



Full wwPDB EM Validation Report ⓘ

Mar 20, 2026 – 11:11 AM UTC

PDB ID : 7B5H / pdb_00007b5h
EMDB ID : EMD-12029
Title : Cryo-EM structure of the contractile injection system base plate from Anabaena PCC7120
Authors : Eisenstein, F.; Weiss, G.L.; Pilhofer, M.
Deposited on : 2020-12-03
Resolution : 3.20 Å(reported)

This is a Full wwPDB EM Validation Report for a publicly released PDB entry.

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

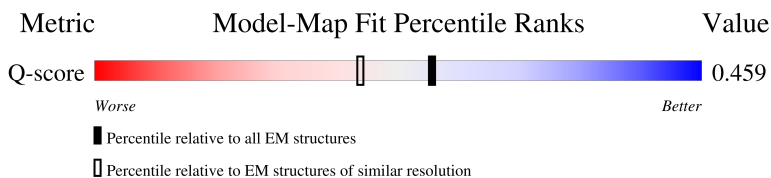
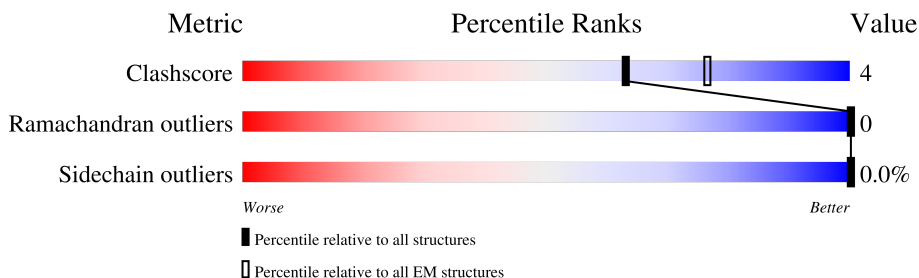
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.20 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.



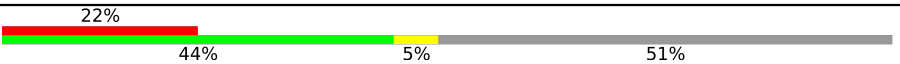
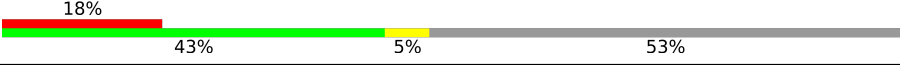
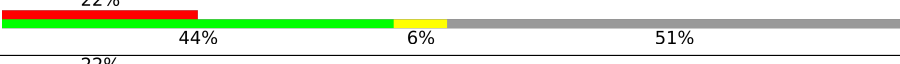
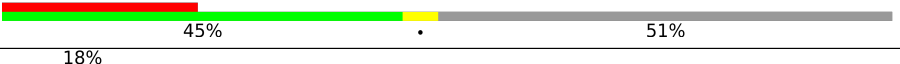
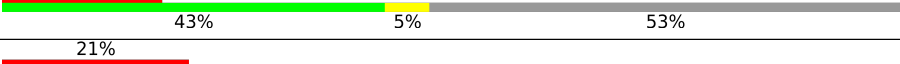
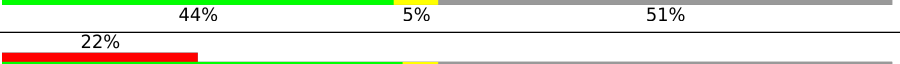
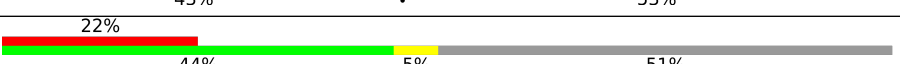
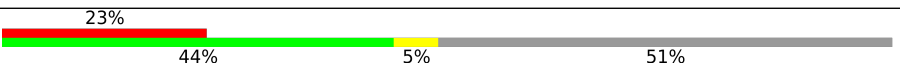
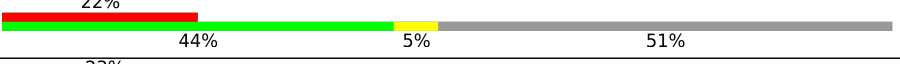
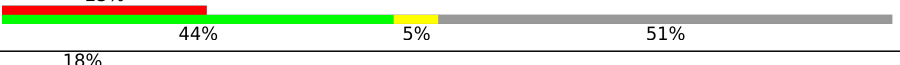
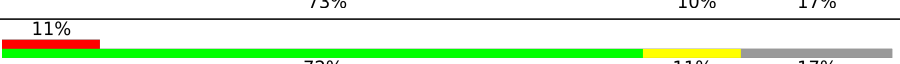
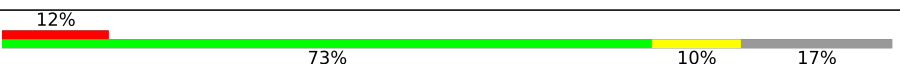
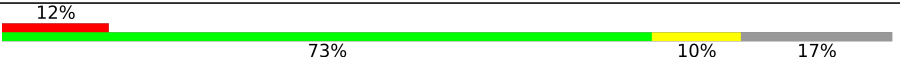
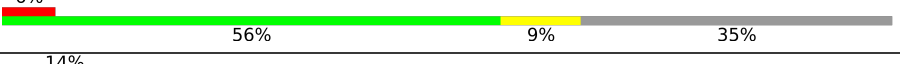
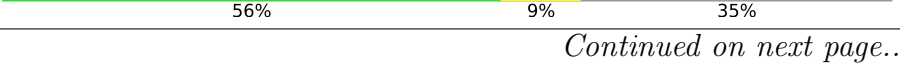
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	15020 (2.70 - 3.70)

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	AA	1476	22% 44% 5% 51%
1	AB	1476	22% 45% 5% 51%
1	AC	1476	18% 43% . 53%
1	BA	1476	22% 44% 5% 51%

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Mol	Chain	Length	Quality of chain
1	BB	1476	
1	BC	1476	
1	CA	1476	
1	CB	1476	
1	CC	1476	
1	DA	1476	
1	DB	1476	
1	DC	1476	
1	EA	1476	
1	EB	1476	
1	EC	1476	
1	FA	1476	
1	FB	1476	
1	FC	1476	
2	AD	1335	
2	BD	1335	
2	CD	1335	
2	DD	1335	
2	ED	1335	
2	FD	1335	
3	AE	154	
3	AF	154	
3	AG	154	
3	BE	154	
3	BF	154	

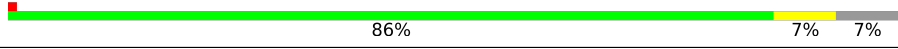
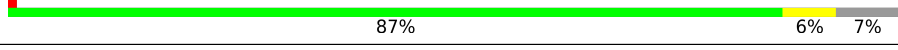
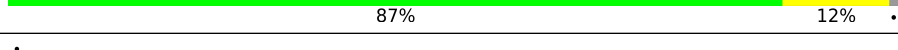
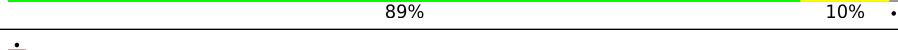
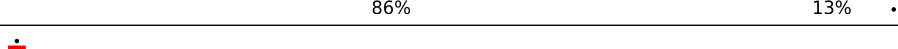
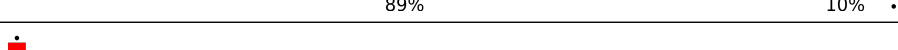
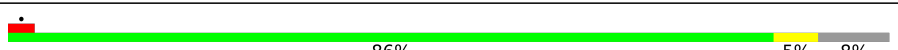
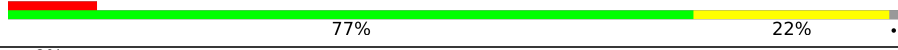
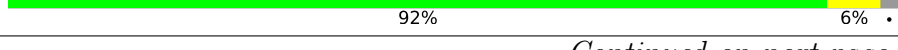
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Mol	Chain	Length	Quality of chain
3	BG	154	
3	CE	154	
3	CF	154	
3	CG	154	
3	DE	154	
3	DF	154	
3	DG	154	
3	EE	154	
3	EF	154	
3	EG	154	
3	FE	154	
3	FF	154	
3	FG	154	
4	AH	1231	
4	BH	1231	
4	CH	1231	
4	DH	1231	
4	EH	1231	
4	FH	1231	
5	AJ	589	
5	CJ	589	
5	EJ	589	
6	AL	50	
6	CL	50	
6	EL	50	

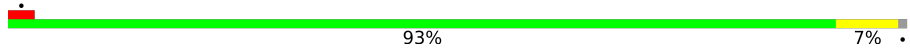
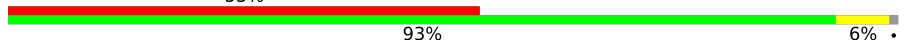
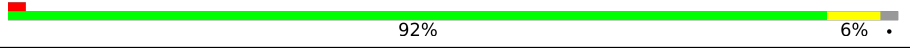
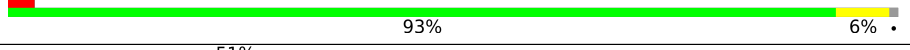
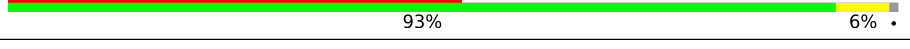
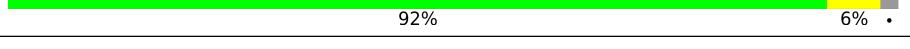
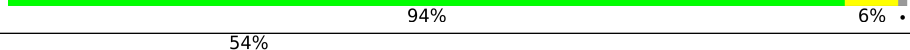
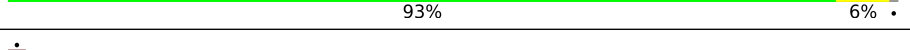
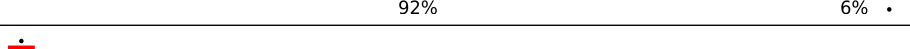
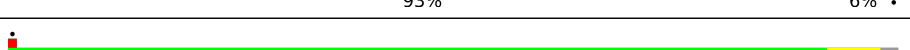
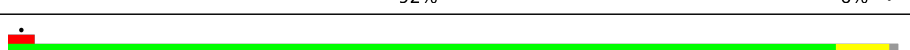
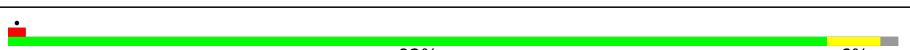
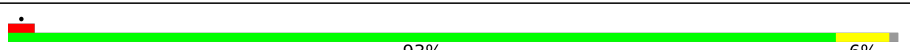
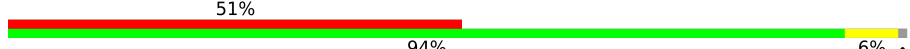
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Mol	Chain	Length	Quality of chain
7	AI	149	
7	BI	149	
7	CI	149	
7	DI	149	
7	EI	149	
7	FI	149	
8	AK	234	
8	BK	234	
8	CK	234	
8	DK	234	
8	EK	234	
8	FK	234	
9	AM	167	
9	BM	167	
9	CM	167	
9	DM	167	
9	EM	167	
9	FM	167	
10	AN	143	
10	BN	143	
10	CN	143	
10	DN	143	
10	EN	143	
10	FN	143	
11	AO	484	

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Mol	Chain	Length	Quality of chain
11	AP	484	
11	AQ	484	
11	BO	484	
11	BP	484	
11	BQ	484	
11	CO	484	
11	CP	484	
11	CQ	484	
11	DO	484	
11	DP	484	
11	DQ	484	
11	EO	484	
11	EP	484	
11	EQ	484	
11	FO	484	
11	FP	484	
11	FQ	484	

2 Entry composition [i](#)

There are 11 unique types of molecules in this entry. The entry contains 346635 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 All3314 protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	AA	729	Total	C	N	O	S	0	0
			5899	3784	991	1111	13		
1	AB	724	Total	C	N	O	S	0	0
			5886	3781	989	1103	13		
1	AC	700	Total	C	N	O	S	0	0
			5690	3659	957	1063	11		
1	BA	729	Total	C	N	O	S	0	0
			5899	3784	991	1111	13		
1	BB	724	Total	C	N	O	S	0	0
			5886	3781	989	1103	13		
1	BC	700	Total	C	N	O	S	0	0
			5690	3659	957	1063	11		
1	CA	729	Total	C	N	O	S	0	0
			5899	3784	991	1111	13		
1	CB	724	Total	C	N	O	S	0	0
			5886	3781	989	1103	13		
1	CC	700	Total	C	N	O	S	0	0
			5690	3659	957	1063	11		
1	DA	729	Total	C	N	O	S	0	0
			5899	3784	991	1111	13		
1	DB	724	Total	C	N	O	S	0	0
			5886	3781	989	1103	13		
1	DC	700	Total	C	N	O	S	0	0
			5690	3659	957	1063	11		
1	EA	729	Total	C	N	O	S	0	0
			5899	3784	991	1111	13		
1	EB	724	Total	C	N	O	S	0	0
			5886	3781	989	1103	13		
1	EC	700	Total	C	N	O	S	0	0
			5690	3659	957	1063	11		
1	FA	729	Total	C	N	O	S	0	0
			5899	3784	991	1111	13		
1	FB	724	Total	C	N	O	S	0	0
			5886	3781	989	1103	13		

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	FC	700	Total	C	N	O	S	0	0
			5690	3659	957	1063	11		

- Molecule 2 is a protein called All3315 protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	AD	1109	Total	C	N	O	S	0	0
			9112	5798	1557	1744	13		
2	BD	1109	Total	C	N	O	S	0	0
			9112	5798	1557	1744	13		
2	CD	1109	Total	C	N	O	S	0	0
			9112	5798	1557	1744	13		
2	DD	1109	Total	C	N	O	S	0	0
			9112	5798	1557	1744	13		
2	ED	1109	Total	C	N	O	S	0	0
			9112	5798	1557	1744	13		
2	FD	1109	Total	C	N	O	S	0	0
			9112	5798	1557	1744	13		

- Molecule 3 is a protein called All3316 protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	AE	100	Total	C	N	O	S	0	0
			845	532	148	163	2		
3	AF	100	Total	C	N	O	S	0	0
			845	532	148	163	2		
3	AG	100	Total	C	N	O	S	0	0
			845	532	148	163	2		
3	BE	100	Total	C	N	O	S	0	0
			845	532	148	163	2		
3	BF	100	Total	C	N	O	S	0	0
			845	532	148	163	2		
3	BG	100	Total	C	N	O	S	0	0
			845	532	148	163	2		
3	CE	100	Total	C	N	O	S	0	0
			845	532	148	163	2		
3	CF	100	Total	C	N	O	S	0	0
			845	532	148	163	2		
3	CG	100	Total	C	N	O	S	0	0
			845	532	148	163	2		
3	DE	100	Total	C	N	O	S	0	0
			845	532	148	163	2		

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Mol	Chain	Residues	Atoms					AltConf	Trace
3	DF	100	Total	C	N	O	S	0	0
			845	532	148	163	2		
3	DG	100	Total	C	N	O	S	0	0
			845	532	148	163	2		
3	EE	100	Total	C	N	O	S	0	0
			845	532	148	163	2		
3	EF	100	Total	C	N	O	S	0	0
			845	532	148	163	2		
3	EG	100	Total	C	N	O	S	0	0
			845	532	148	163	2		
3	FE	100	Total	C	N	O	S	0	0
			845	532	148	163	2		
3	FF	100	Total	C	N	O	S	0	0
			845	532	148	163	2		
3	FG	100	Total	C	N	O	S	0	0
			845	532	148	163	2		

- Molecule 4 is a protein called All3317 protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	AH	1227	Total	C	N	O	S	0	0
			9792	6278	1676	1825	13		
4	BH	1227	Total	C	N	O	S	0	0
			9792	6278	1676	1825	13		
4	CH	1227	Total	C	N	O	S	0	0
			9792	6278	1676	1825	13		
4	DH	1227	Total	C	N	O	S	0	0
			9792	6278	1676	1825	13		
4	EH	1227	Total	C	N	O	S	0	0
			9792	6278	1676	1825	13		
4	FH	1227	Total	C	N	O	S	0	0
			9792	6278	1676	1825	13		

- Molecule 5 is a protein called All3320 protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	AJ	585	Total	C	N	O	S	0	0
			4438	2782	775	870	11		
5	CJ	585	Total	C	N	O	S	0	0
			4438	2782	775	870	11		
5	EJ	585	Total	C	N	O	S	0	0
			4438	2782	775	870	11		

- Molecule 6 is a protein called Asl3322 protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	AL	37	Total	C	N	O	S	0	0
			285	179	49	56	1		
6	CL	37	Total	C	N	O	S	0	0
			285	179	49	56	1		
6	EL	37	Total	C	N	O	S	0	0
			285	179	49	56	1		

- Molecule 7 is a protein called All3318 protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	AI	138	Total	C	N	O	S	0	0
			1098	696	184	215	3		
7	BI	138	Total	C	N	O	S	0	0
			1098	696	184	215	3		
7	CI	138	Total	C	N	O	S	0	0
			1098	696	184	215	3		
7	DI	138	Total	C	N	O	S	0	0
			1098	696	184	215	3		
7	EI	138	Total	C	N	O	S	0	0
			1098	696	184	215	3		
7	FI	138	Total	C	N	O	S	0	0
			1098	696	184	215	3		

- Molecule 8 is a protein called All3321 protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	AK	232	Total	C	N	O	S	0	0
			1898	1210	328	357	3		
8	BK	232	Total	C	N	O	S	0	0
			1898	1210	328	357	3		
8	CK	232	Total	C	N	O	S	0	0
			1898	1210	328	357	3		
8	DK	232	Total	C	N	O	S	0	0
			1898	1210	328	357	3		
8	EK	232	Total	C	N	O	S	0	0
			1898	1210	328	357	3		
8	FK	232	Total	C	N	O	S	0	0
			1898	1210	328	357	3		

- Molecule 9 is a protein called All3323 protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	AM	153	Total	C	N	O	S	0	0
			1254	808	208	232	6		
9	BM	153	Total	C	N	O	S	0	0
			1254	808	208	232	6		
9	CM	153	Total	C	N	O	S	0	0
			1254	808	208	232	6		
9	DM	153	Total	C	N	O	S	0	0
			1254	808	208	232	6		
9	EM	153	Total	C	N	O	S	0	0
			1254	808	208	232	6		
9	FM	153	Total	C	N	O	S	0	0
			1254	808	208	232	6		

