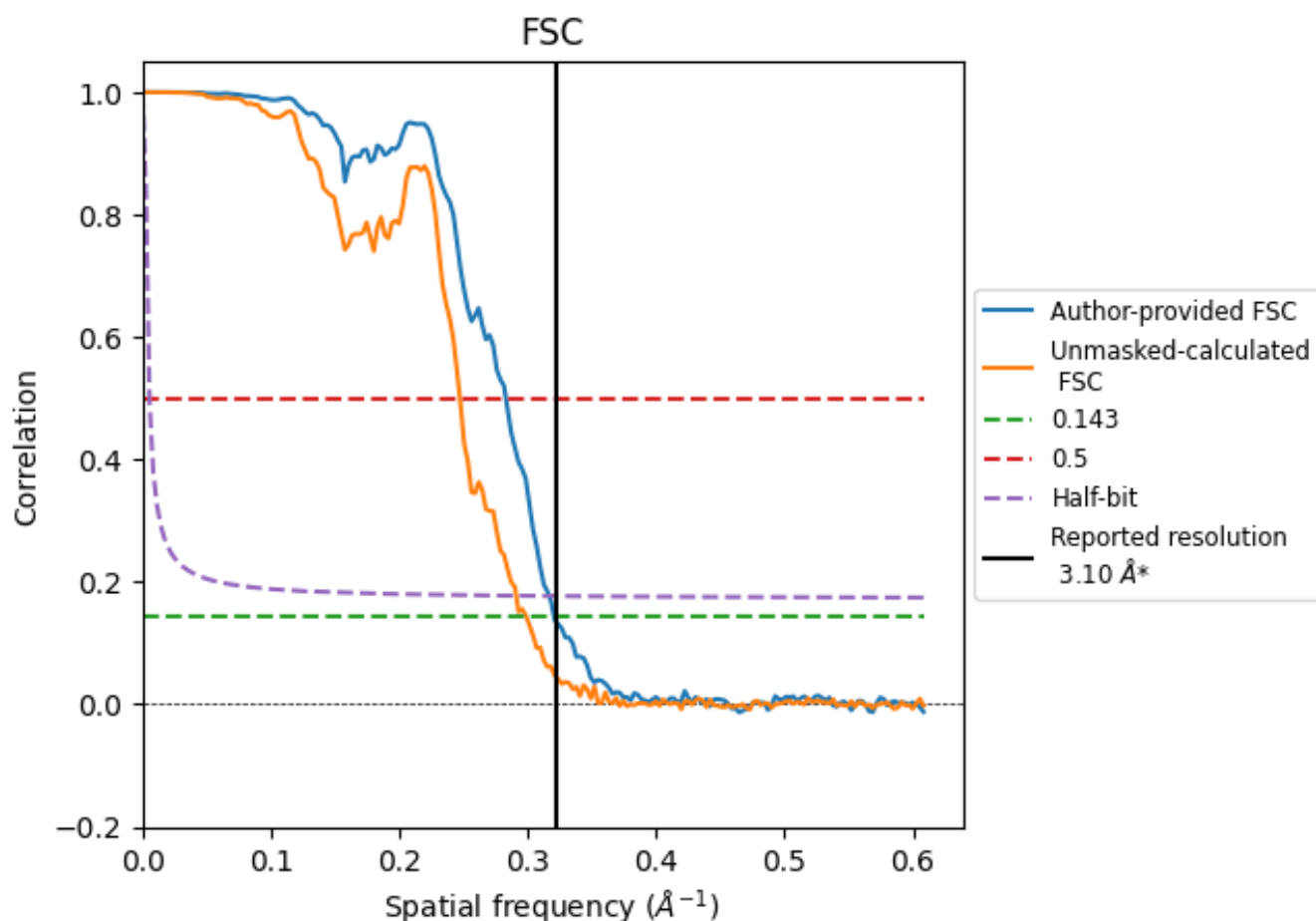


*Reported resolution corresponds to spatial frequency of 0.323 Å⁻¹

8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.323 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

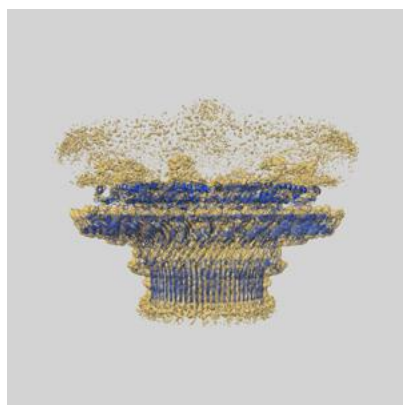
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.10	-	-
Author-provided FSC curve	3.12	3.53	3.16
Unmasked-calculated*	3.35	4.04	3.44

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

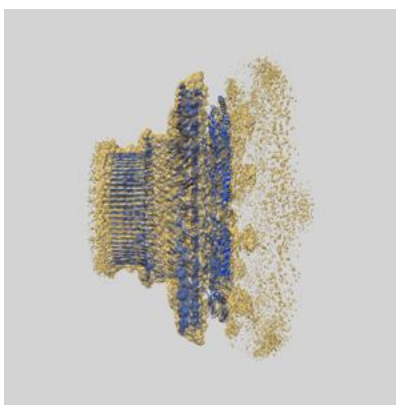
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-10143 and PDB model 6SCN. Per-residue inclusion information can be found in [section 3](#) on [page 7](#).