- Molecule 10 is a protein called All3324 protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	AN	142	Total	C	N	O	S	0	0
			1152	734	198	217	3		
10	BN	142	Total	C	N	O	S	0	0
			1152	734	198	217	3		
10	CN	142	Total	C	N	O	S	0	0
			1152	734	198	217	3		
10	DN	142	Total	C	N	O	S	0	0
			1152	734	198	217	3		
10	EN	142	Total	C	N	O	S	0	0
			1152	734	198	217	3		
10	FN	142	Total	C	N	O	S	0	0
			1152	734	198	217	3		

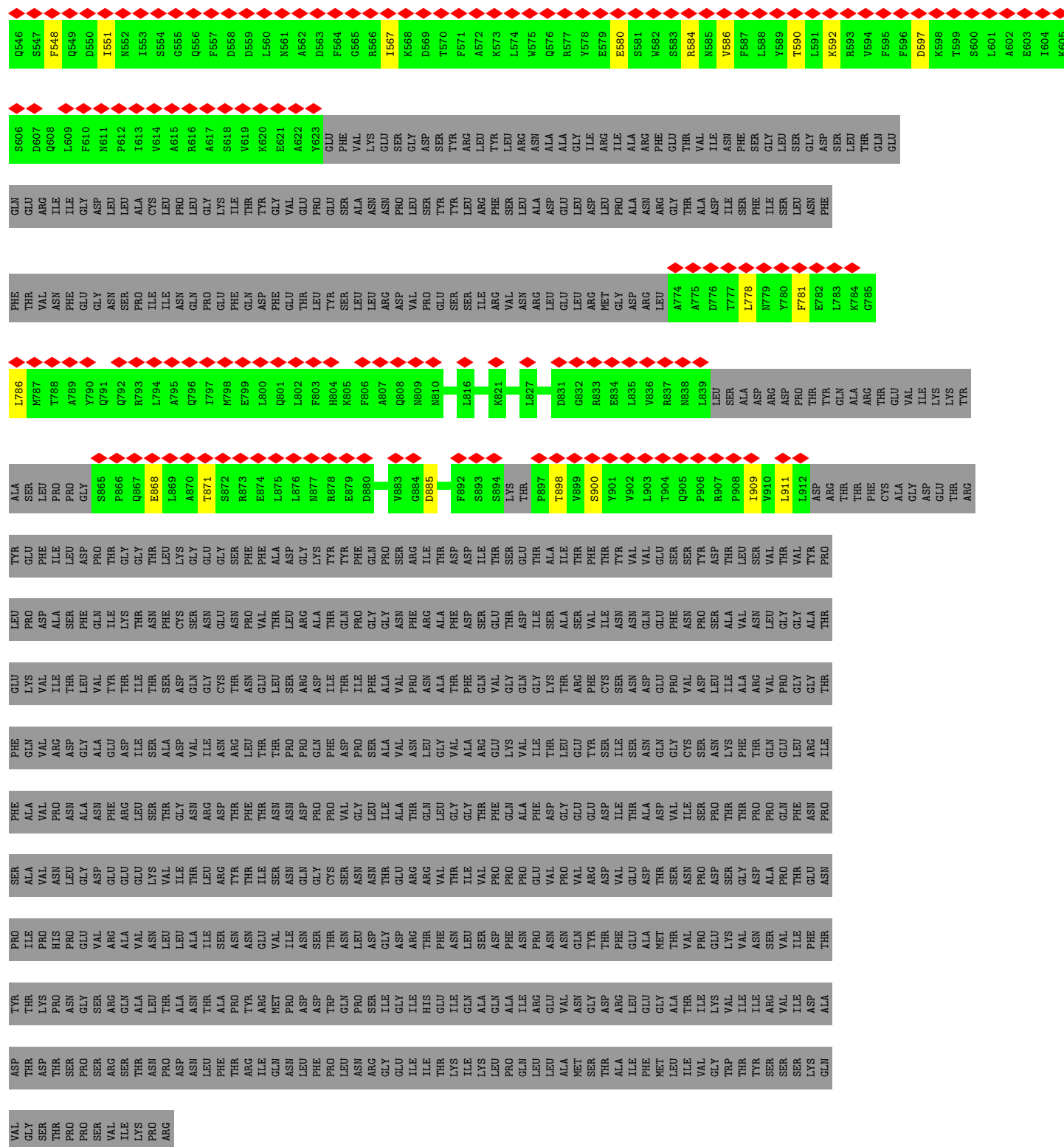
- Molecule 11 is a protein called All3325 protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	AO	473	Total	C	N	O	S	0	0
			3663	2328	616	705	14		
11	AP	480	Total	C	N	O	S	0	0
			3716	2365	624	713	14		
11	AQ	480	Total	C	N	O	S	0	0
			3716	2365	624	713	14		
11	BO	473	Total	C	N	O	S	0	0
			3663	2328	616	705	14		
11	BP	480	Total	C	N	O	S	0	0
			3716	2365	624	713	14		
11	BQ	480	Total	C	N	O	S	0	0
			3716	2365	624	713	14		

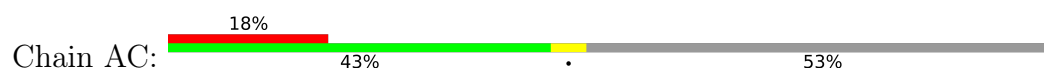
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Mol	Chain	Residues	Atoms					AltConf	Trace
11	CO	473	Total 3663	C 2328	N 616	O 705	S 14	0	0
11	CP	480	Total 3716	C 2365	N 624	O 713	S 14	0	0
11	CQ	480	Total 3716	C 2365	N 624	O 713	S 14	0	0
11	DO	473	Total 3663	C 2328	N 616	O 705	S 14	0	0
11	DP	480	Total 3716	C 2365	N 624	O 713	S 14	0	0
11	DQ	480	Total 3716	C 2365	N 624	O 713	S 14	0	0
11	EO	473	Total 3663	C 2328	N 616	O 705	S 14	0	0
11	EP	480	Total 3716	C 2365	N 624	O 713	S 14	0	0
11	EQ	480	Total 3716	C 2365	N 624	O 713	S 14	0	0
11	FO	473	Total 3663	C 2328	N 616	O 705	S 14	0	0
11	FP	480	Total 3716	C 2365	N 624	O 713	S 14	0	0
11	FQ	480	Total 3716	C 2365	N 624	O 713	S 14	0	0



• Molecule 1: All3314 protein



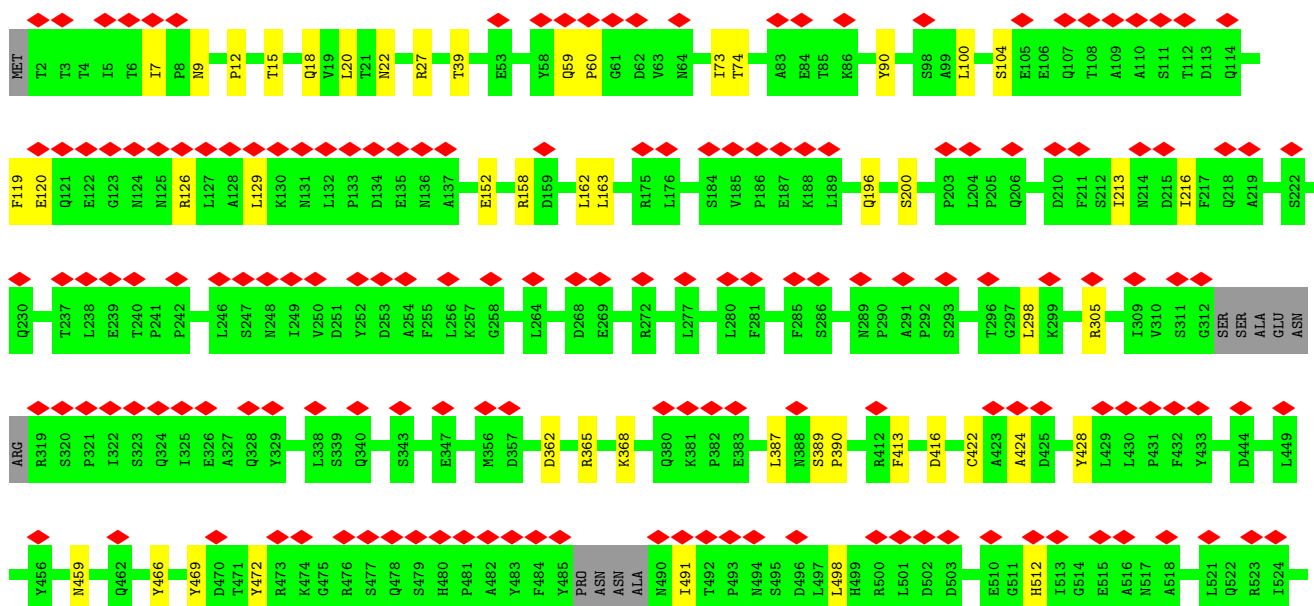


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GLN	PRO	SER	ILE	GLY	ILE	ARG	THR	THR	GLU	THR	GLN	ALA	GLN	GLN	ARG	PRO	ALA	ILE	GLN	VAL	LEU	ALA	ALA	MET	ASN	VAL	GLY	THR	ASP	THR	GLY	ALA	PHE	GLU	GLY	THR	ILE	VAL	TRP	LYS	GLY	THR	ILE	VAL	GLN	ASN	THR	PRO	ASP	THR	LEU	PRO	GLN	PRO	ASN	THR	TRP
LEU	ASN	ARG	GLY	GLU	ILE	ILE	THR	THR	LYS	ILE	LYS	VAL	GLN	PRO	GLN	LEU	GLU	VAL	ASN	ALA	ALA	MET	ASN	GLY	THR	THR	ASP	THR	GLY	ALA	PHE	GLU	GLY	THR	ILE	VAL	TRP	LYS	GLY	THR	ILE	VAL	GLN	ASN	THR	PRO	ASP	THR	LEU	PRO	GLN	PRO	ASN	THR	TRP		

● Molecule 1: All3314 protein



MET	T2	T3	T4	I5	T6	I7	P8	I9	T15	P16	L20	T21	N22	R27	R37	L38	T39	R40	V41	Y42	E53	I57	Y58	Q59	P60	G61	D62	V63	N64	A83	S85	L100	E105	E106	Q107	T108	A109	S110	S111	T112	D113	Q114	Q121	E122	G123	N124	N125	R126													
L132	V150	L153	Q156	L163	D164	C165	D166	D167	V185	P186	E187	K188	L189	E192	Q196	S200	R201	E202	P203	L204	W208	R209	D210	F211	L213	L216	N226	F227	Q230	V231	F234	Q235	Y236	T237	L238	E239	T240	P241	V243	T244	R245	L246	S247																		
N248	T249	V250	D251	Y252	D253	A254	F255	L256	K257	G258	Y259	Q260	Q261	V262	C263	L264	Q265	A266	L267	D268	E269	L270	D271	R272	T273	F274	P275	W276	L277	P283	A291	P292	D294	F295	T296	Q297	K299	T300	L301	L302	N303	Q304	R305	L306	S307	D308	I309	V310	S311	G312	SER	SER	ALA	GLU	ASN						
ARG	ARG	S320	P321	I322	S323	Q324	I325	E326	A327	Q328	Y329	A330	L331	Q332	Y333	F334	Y335	L341	A344	F345	R346	A349	A489	E350	S351	D354	D358	A359	T360	T363	K368	K381	P382	E383	V384	Y385	A386	L387	M404	V408	K409	F413	L414	Y415	A423	A424	D425	S426													
F427	Y428	L429	L430	P431	D434	L437	K438	L439	A446	Y456	Y457	Q462	Y466	Y483	N487	M488	A489	N490	D496	R500	S505	L509	E510	O511	H512	E515	A516	T519	R523	T542	G543	N544	L545	Q546	S547	F548	Q549	D550	I551	N552	I553	S554																			
G555	Q556	F557	D558	D559	L560	N561	A562	D563	F564	G565	R566	I567	K568	D569	L570	F571	A572	K573	L574	W575	Q576	ARG	TYR	GLU	GLU	SER	TRP	SER	ARG	ASN	VAL	PHE	LEU	TYR	T590	L591	K592	R593	V594	F595	F596	D597	K598	T599	S600	L601	A602	E603	I604	K605	S606	D607	Q608	L609	F610	N611	PRO	ILE	VAL		
ALA	ARG	ALA	SER	VAL	LYS	GLU	ALA	TYR	PHE	GLY	VAL	LYS	GLU	PRO	GLU	SER	GLY	ASP	ASN	TYR	ARG	ALA	GLY	ILE	ALA	ASP	GLU	LEU	ASP	PHE	ILE	ASN	ARG	GLY	THR	SER	GLY	ILE	SER	LEU	THR	ASN	PHE	GLU	VAL	ASN	GLY	LEU	LEU												
ALA	CYS	LEU	PRO	GLY	LYS	ILE	THR	THR	GLY	GLY	VAL	GLU	PRO	GLU	SER	SER	GLY	ALA	ASN	ASN	PRO	ARG	LEU	TYR	TYR	ARG	ASN	LEU	LEU	VAL	ASN	ARG	GLY	THR	SER	GLY	ILE	ASN	PHE	GLU	VAL	ASN	GLY	LEU	LEU	SER															
PRO	ILE	ILE	ASN	GLN	PRO	GLY	PHE	GLN	ASP	PHE	GLU	THR	LEU	TYR	ASP	SER	LEU	LEU	VAL	ASN	ARG	LEU	GLY	ASP	GLY	MET	ARG	GLY	ASP	ALA	ASN	ARG	LEU	A774	A775	D776	T777	L778	W779	Y780	F781	E782	L783	K784	G785	L786	H787	T788	A789	S860	L861	P862	P863	G864	S865	P866	Q867	E868	L869	A870	T871
A795	Q796	I797	M798	E799	L800	Q801	L802	F803	H804	K805	F806	A807	G812	M813	Y829	W830	D831	G832	R833	E834	L835	W836	R837	N838	L839	L840	S841	A842	D843	R844	D845	P846	T847	Y848	Q849	A850	R851	T852	E853	W854	K855	K857	Y858	A859	S860	L861	P862	P863	G864	S865	P866	Q867	E868	L869	A870	T871					

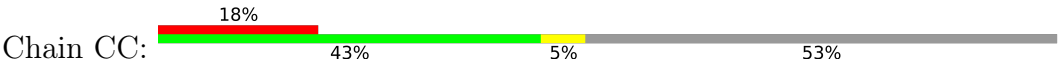






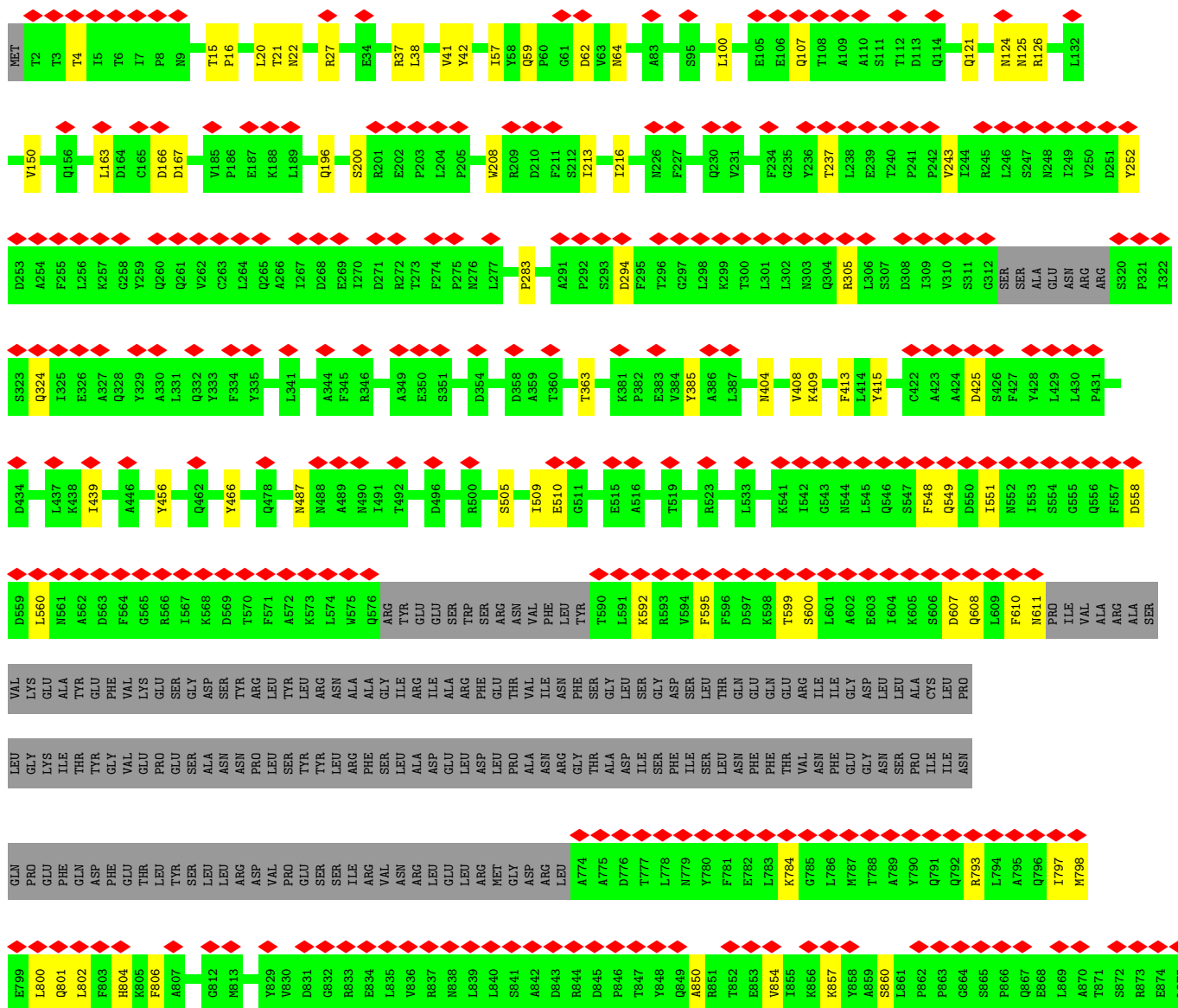
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A617	S618	V619	K620	E621	A622	Y623	GLU	PHE	VAL	LYS	GLU	SER	GLY	ASN	SER	TYR	ARG	LEU	ASN	ALA	GLY	ILE	ILE	ALA	ARG	PHE	GLU	ALA	THR	VAL	ILE	ASN	PHE	SER	GLY	ASP	SER	LEU	THR	GLN	GLU	GLU	ARG	ILE	ILE	GLY	ASN	SER	PRO	LEU	LEU	ALA	CYS								
LEU	PRO	GLY	LEU	ILE	THR	TYR	GLY	VAL	GLU	PRO	GLU	SER	ALA	ASN	ASN	PRO	LEU	ARG	PHE	SER	ALA	GLY	ILE	LEU	ASP	LEU	PRO	ALA	ASN	ARG	GLY	THR	ALA	ASP	ILE	PHE	SER	LEU	THR	GLN	VAL	THR	PHE	ASN	GLY	ASN	SER	PRO	ILE												
ILE	ASN	GLN	PRO	GLU	PHE	GLN	ASP	PHE	THR	LEU	LEU	ARG	ASP	VAL	PRO	GLU	SER	ILE	ARG	VAL	ASN	ARG	LEU	ARG	MET	GLY	ASP	ARG	LEU	A774	A775	D776	T777	L778	W779	Y780	F781	E782	L783	K784	G785	L786	W787	T788	A789	Y790	Q791	Q792	L794	A795	Q796										
I797	M798	E799	L800	Q801	L802	F803	H804	K805	F806	A807	Q808	N809	N810	E814	H815	L816	G817	K821	L827	D831	Q832	R833	E834	L835	V836	R837	N838	L839	LEU	SER	ALA	ASP	ARG	ASP	PRO	THR	TYR	GLN	ALA	THR	THR	GLU	VAL	ILE	LYS	TYR	ALA	PRO	GLY	S865	P866										
Q867	E868	L869	A870	T871	S872	R873	E874	L875	L876	N877	R878	E879	D880	V883	G884	D885	S893	S894	LYS	THR	P897	T898	W899	S900	Y901	V902	L903	T904	Q905	P906	R907	P908	I909	V910	L911	L912	ASP	ARG	THR	THR	PHE	CYS	ALA	GLY	ASP	GLU	THR	ARG	TYR	PHE	ILE	LEU	THR	GLY							
GLY	THR	LEU	CYS	GLY	GLY	SER	PHE	ALA	ASP	GLY	LYS	TYR	PHE	GLN	TYR	ILE	GLY	PRO	SER	ILE	THR	GLU	THR	ILE	ALA	ILE	THR	THR	VAL	GLU	SER	THR	ASP	THR	LEU	SER	VAL	THR	PRO	LEU	PRO	THR	ALA	GLN	VAL	THR	GLY	THR	GLY	THR	THR	GLY									
THR	ASN	CYS	ASN	GLU	ASN	PRO	VAL	THR	LEU	ASP	ALA	THR	GLN	PRO	GLY	GLY	ASN	GLY	ASN	PHE	ASP	SER	ILE	ALA	ALA	VAL	GLU	ASN	ASN	PRO	PRO	ILE	ALA	VAL	ASN	LEU	VAL	GLY	THR	GLN	LYS	VAL	VAL	ILE	THR	LEU	VAL	TYR	THR												
ILE	THR	SER	ASN	GLY	CYS	THR	ASN	THR	SER	ARG	ASP	ILE	THR	ILE	PHE	ALA	VAL	GLN	THR	VAL	GLY	GLY	THR	LYS	THR	ARG	PHE	CYS	THR	VAL	VAL	ASP	LEU	ILE	ALA	PHE	THR	GLN	VAL	VAL	VAL	ASP	ARG	THR	PHE	GLN	VAL	VAL	PRO	ASN	ASN	GLY	ALA	ASP							
ILE	SER	ALA	VAL	ILE	ASN	ARG	THR	THR	PRO	GLN	VAL	ASN	GLY	VAL	ALA	VAL	ARG	GLU	LYS	VAL	GLY	THR	LEU	GLU	THR	GLY	TYR	SER	ILE	CYS	VAL	PRO	ASN	LYS	PHE	THR	GLN	ALA	ARG	THR	PHE	GLN	VAL	VAL	PRO	ASN	ASN	GLY	ALA	ASP	PHE	ARG									
LEU	SER	THR	GLY	ASN	ASP	THR	PHE	THR	ASN	PRO	GLY	VAL	LEU	ILE	ALA	ALA	THR	PHE	THR	PHE	GLY	THR	GLY	ASP	GLY	ASP	GLU	ASP	ILE	ILE	ASP	PRO	THR	THR	THR	PRO	THR	ASN	PRO	THR	ASN	PRO	ILE	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR							
GLU	LYS	VAL	ILE	THR	ARG	TYR	ILE	ASN	GLY	THR	GLU	ARG	THR	ILE	THR	VAL	VAL	PRO	PRO	PRO	GLY	THR	VAL	PRO	VAL	VAL	ASP	THR	ASP	VAL	VAL	PRO	THR	GLY	THR	ILE	PHE	ASN	PRO	ASN	PRO	ILE	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR						
VAL	ASN	LEU	ALA	ILE	SER	ASN	ASN	VAL	ILE	ASN	THR	ASN	LEU	GLY	ASP	THR	PHE	ASN	SER	ILE	GLN	ALA	GLY	ASN	GLN	THR	THR	THR	VAL	VAL	VAL	GLY	THR	VAL	ASN	PHE	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR					
ALA	LEU	THR	ASN	THR	ALA	PRO	TYR	MET	PRO	ASP	TRP	GLN	PRO	ASN	ARG	GLY	ILE	GLY	GLY	ILE	HIS	GLU	ILE	VAL	ASN	GLY	THR	ALA	ARG	ILE	ILE	VAL	GLY	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR				
THR	ASN	PRO	ASN	LEU	PHE	THR	ARG	GLN	ASN	LEU	PHE	PRO	ASN	ARG	GLY	GLU	ILE	LYS	LYS	LEU	PRO	GLN	LEU	LEU	ALA	MET	SER	THR	ALA	ILE	THR	VAL	GLY	TRP	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
LYS	PRO	ARG																																																											

● Molecule 1: All3314 protein

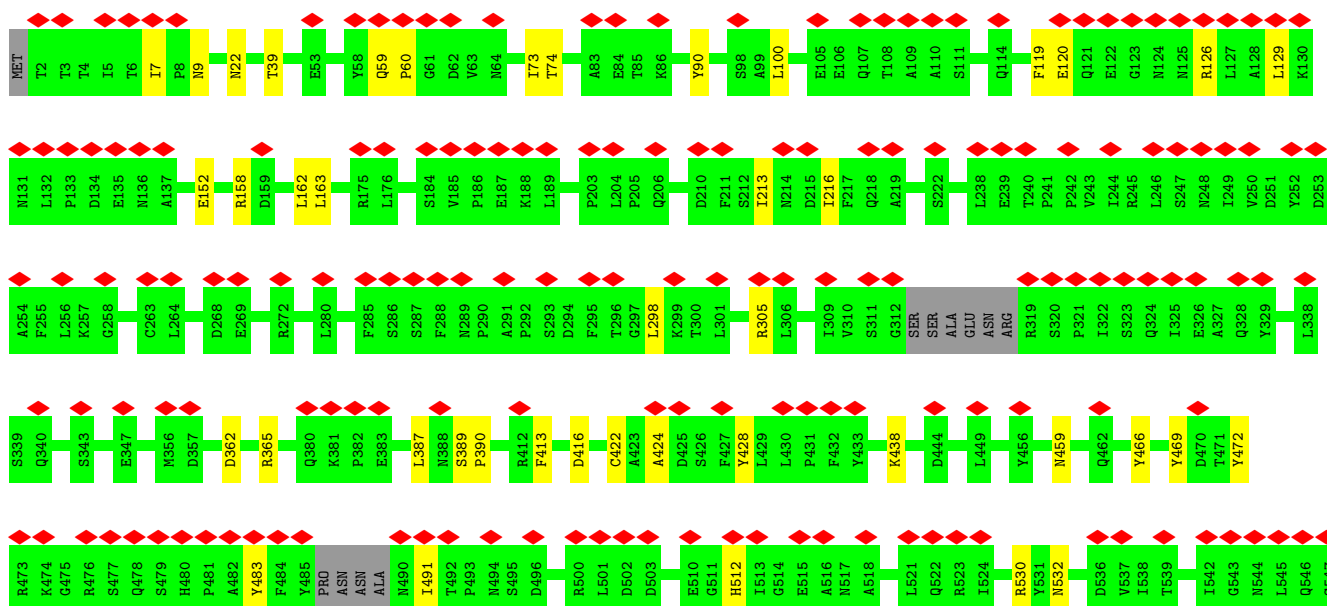




- Molecule 1: All3314 protein



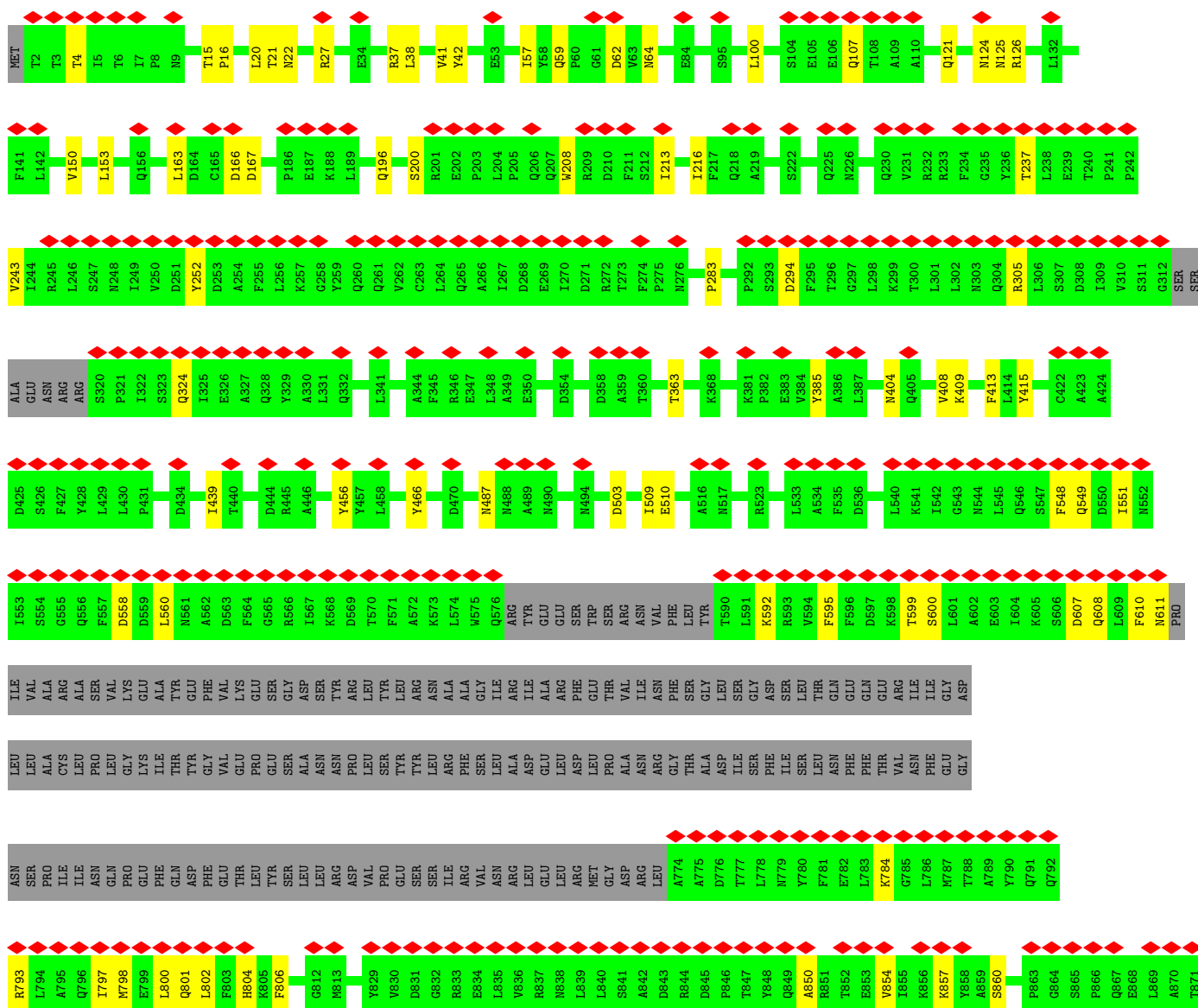
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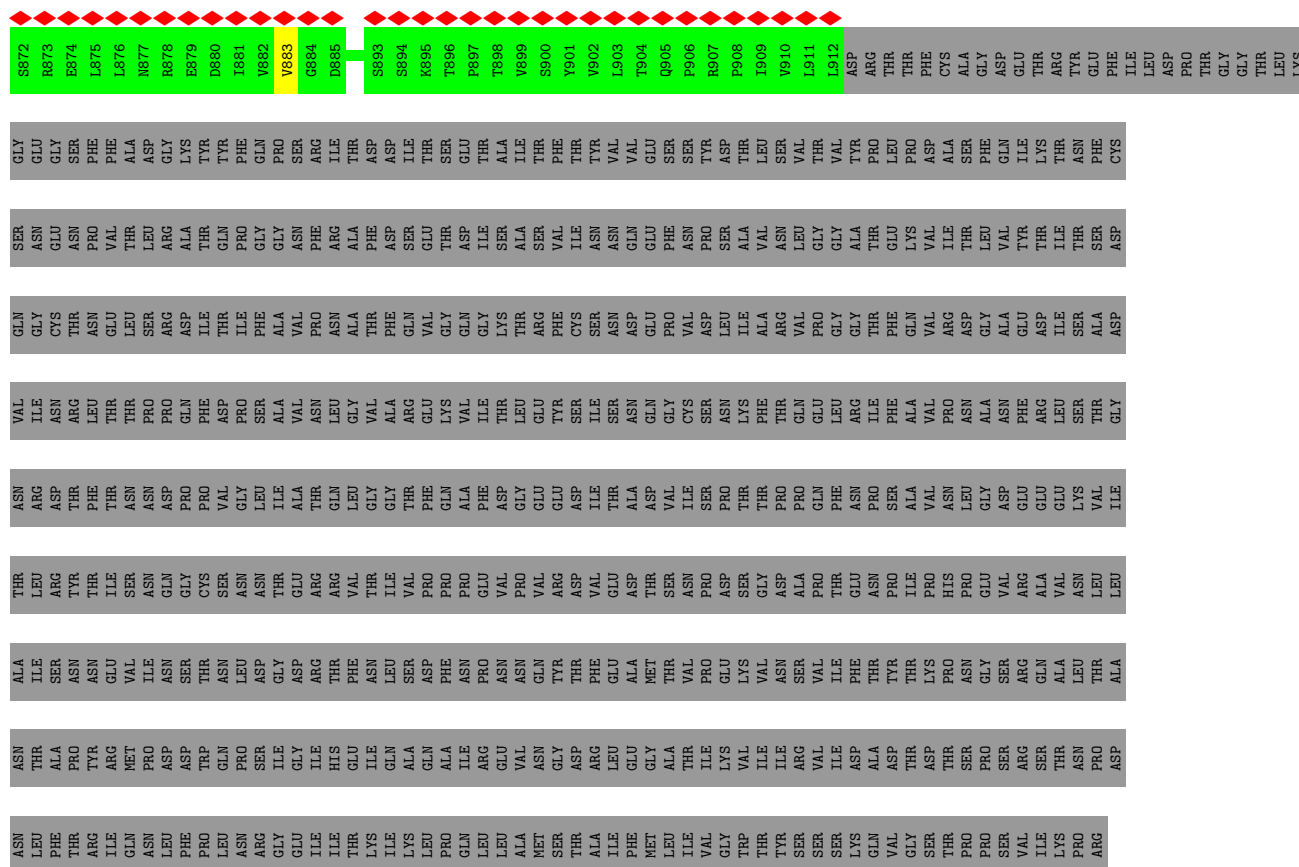