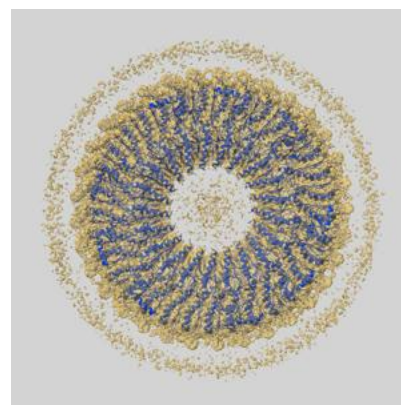
9.1 Map-model overlay [i](#)



X



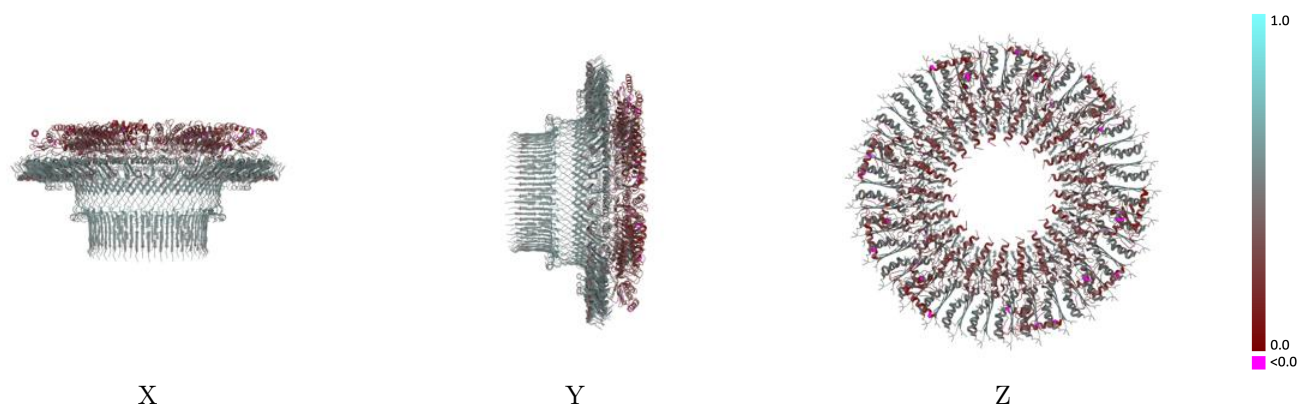
Y



Z

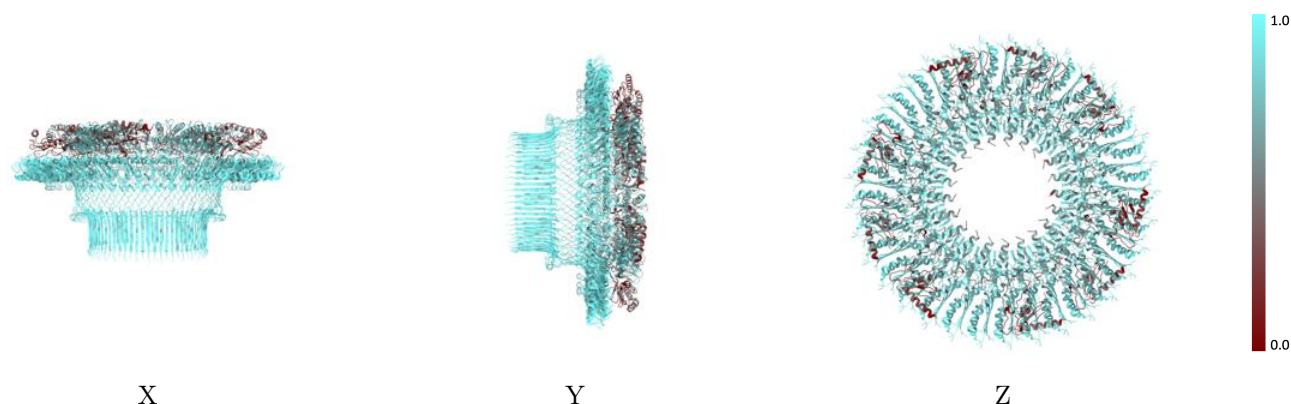
The images above show the 3D surface view of the map at the recommended contour level 0.005 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