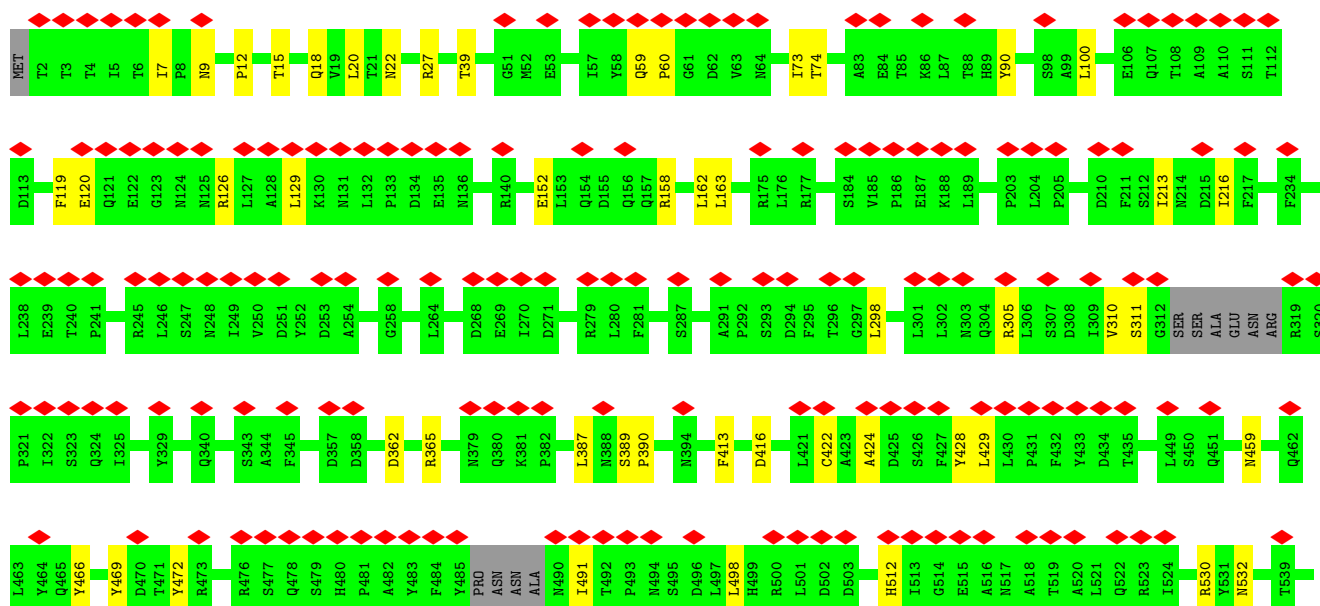


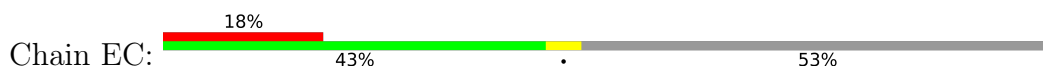
- Molecule 1: All3314 protein





• Molecule 1: All3314 protein

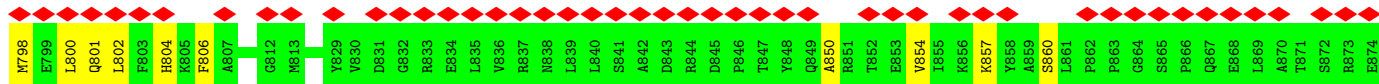


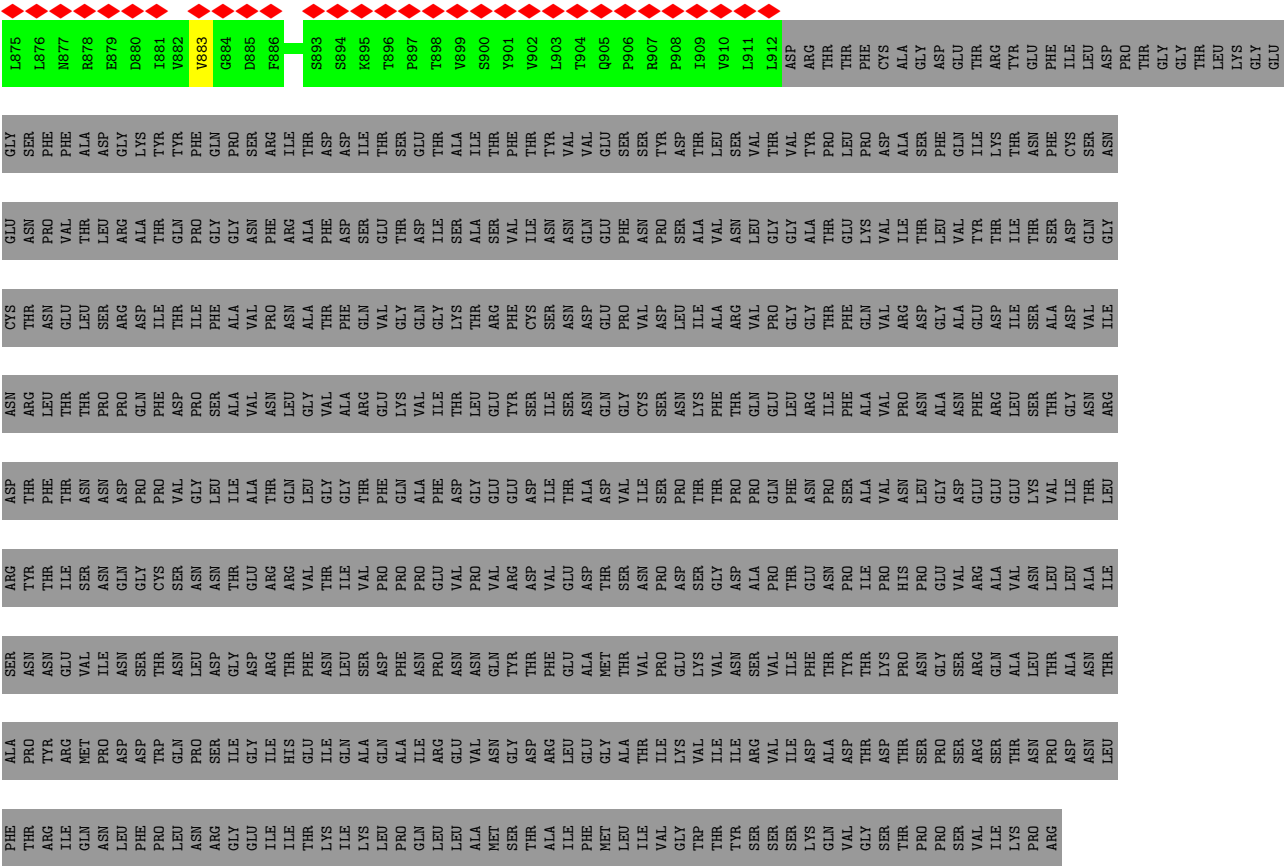


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Q107	T108	A109	A110	S111	T112	D113	Q114	L118	F119	E120	Q121	E122	G123	N124	N125	R126	L127	A128	L129	K130	N131	L132	P133	D134	E135	N136	A137	F138	A139	R140	V141	L142	A143	D144	Q145	E152	L153	Q157	R158	ASP	SER	CYS	LEU	LEU	ASP	CYS	ASP	THR	GLY	K170	N173	F174	R175
F179	L180	P182	R183	S184	V185	K188	L189	L194	E202	P203	F217	Q220	F224	F228	Y236	T237	L238	L246	S247	N248	I249	D253	L277	S282	S287	A291	P292	S293	L298	I309	V310	S311	G312	SER	ALA	GLU	ASN	ARG	ARG	PRO													
I322	S323	Q324	I325	E326	Q327	Q328	Y329	A330	L348	A349	E350	S351	D354	D357	D358	A359	D362	T363	R364	G373	L374	V375	P376	L377	P378	N379	E383	V384	Y385	A386	L387	R392	F413	D416	L421	A424	L430	D434	L437	K438	I439	R445	Y466										
T471	R476	A482	N487	N488	A489	N490	I491	T492	P493	N494	S495	D496	L497	L498	H499	R500	L501	D502	D503	I509	E510	G511	N517	A518	T519	A520	L521	Q522	R523	I524	L525	D526	R530	D536	V537	I538	K541	I542	G543	N544	L545	Q546	S547	PHE	GLN	ASP	ILE	ASN	I553	S554			
G556	Q556	F557	D558	D559	L560	N561	A562	D563	F564	G565	R566	I567	K568	D569	T570	F571	A572	K573	L574	M575	Q576	R577	Y578	E579	E580	S581	M582	SER	ARG	ASN	VAL	F587	L588	Y589	T590	L591	K592	VAL	PHE	PHE	ASP	LYS	THR	SER	LEU	ALA	GLU	ASP	LEU	VAL			
ALA	ARG	ALA	ASN	VAL	LYS	GLU	ALA	TYR	PHE	VAL	LYS	GLU	SER	GLY	ASP	SER	TYR	ARG	ALA	ALA	GLY	ILE	ARG	ILE	ALA	GLU	ASP	PHE	GLU	THR	VAL	ILE	ASN	ARG	VAL	PHE	GLN	GLU	GLU	GLU	ARG	ILE	THR	ASN	GLN	LEU	THR	GLN	VAL				
ALA	CYS	LEU	PRO	GLY	LYS	ILE	THR	TYR	GLY	VAL	PRO	GLU	PRO	GLU	SER	ALA	ASN	ASN	PRO	ARG	PHE	SER	LEU	ASP	GLU	MET	GLY	PRO	ALA	ASN	ARG	GLY	THR	PHE	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR		
PRO	ILE	ILE	ASN	GLN	PRO	GLY	PHE	GLY	ASP	PHE	GLY	THR	LEU	TYR	SER	LEU	LEU	ARG	ASP	VAL	PRO	GLU	GLU	LEU	LEU	ASP	GLU	MET	GLY	ASP	ARG	LEU	A774	A775	D776	T777	N779	Y780	F781	E782	L783	K784	G785	L786	M787	T788	A789	Y790	Q791	Q792	R793	L794	
A795	Q796	I797	M798	E799	L800	Q801	L802	F803	H804	F806	A807	G812	T824	F825	V826	Y829	V830	D831	G832	R833	E834	R837	N838	L839	A842	D843	R844	D845	P846	Q849	A850	E853	K856	K857	Y858	A859	S860	L861	P862	G864	S865	P866	Q867	E868	L869	A870	R873	E874					
L875	L876	N877	R878	E879	D880	G884	D885	F889	S893	S894	K895	T896	P897	T898	V899	S900	Y901	V902	L903	T904	Q905	P906	R907	P908	I909	V910	L911	LEU	ASP	ARG	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	
PHE	PHE	ALA	ASP	GLY	LYS	TYR	PHE	GLN	PRO	ASN	ARG	THR	SER	GLU	GLY	THR	THR	PHE	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
PRO	VAL	THR	LEU	ARG	ALA	THR	GLN	THR	GLY	ASN	PHE	ARG	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	
ASN	GLU	LEU	SER	ARG	ASP	ILE	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	
LEU	THR	THR	PRO	PRO	GLN	PHE	ASP	PRO	GLY	ALA	VAL	ASN	LEU	GLY	ALA	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
PHE	THR	ASN	ASP	PRO	PRO	VAL	GLY	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR

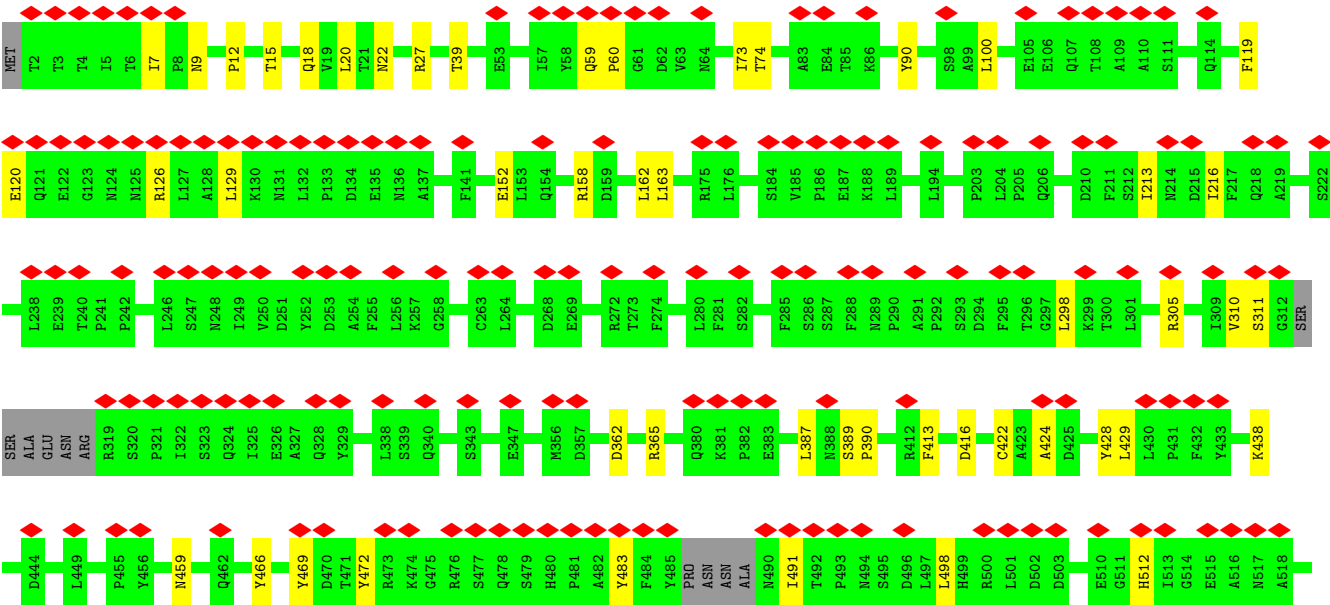
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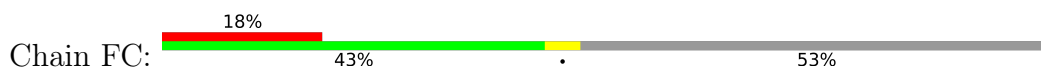
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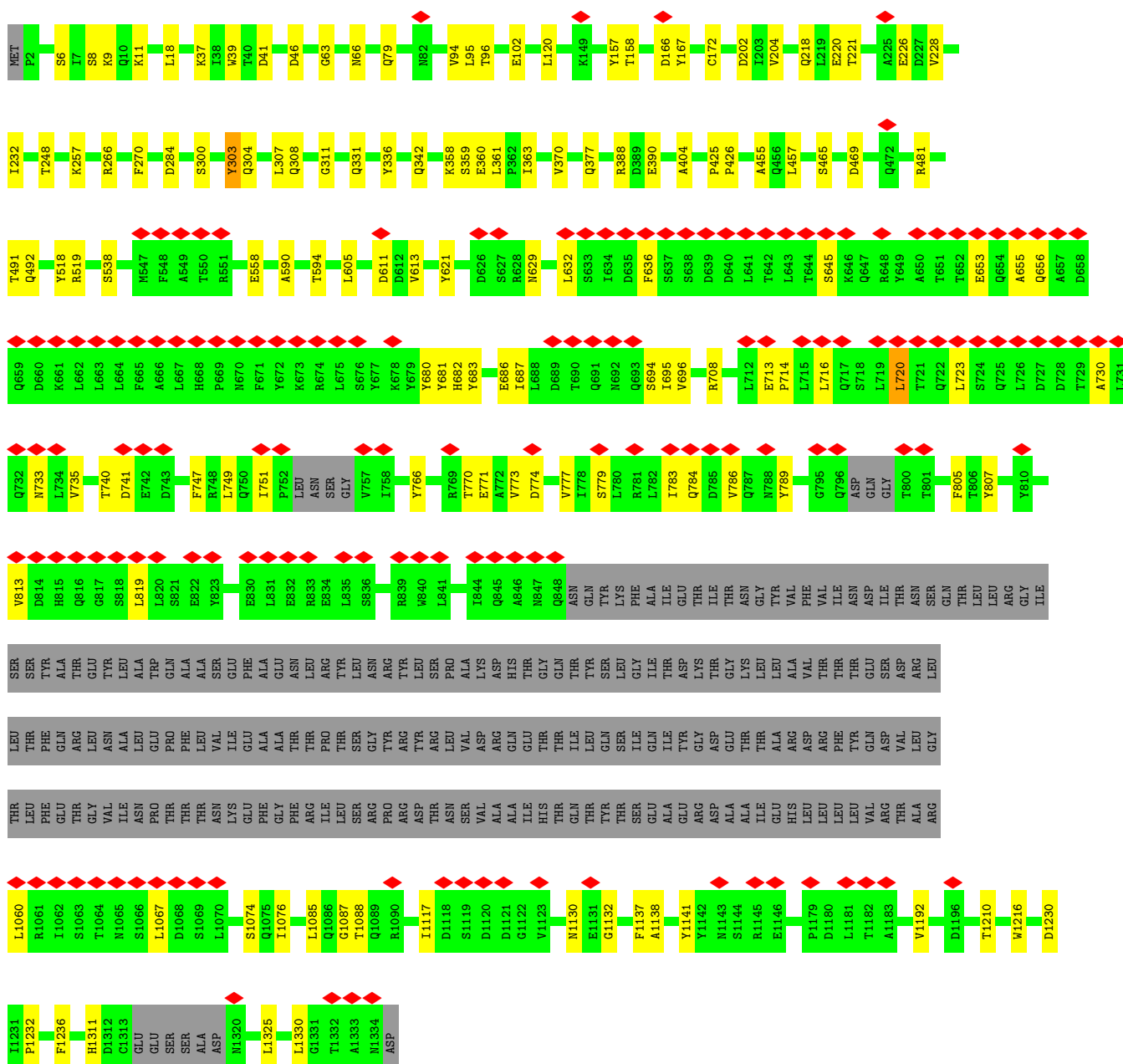


● Molecule 1: All3314 protein

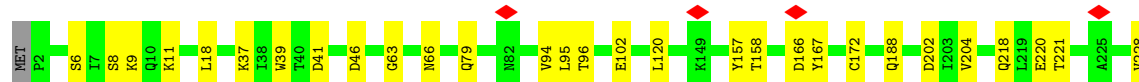
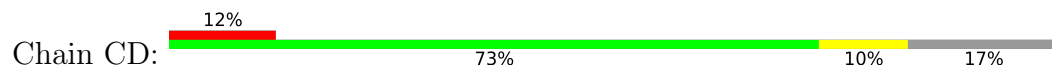


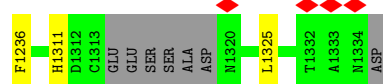




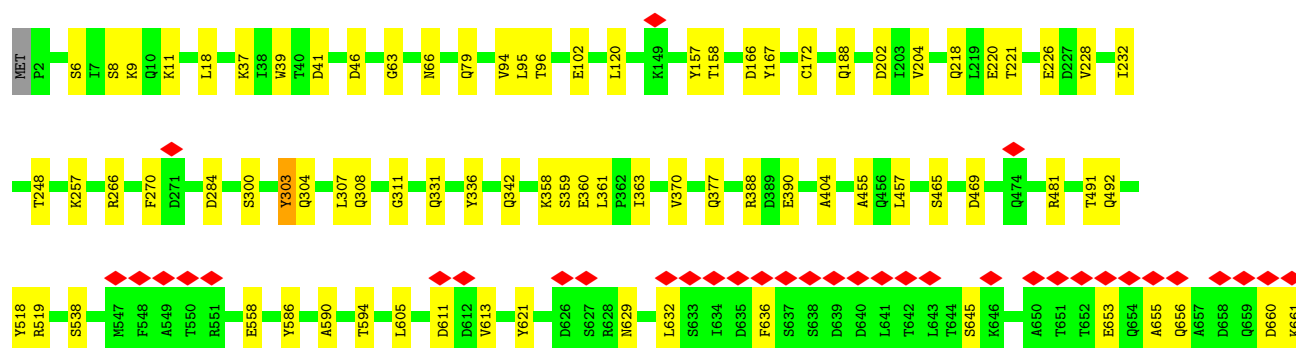


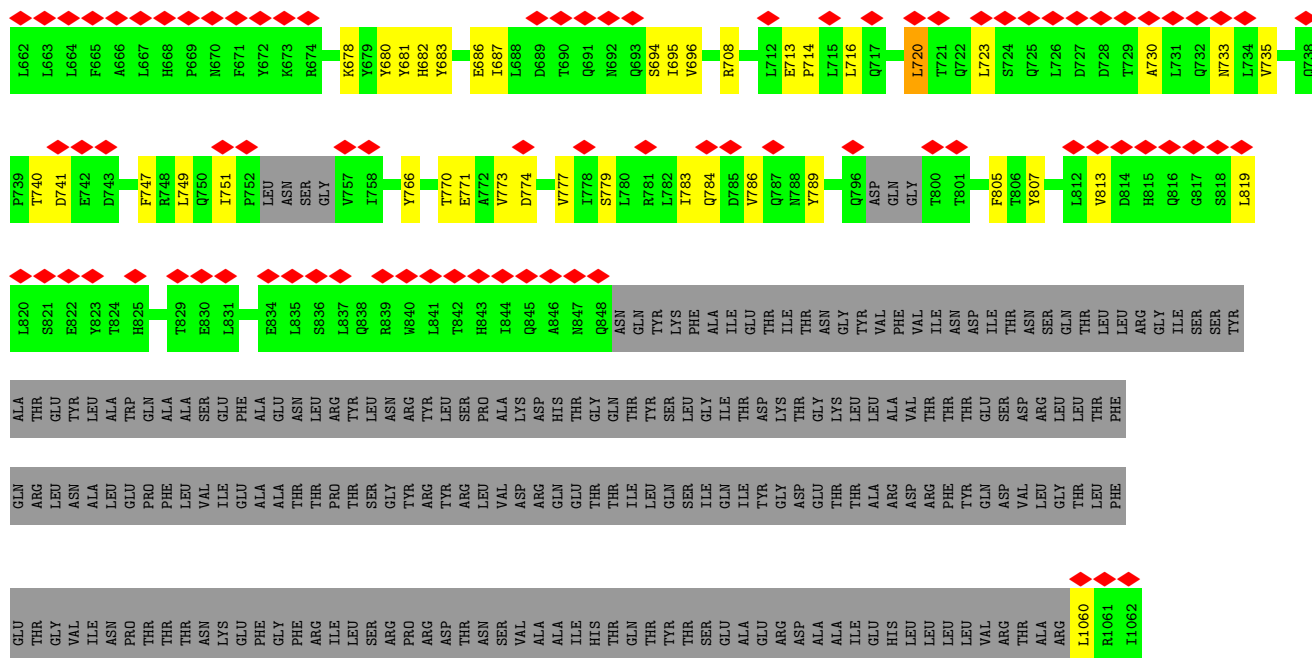
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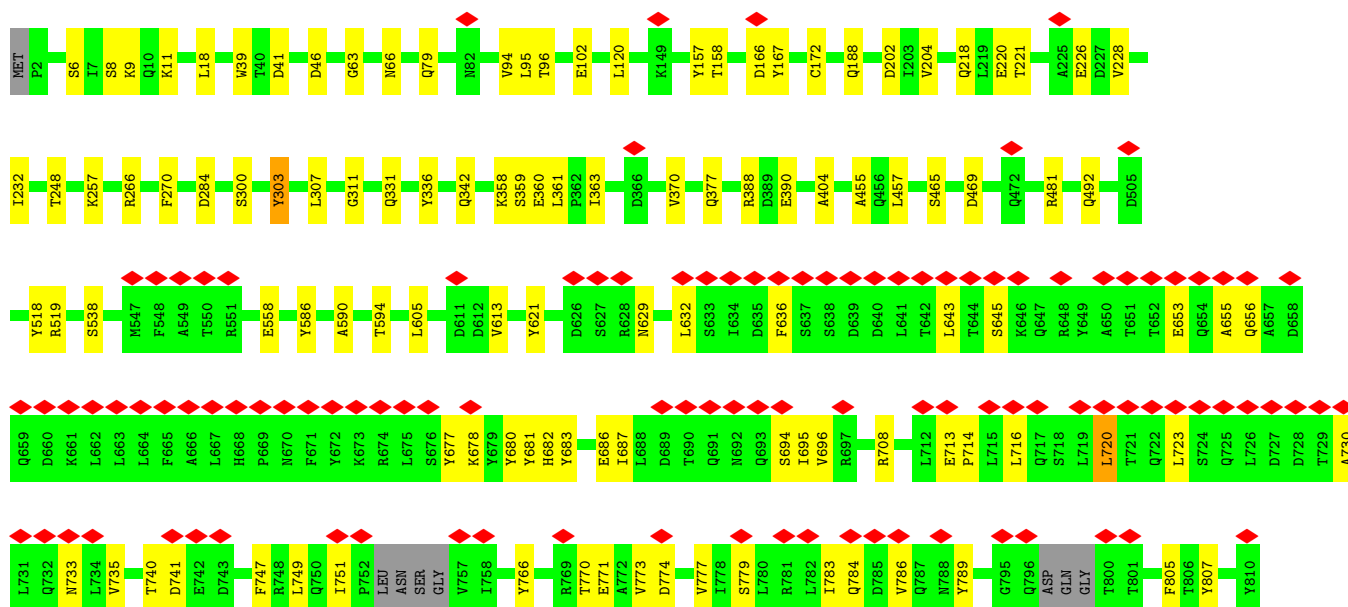
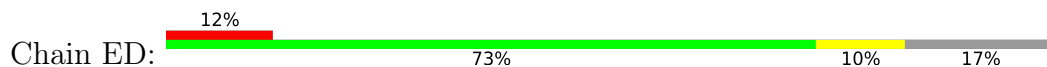


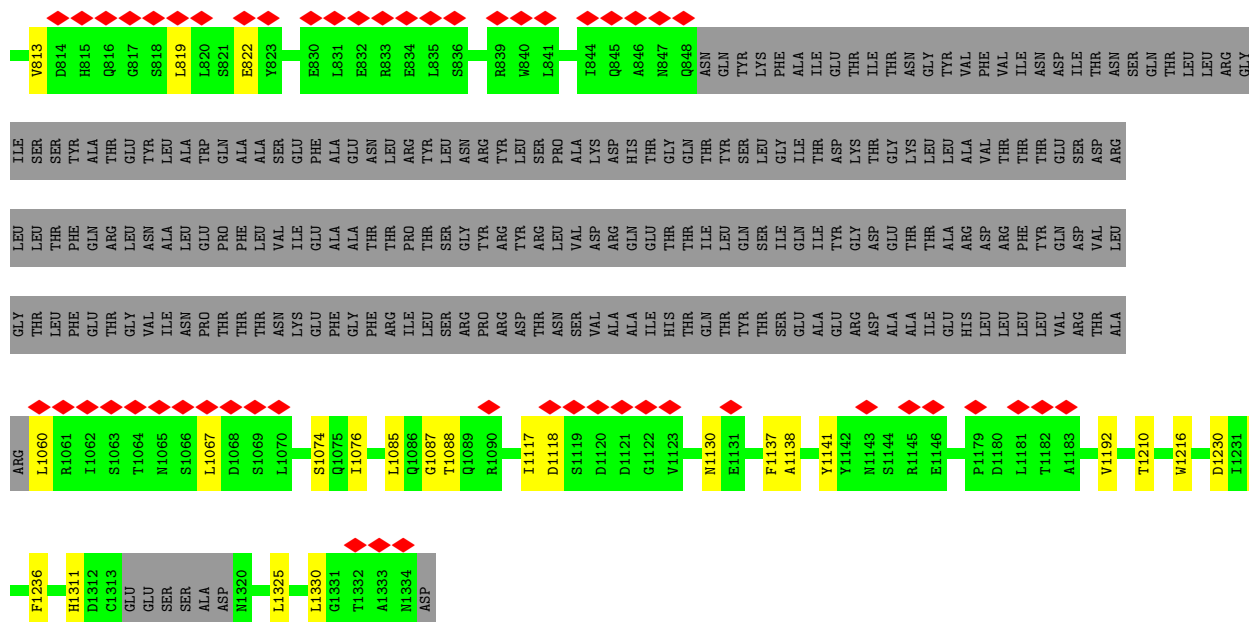
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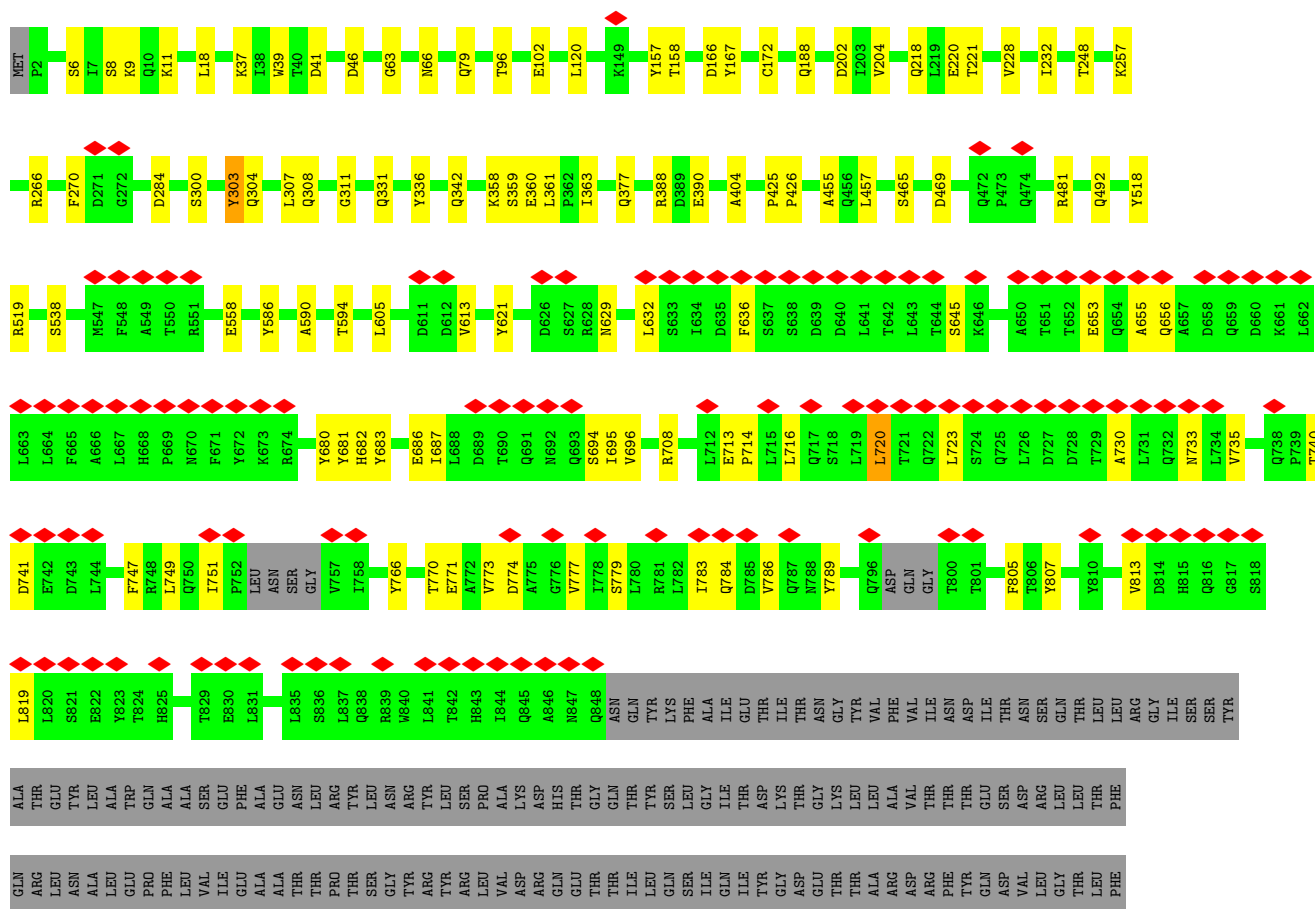
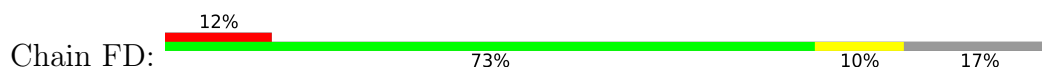


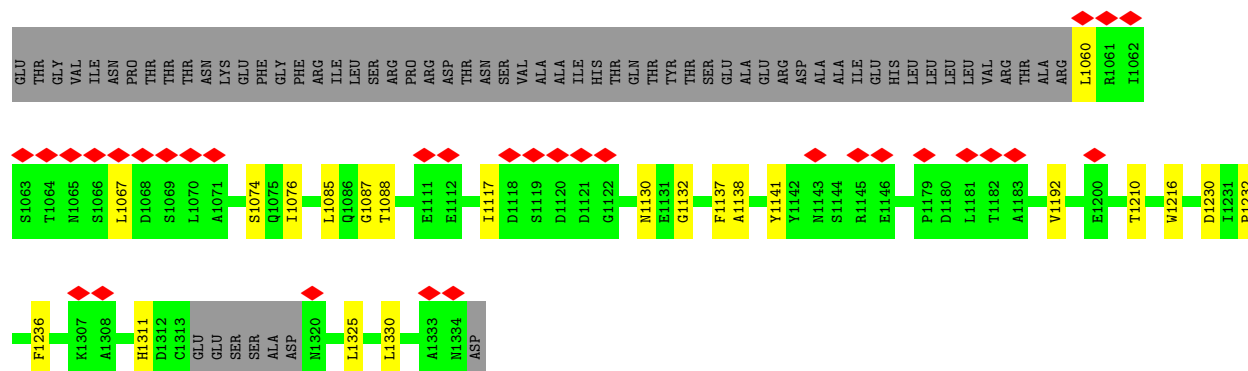
• Molecule 2: All3315 protein



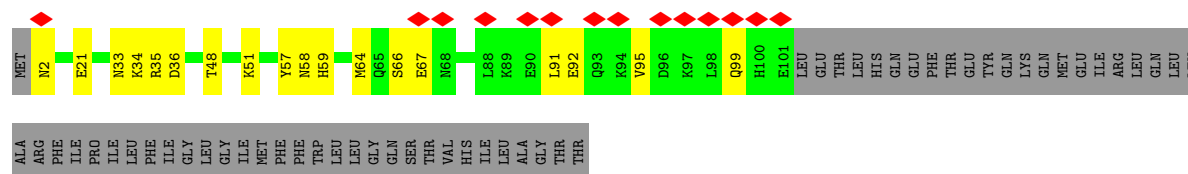


• Molecule 2: All3315 protein

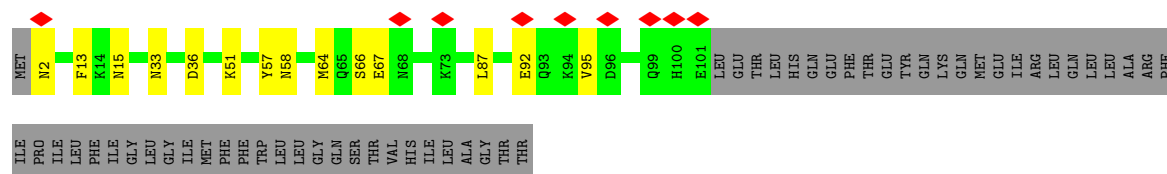




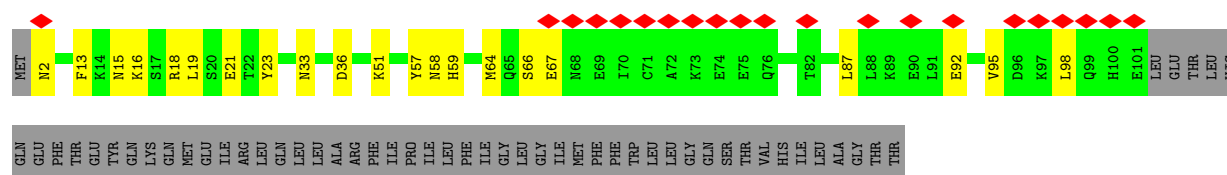
• Molecule 3: All3316 protein



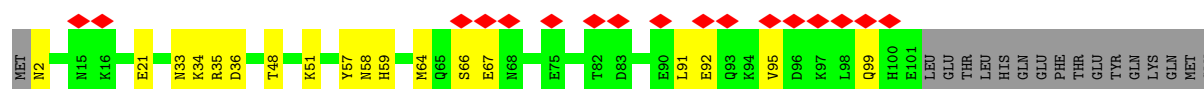
• Molecule 3: All3316 protein



• Molecule 3: All3316 protein



• Molecule 3: All3316 protein



Amino Acid	Count (MET)
N2	1
F13	1
K14	1
R15	1
K16	1
S17	1
R18	1
L19	1
S20	1
E21	1
T22	1
Y23	1
N33	1
D36	1
K51	1
Y57	1
N58	1
H59	1
M64	1
Q65	1
S66	1
E67	1
N68	1
E69	1
I70	1
C71	1
A72	1
K73	1
E74	1
E75	1
Q76	1
I80	1
S81	1
T82	1
L87	1
L88	1
E92	1
V95	1
D96	1
K97	1
L98	1
Q99	1
H100	1
E101	1
LEU	1
GLU	1
THR	1
LEU	1

GLN
GLU
PHE
THR
LEU
TYR
GLN
LYS
MET
GLU
ILE
ARG
LEU
GLN
LEU
LEU
ALA
ARG
PHE
ILE
PRO
ILE
PHE
ILE
GLY
GLY
MET
PHE
PHE
TRP
LEU
LEU
GLY
GLN
SER
THR
VAL
HIS
ILE
LEU
ALA
GLY
THR

• Molecule 3: All3316 protein



MET N2 N15 K16 E21 T22 Y23 N33 K34 R35 D36 T48 K51 Y57 N58 H59 M64 Q65 S66 E67 N68 T82 E90 L91 E92 Q93 D96 K97 L98 Q99 H100 E101 LEU THR LEU HIS GLN GLU PHE THR TYR GLN LYS MET GLU ILE ARG

LEU
GLN
LEU
ALA
ARG
PHE
ILE
PRO
LEU
PHE
ILE
GLY
LEU
GLY
ILE
MET
PHE
TRP
LEU
GLY
GLN
SER
THR
VAL
HIS
ILE
LEU
ALA
GLY
THR

• Molecule 3: All3316 protein



MET N2 F13 K14 N15 N33 D36 K51 Y57 N58 M64 Q65 S66 E67 E75 L87 L88 L91 E92 Q93 Q94 V95 D96 K97 L98 Q99 H100 E101 LEU THR LEU HIS GLN GLU PHE THR TYR GLN LYS MET GLU ARG ILE LEU GLN LEU ALA

ARG
PHE
ILE
PRO
LEU
PHE
ILE
GLY
LEU
GLY
ILE
MET
PHE
PHE
TRP
LEU
GLY
GLN
SER
THR
VAL
HIS
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LEU
ALA
GLY
THR

• Molecule 3: All3316 protein



MET N2 F13 K14 N15 K16 S17 R18 L19 S20 E21 T22 Y23 N33 D36 Q46 Q47 T48 K51 Y57 N58 H59 M64 Q65 S66 E67 N68 E69 I70 C71 A72 K73 E74 E75 Q76 I80 L87 L88 E92 V95 D96 K97 L98 Q99 H100 E101 LEU GLU THR

LEU
HIS
GLU
PHE
THR
GLU
TYR
GLN
LYS
MET
GLU
ILE
ARG
LEU
GLN
ALA
ARG
PHE
ILE
PRO
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LEU
PHE
ILE
GLY
GLY
ILE
MET
PHE
PHE
TRP
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ALA
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THR