9.2 Q-score mapped to coordinate model [i](#)



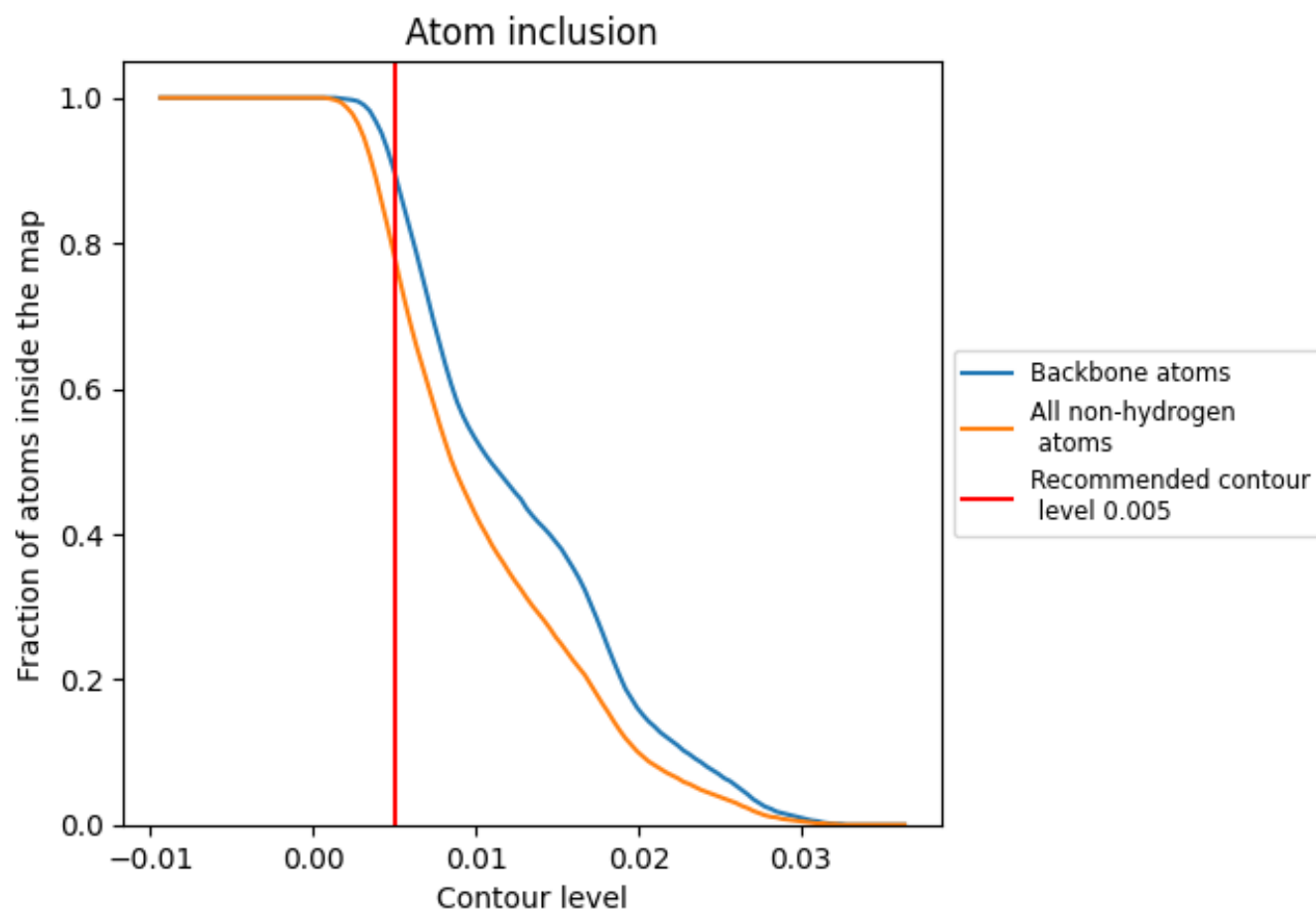
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

9.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.005).

9.4 Atom inclusion [i](#)



At the recommended contour level, 90% of all backbone atoms, 78% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (0.005) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7810	 0.4300
A	 0.8120	 0.4280
B	 0.6620	 0.3990
C	 0.8120	 0.4270
D	 0.8090	 0.4390
E	 0.6910	 0.4140
F	 0.8120	 0.4320
G	 0.8190	 0.4300
H	 0.6730	 0.4120
I	 0.8230	 0.4280
J	 0.8210	 0.4340
K	 0.9060	 0.5080
L	 0.8120	 0.4270
M	 0.6610	 0.4000
N	 0.8160	 0.4290
O	 0.8120	 0.4350
P	 0.6910	 0.4160
Q	 0.8120	 0.4340
R	 0.8200	 0.4330
S	 0.6710	 0.4150
T	 0.8190	 0.4300
U	 0.8250	 0.4360
V	 0.9080	 0.5080
W	 0.8110	 0.4280
X	 0.6590	 0.4040
Y	 0.8120	 0.4290
Z	 0.8120	 0.4390
a	 0.6890	 0.4150
b	 0.8110	 0.4320
c	 0.8190	 0.4330
d	 0.6720	 0.4130
e	 0.8180	 0.4280
f	 0.8210	 0.4330
g	 0.9060	 0.5090