• Molecule 3: All3316 protein



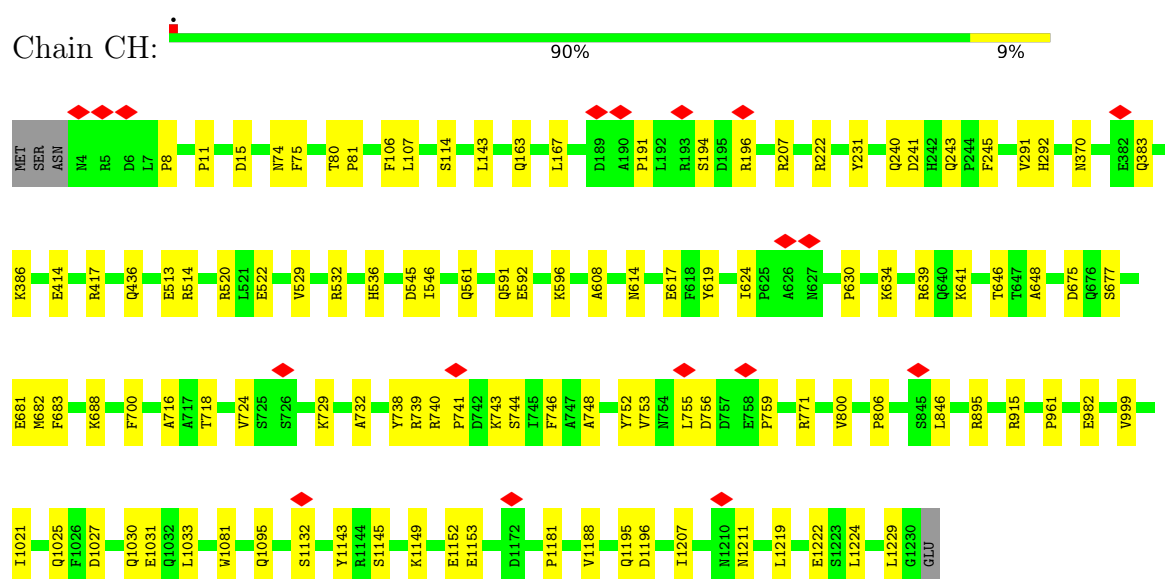
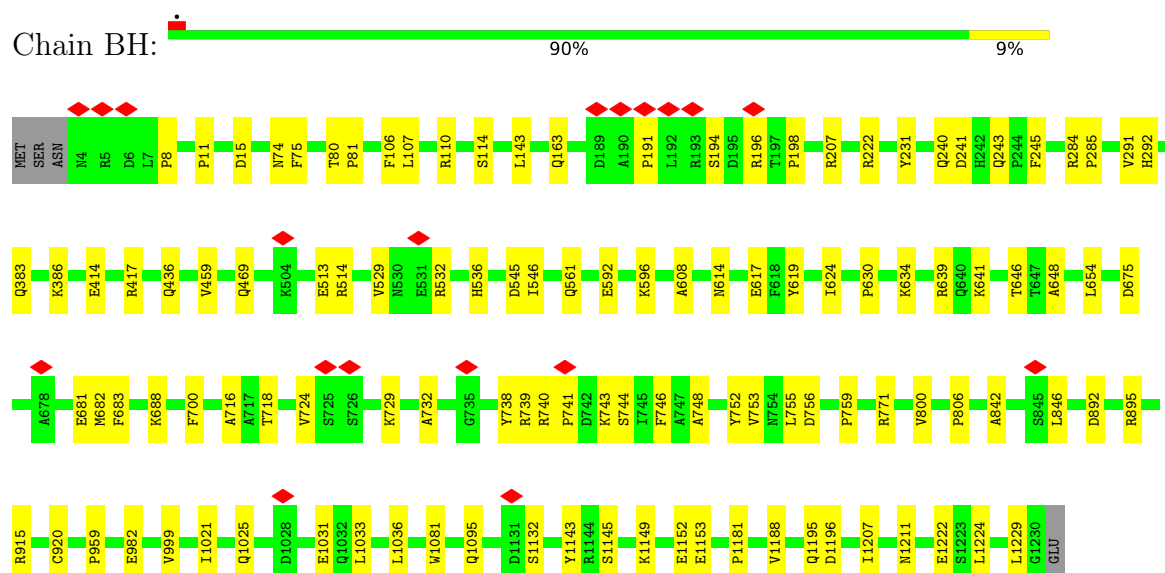
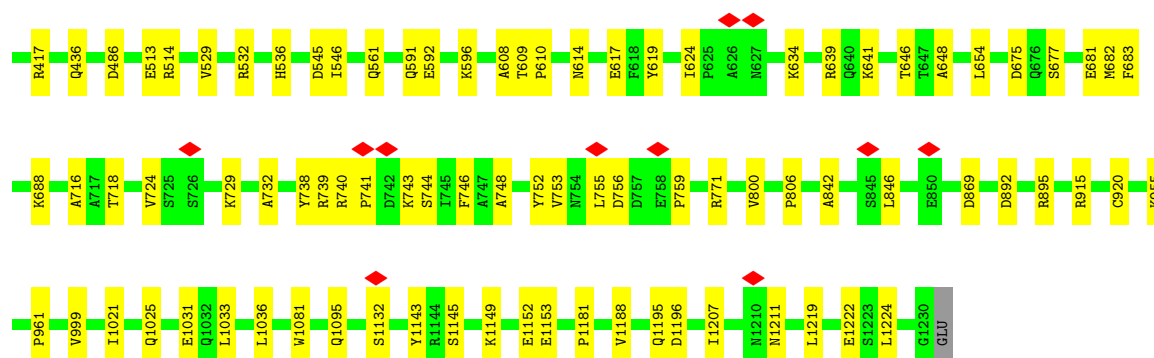
MET N2 E21 N33 K34 D36 T48 K51 Y57 N58 H59 M64 Q65 S66 E67 N68 E74 E90 L91 E92 Q93 K94 V95 D96 K97 L98 Q99 H100 E101 LEU THR LEU HIS GLN GLU PHE THR TYR GLN LYS MET GLU ARG ILE LEU GLN LEU

ALA
ARG
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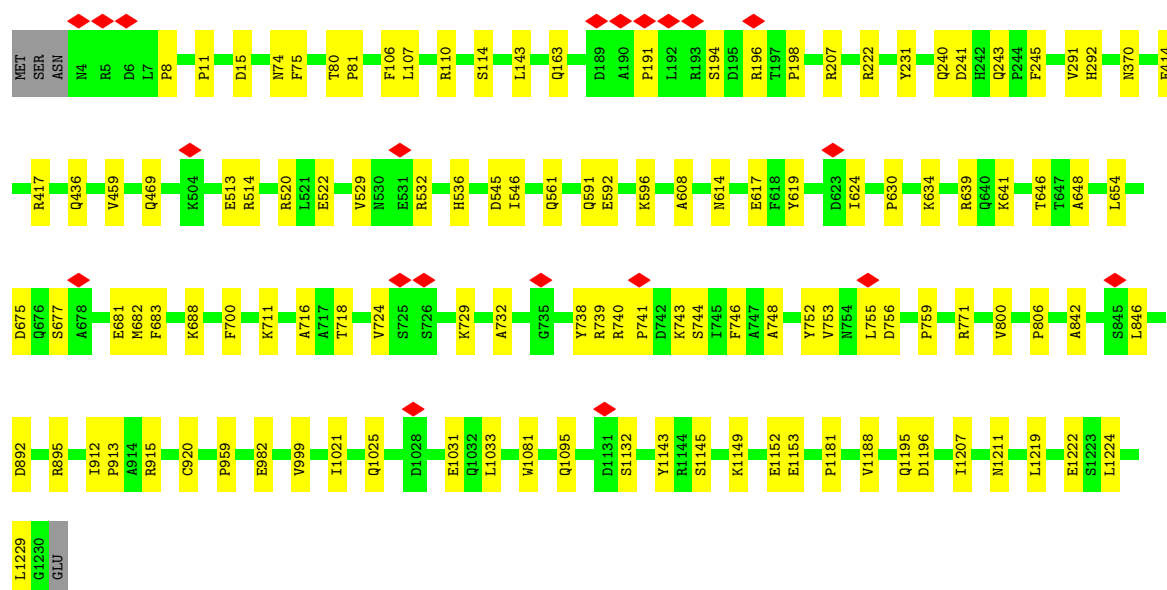
• Molecule 3: All3316 protein



MET N2 F13 N33 D36 K51 Y57 N58 M64 Q65 S66 E67 N68 K73 L87 E92 Q93 K94 V95 D96 Q99 H100 E101 LEU THR LEU HIS GLN GLU PHE THR TYR GLN LYS MET GLU ARG ILE LEU GLN LEU ALA ARG PHE ILE PRO

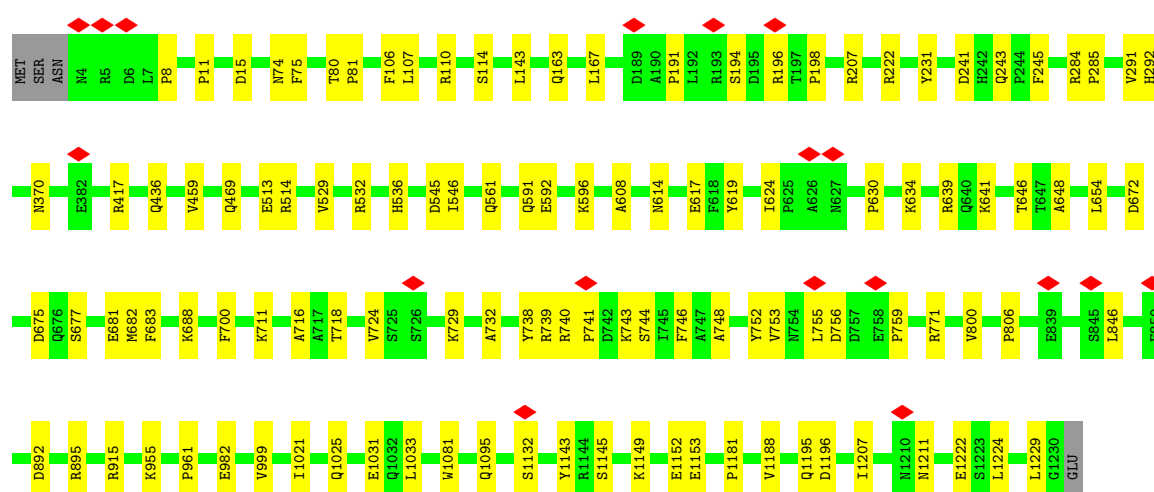


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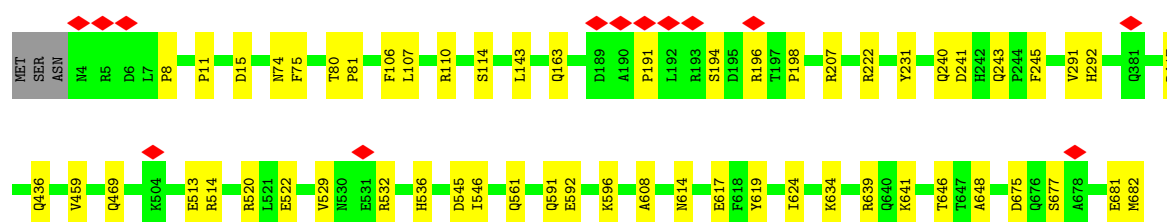
- Molecule 4: All3317 protein

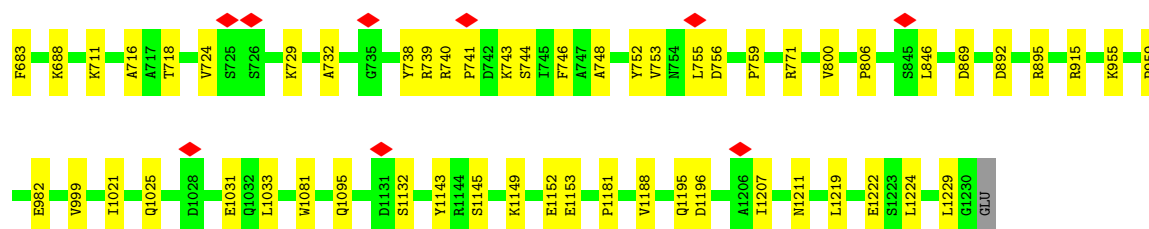
Chain EH: 



- Molecule 4: All3317 protein

Chain FH: 





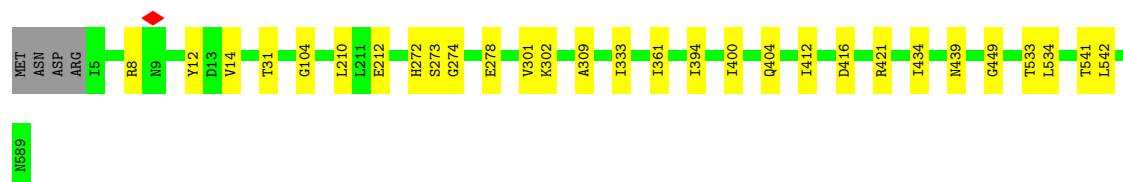
• Molecule 5: All3320 protein

Chain AJ: 95% 5%



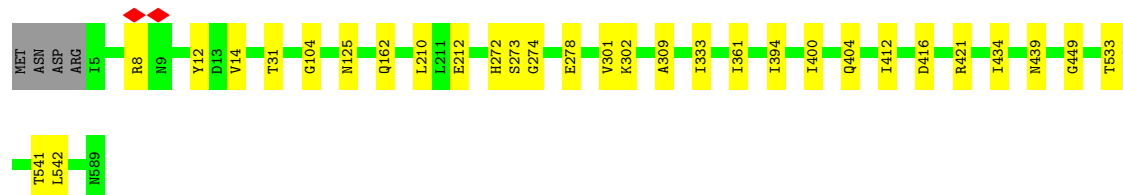
• Molecule 5: All3320 protein

Chain CJ: 94% 5%



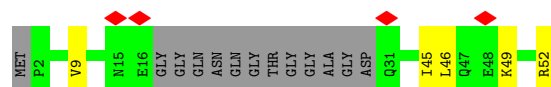
• Molecule 5: All3320 protein

Chain EJ: 94% 5%



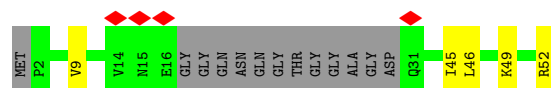
• Molecule 6: Asl3322 protein

Chain AL: 8% 64% 10% 26%

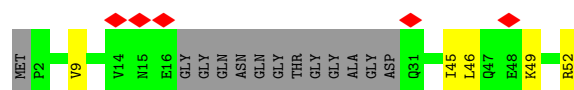


• Molecule 6: Asl3322 protein

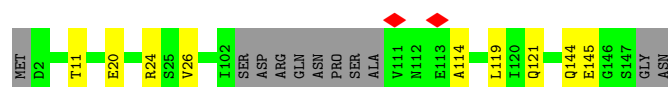
Chain CL: 8% 64% 10% 26%



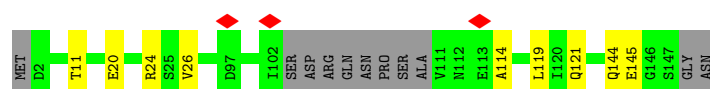
• Molecule 6: Asl3322 protein



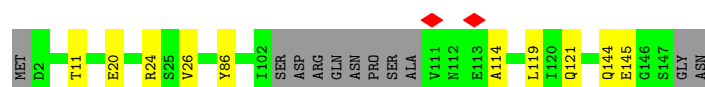
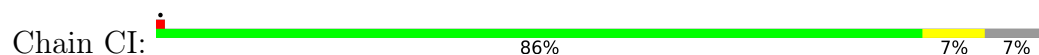
• Molecule 7: All3318 protein



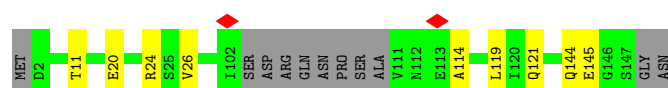
• Molecule 7: All3318 protein



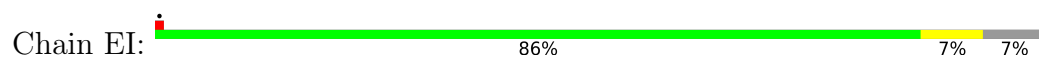
• Molecule 7: All3318 protein



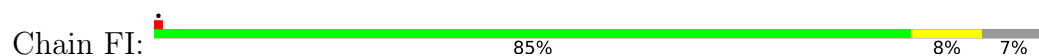
• Molecule 7: All3318 protein



• Molecule 7: All3318 protein

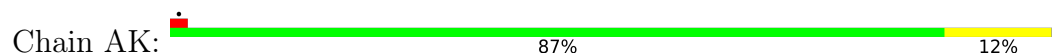


• Molecule 7: All3318 protein

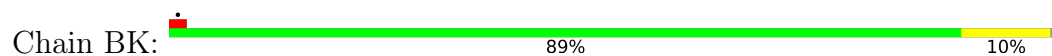




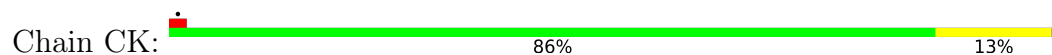
- Molecule 8: All3321 protein



- Molecule 8: All3321 protein



- Molecule 8: All3321 protein



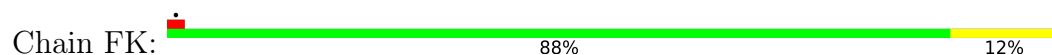
- Molecule 8: All3321 protein



- Molecule 8: All3321 protein

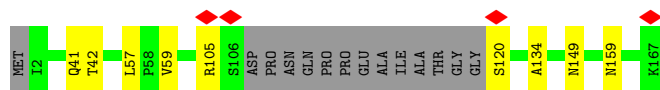


- Molecule 8: All3321 protein



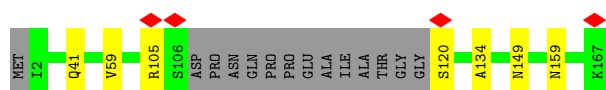
- Molecule 9: All3323 protein

Chain AM:  86% 5% 8%



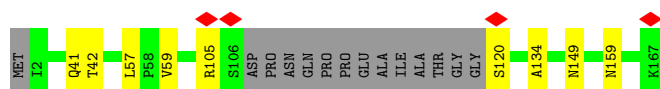
- Molecule 9: All3323 protein

Chain BM:  87% 5% 8%



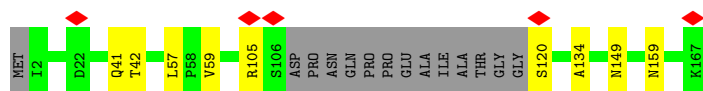
- Molecule 9: All3323 protein

Chain CM:  86% 5% 8%



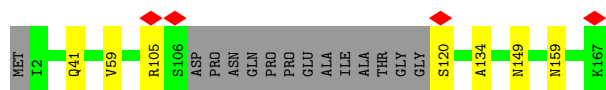
- Molecule 9: All3323 protein

Chain DM:  86% 5% 8%



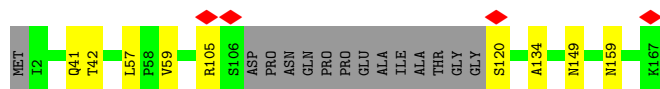
- Molecule 9: All3323 protein

Chain EM:  87% 5% 8%



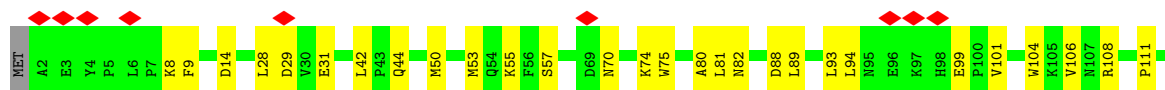
- Molecule 9: All3323 protein

Chain FM:  86% 5% 8%



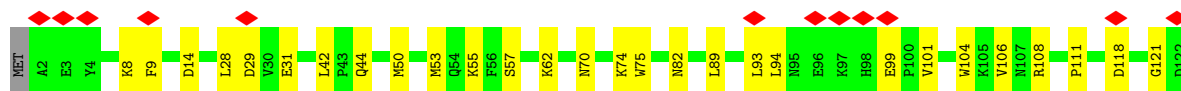
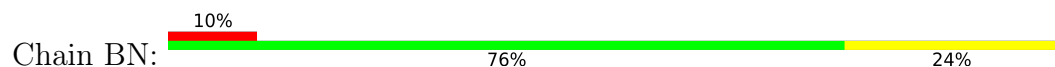
- Molecule 10: All3324 protein

Chain AN:  9% 75% 24%

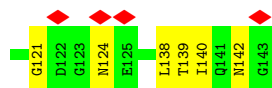
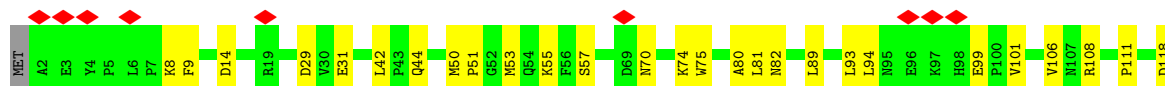
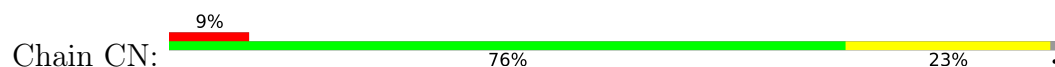




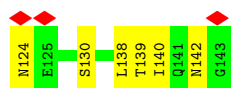
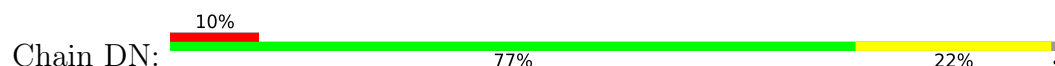
- Molecule 10: All3324 protein



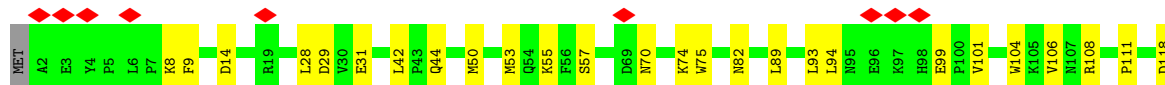
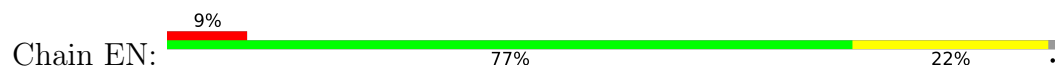
- Molecule 10: All3324 protein



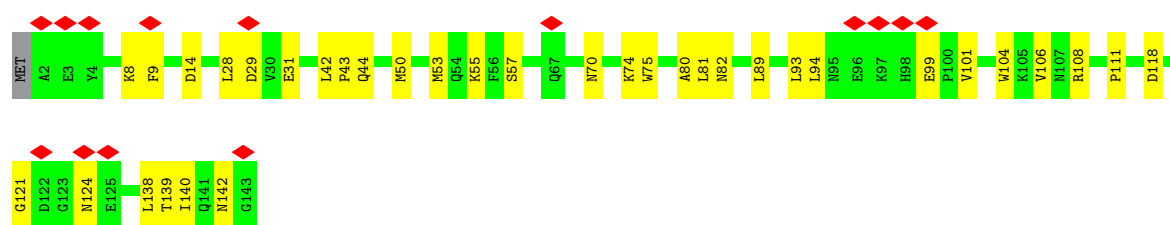
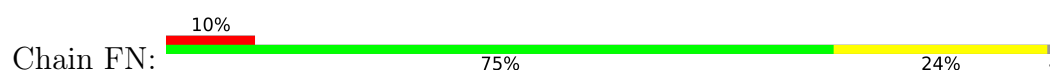
- Molecule 10: All3324 protein



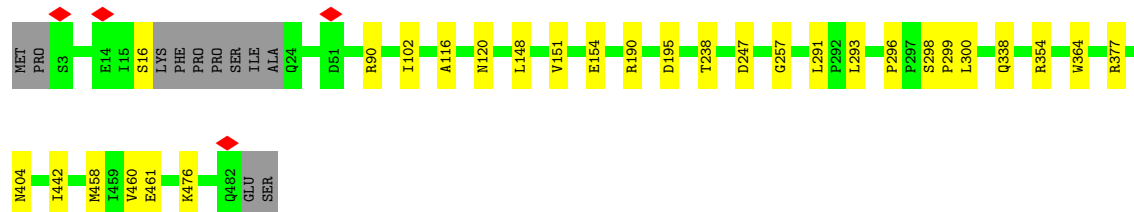
- Molecule 10: All3324 protein



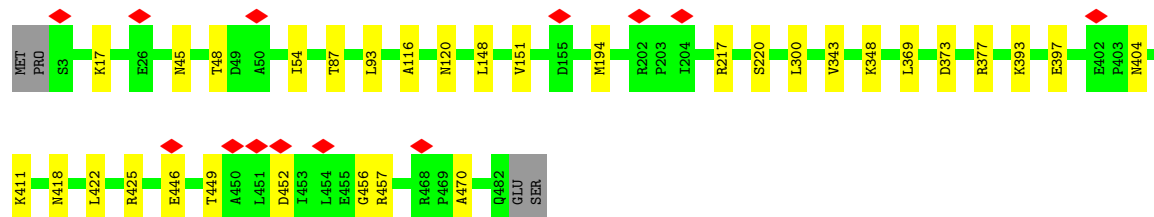
- Molecule 10: All3324 protein



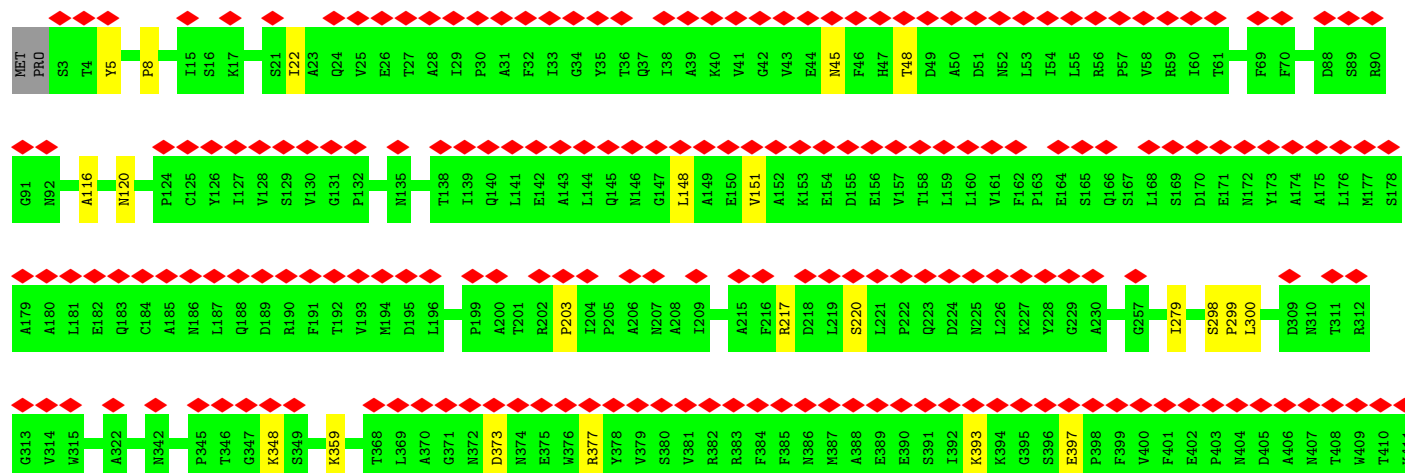
- Molecule 11: All3325 protein

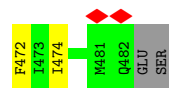
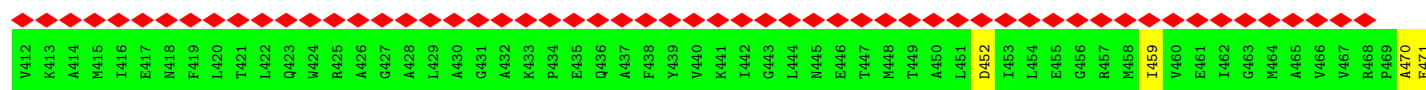


- Molecule 11: All3325 protein

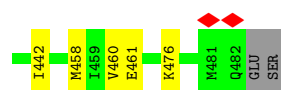


- Molecule 11: All3325 protein

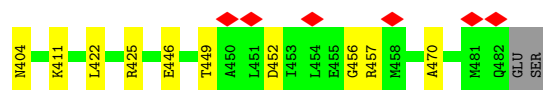
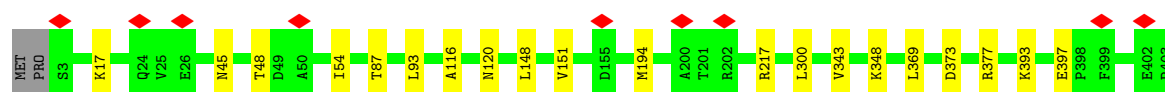




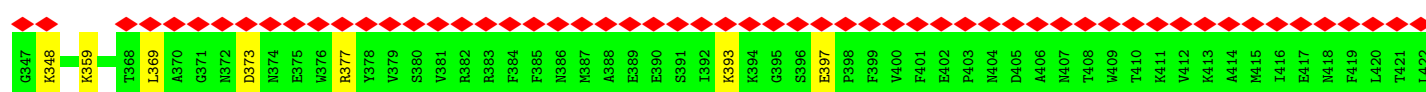
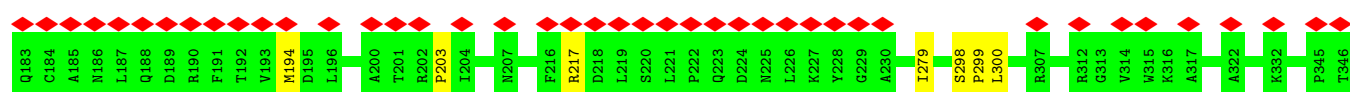
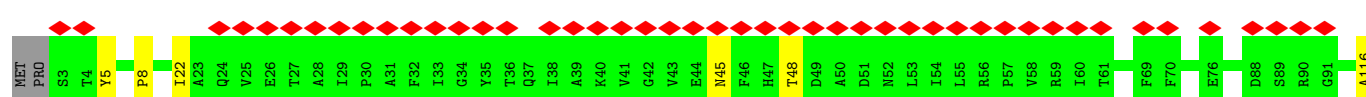
- Molecule 11: All3325 protein

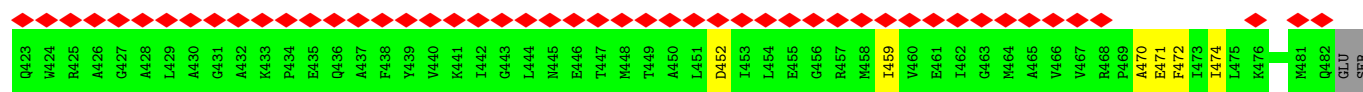


- Molecule 11: All3325 protein

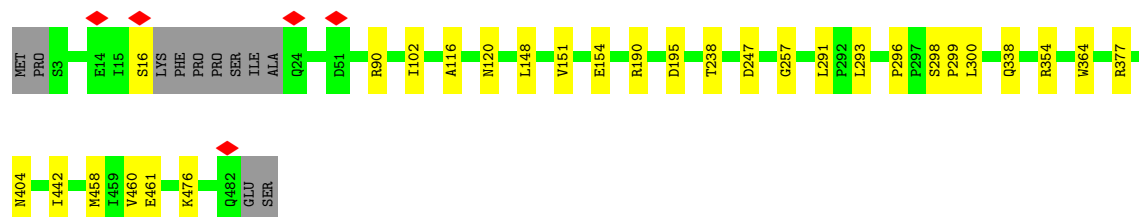


- Molecule 11: All3325 protein

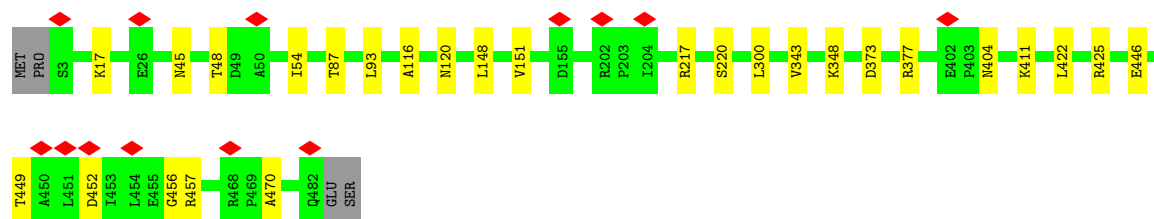




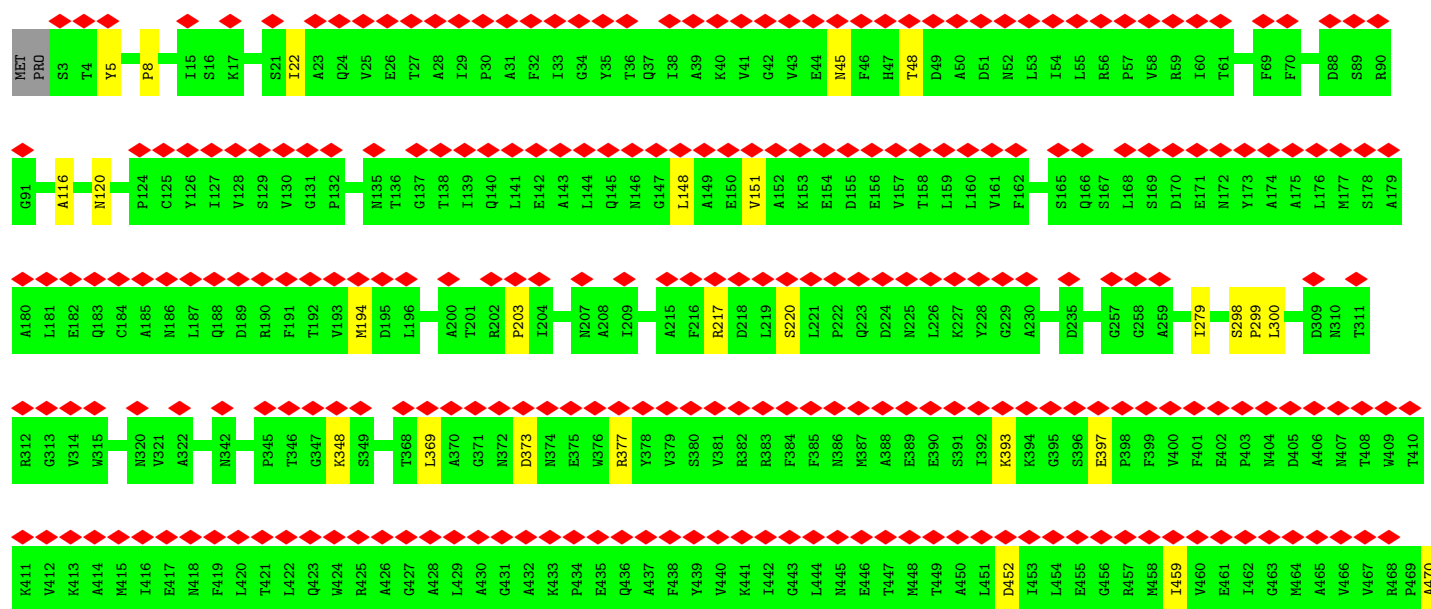
• Molecule 11: All3325 protein

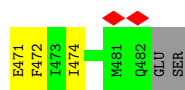


• Molecule 11: All3325 protein



• Molecule 11: All3325 protein

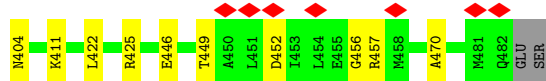
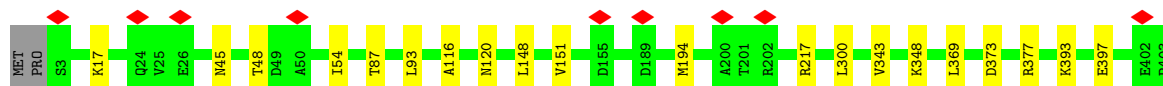




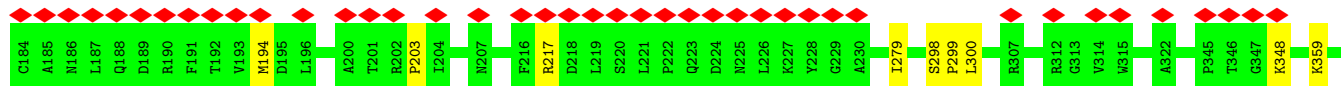
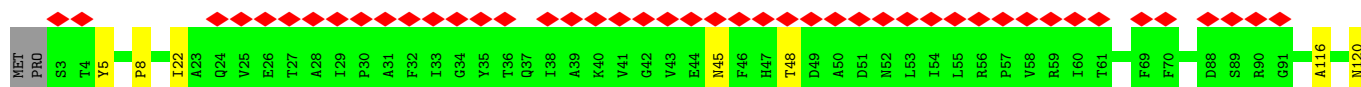
- Molecule 11: All3325 protein



- Molecule 11: All3325 protein

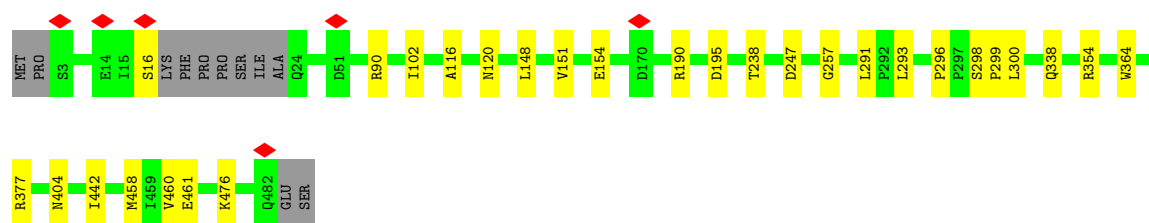


- Molecule 11: All3325 protein



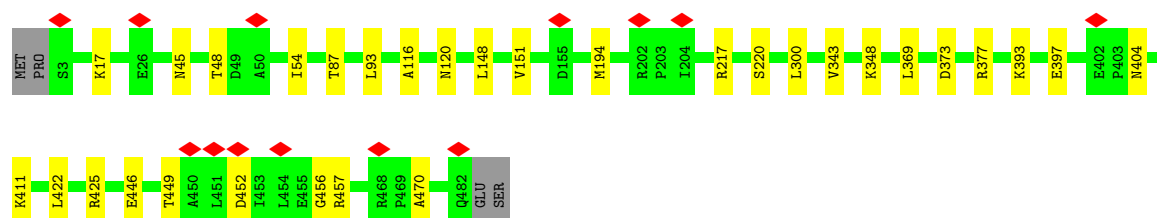
- Molecule 11: All3325 protein

Chain EO:  92% 6%



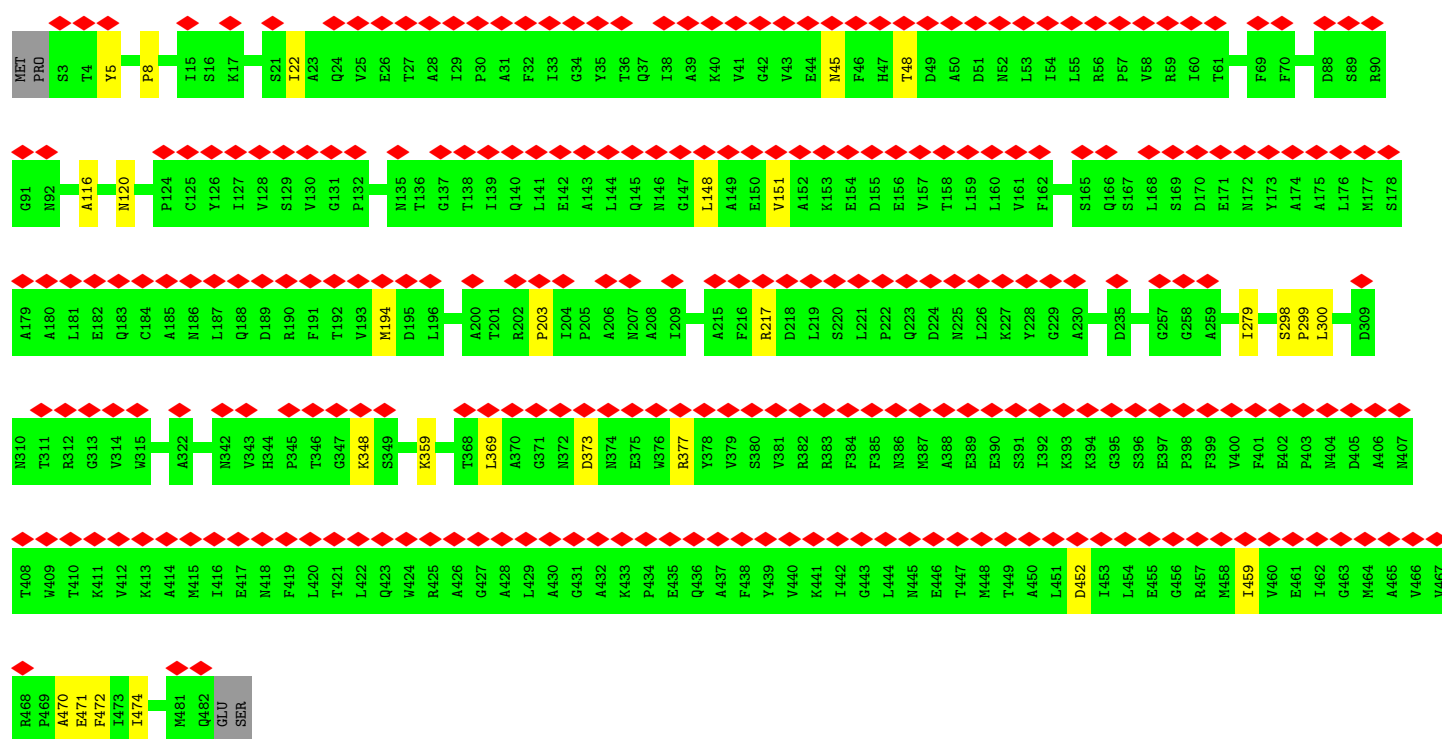
• Molecule 11: All3325 protein

Chain EP:  93% 6%



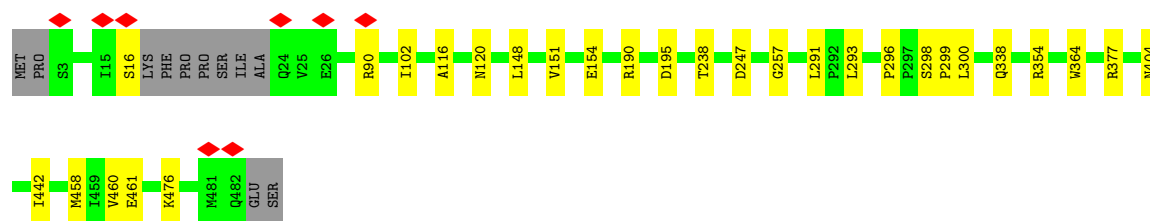
• Molecule 11: All3325 protein

Chain EQ:  54% 94% 6%

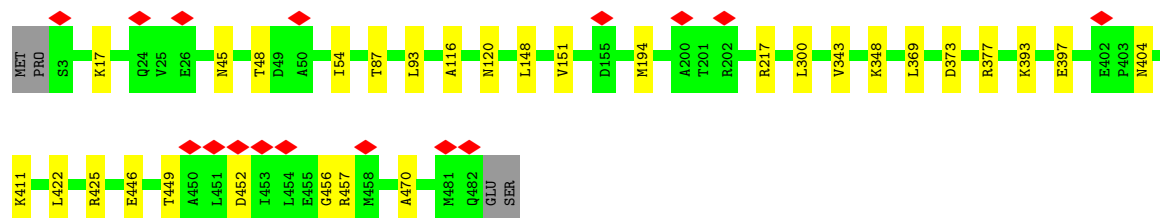


• Molecule 11: All3325 protein

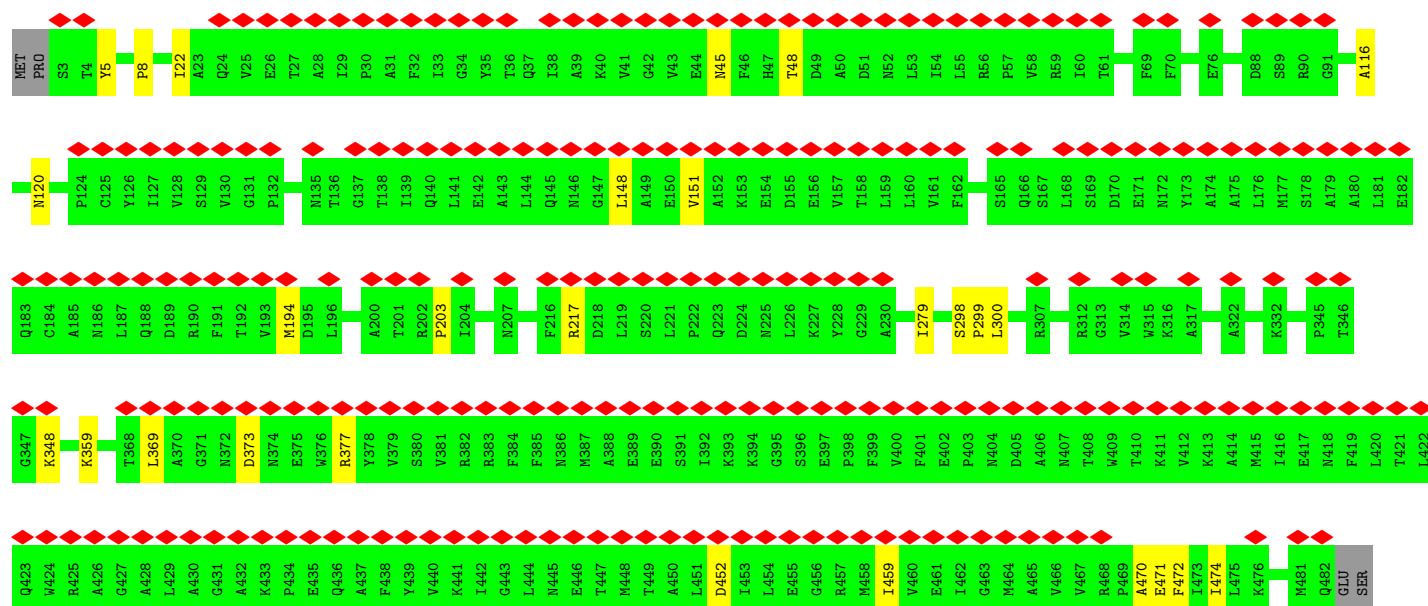
Chain FO:  92% 6%



- Molecule 11: All3325 protein



- Molecule 11: All3325 protein



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C3	Depositor
Number of particles used	36909	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 ($e^-/\text{\AA}^2$)	52	Depositor
Minimum defocus (nm)	900	Depositor
Maximum defocus (nm)	1500	Depositor
Magnification	Not provided	
Image detector	GATAN K2 QUANTUM (4k x 4k)	Depositor
Maximum map value	0.125	Depositor
Minimum map value	-0.048	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.006	Depositor
Recommended contour level	0.0275	Depositor
Map size (Å)	563.2, 563.2, 563.2	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.1, 1.1, 1.1	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	AA	0.32	0/6041	0.47	0/8212
1	AB	0.29	0/6027	0.44	0/8186
1	AC	0.31	0/5830	0.45	0/7924
1	BA	0.33	0/6041	0.47	0/8212
1	BB	0.29	0/6027	0.44	0/8186
1	BC	0.31	0/5830	0.45	0/7924
1	CA	0.33	0/6041	0.47	0/8212
1	CB	0.29	0/6027	0.44	0/8186
1	CC	0.31	0/5830	0.45	0/7924
1	DA	0.33	0/6041	0.47	0/8212
1	DB	0.29	0/6027	0.44	0/8186
1	DC	0.31	0/5830	0.45	0/7924
1	EA	0.32	0/6041	0.47	0/8212
1	EB	0.29	0/6027	0.44	0/8186
1	EC	0.31	0/5830	0.45	0/7924
1	FA	0.33	0/6041	0.47	0/8212
1	FB	0.29	0/6027	0.44	0/8186
1	FC	0.31	0/5830	0.45	0/7924
2	AD	0.24	0/9323	0.48	0/12684
2	BD	0.24	0/9323	0.48	0/12684
2	CD	0.24	0/9323	0.48	0/12684
2	DD	0.24	0/9323	0.48	0/12684
2	ED	0.24	0/9323	0.48	0/12684
2	FD	0.24	0/9323	0.48	0/12684
3	AE	0.41	0/862	0.58	0/1157
3	AF	0.33	0/862	0.43	0/1157
3	AG	0.34	0/862	0.51	0/1157
3	BE	0.41	0/862	0.58	0/1157
3	BF	0.34	0/862	0.43	0/1157
3	BG	0.34	0/862	0.51	0/1157
3	CE	0.41	0/862	0.58	0/1157
3	CF	0.33	0/862	0.43	0/1157
3	CG	0.34	0/862	0.51	0/1157
3	DE	0.41	0/862	0.58	0/1157

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
3	DF	0.34	0/862	0.43	0/1157
3	DG	0.34	0/862	0.51	0/1157
3	EE	0.41	0/862	0.58	0/1157
3	EF	0.34	0/862	0.43	0/1157
3	EG	0.34	0/862	0.51	0/1157
3	FE	0.41	0/862	0.58	0/1157
3	FF	0.33	0/862	0.43	0/1157
3	FG	0.34	0/862	0.51	0/1157
4	AH	0.26	0/10021	0.47	0/13644
4	BH	0.26	0/10021	0.48	0/13644
4	CH	0.26	0/10021	0.48	0/13644
4	DH	0.26	0/10021	0.48	0/13644
4	EH	0.26	0/10021	0.48	0/13644
4	FH	0.26	0/10021	0.48	0/13644
5	AJ	0.29	0/4507	0.43	0/6122
5	CJ	0.29	0/4507	0.43	0/6122
5	EJ	0.29	0/4507	0.43	0/6122
6	AL	0.35	0/284	0.70	0/380
6	CL	0.35	0/284	0.70	0/380
6	EL	0.35	0/284	0.70	0/380
7	AI	0.28	0/1116	0.54	0/1513
7	BI	0.28	0/1116	0.54	0/1513
7	CI	0.28	0/1116	0.54	0/1513
7	DI	0.28	0/1116	0.55	0/1513
7	EI	0.28	0/1116	0.54	0/1513
7	FI	0.28	0/1116	0.54	0/1513
8	AK	0.32	0/1942	0.56	0/2623
8	BK	0.31	0/1942	0.55	0/2623
8	CK	0.32	0/1942	0.56	0/2623
8	DK	0.31	0/1942	0.55	0/2623
8	EK	0.32	0/1942	0.56	0/2623
8	FK	0.31	0/1942	0.55	0/2623
9	AM	0.28	0/1282	0.55	0/1737
9	BM	0.28	0/1282	0.55	0/1737
9	CM	0.28	0/1282	0.55	0/1737
9	DM	0.28	0/1282	0.55	0/1737
9	EM	0.28	0/1282	0.55	0/1737
9	FM	0.28	0/1282	0.55	0/1737
10	AN	0.47	0/1181	0.76	0/1601
10	BN	0.47	0/1181	0.76	0/1601
10	CN	0.47	0/1181	0.76	0/1601
10	DN	0.47	0/1181	0.76	0/1601
10	EN	0.47	0/1181	0.76	0/1601

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
10	FN	0.47	0/1181	0.76	0/1601
11	AO	0.28	0/3738	0.49	0/5085
11	AP	0.25	0/3795	0.46	0/5165
11	AQ	0.29	0/3795	0.49	0/5165
11	BO	0.28	0/3738	0.49	0/5085
11	BP	0.25	0/3795	0.46	0/5165
11	BQ	0.29	0/3795	0.49	0/5165
11	CO	0.28	0/3738	0.49	0/5085
11	CP	0.25	0/3795	0.46	0/5165
11	CQ	0.29	0/3795	0.49	0/5165
11	DO	0.28	0/3738	0.49	0/5085
11	DP	0.26	0/3795	0.46	0/5165
11	DQ	0.29	0/3795	0.49	0/5165
11	EO	0.28	0/3738	0.49	0/5085
11	EP	0.25	0/3795	0.46	0/5165
11	EQ	0.29	0/3795	0.49	0/5165
11	FO	0.28	0/3738	0.49	0/5085
11	FP	0.25	0/3795	0.46	0/5165
11	FQ	0.29	0/3795	0.49	0/5165
All	All	0.29	0/354435	0.48	0/481566

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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	AA	5899	0	5787	60	0
1	AB	5886	0	5764	50	0
1	AC	5690	0	5581	40	0
1	BA	5899	0	5787	60	0
1	BB	5886	0	5764	50	0
1	BC	5690	0	5581	43	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	CA	5899	0	5787	62	0
1	CB	5886	0	5764	45	0
1	CC	5690	0	5581	42	0
1	DA	5899	0	5787	60	0
1	DB	5886	0	5764	44	0
1	DC	5690	0	5581	39	0
1	EA	5899	0	5787	57	0
1	EB	5886	0	5764	50	0
1	EC	5690	0	5581	41	0
1	FA	5899	0	5787	59	0
1	FB	5886	0	5764	51	0
1	FC	5690	0	5581	40	0
2	AD	9112	0	8875	118	0
2	BD	9112	0	8875	112	0
2	CD	9112	0	8875	110	0
2	DD	9112	0	8875	117	0
2	ED	9112	0	8875	113	0
2	FD	9112	0	8875	112	0
3	AE	845	0	828	13	0
3	AF	845	0	828	11	0
3	AG	845	0	829	19	0
3	BE	845	0	828	14	0
3	BF	845	0	828	11	0
3	BG	845	0	829	19	0
3	CE	845	0	828	15	0
3	CF	845	0	828	11	0
3	CG	845	0	829	20	0
3	DE	845	0	828	14	0
3	DF	845	0	828	11	0
3	DG	845	0	829	18	0
3	EE	845	0	828	14	0
3	EF	845	0	828	10	0
3	EG	845	0	829	19	0
3	FE	845	0	828	14	0
3	FF	845	0	828	11	0
3	FG	845	0	829	18	0
4	AH	9792	0	9799	105	0
4	BH	9792	0	9799	105	0
4	CH	9792	0	9799	103	0
4	DH	9792	0	9799	108	0
4	EH	9792	0	9799	106	0
4	FH	9792	0	9799	103	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	AJ	4438	0	4441	27	0
5	CJ	4438	0	4441	29	0
5	EJ	4438	0	4441	29	0
6	AL	285	0	304	5	0
6	CL	285	0	304	5	0
6	EL	285	0	304	6	0
7	AI	1098	0	1086	12	0
7	BI	1098	0	1086	12	0
7	CI	1098	0	1086	13	0
7	DI	1098	0	1086	12	0
7	EI	1098	0	1086	13	0
7	FI	1098	0	1086	14	0
8	AK	1898	0	1868	31	0
8	BK	1898	0	1868	24	0
8	CK	1898	0	1868	32	0
8	DK	1898	0	1868	24	0
8	EK	1898	0	1868	29	0
8	FK	1898	0	1868	27	0
9	AM	1254	0	1251	5	0
9	BM	1254	0	1251	4	0
9	CM	1254	0	1251	5	0
9	DM	1254	0	1251	5	0
9	EM	1254	0	1251	4	0
9	FM	1254	0	1251	5	0
10	AN	1152	0	1119	34	0
10	BN	1152	0	1119	32	0
10	CN	1152	0	1119	32	0
10	DN	1152	0	1119	31	0
10	EN	1152	0	1119	31	0
10	FN	1152	0	1119	33	0
11	AO	3663	0	3628	23	0
11	AP	3716	0	3686	31	0
11	AQ	3716	0	3686	25	0
11	BO	3663	0	3628	22	0
11	BP	3716	0	3686	31	0
11	BQ	3716	0	3686	24	0
11	CO	3663	0	3628	23	0
11	CP	3716	0	3686	28	0
11	CQ	3716	0	3686	26	0
11	DO	3663	0	3628	22	0
11	DP	3716	0	3686	30	0
11	DQ	3716	0	3686	25	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
11	EO	3663	0	3628	22	0
11	EP	3716	0	3686	32	0
11	EQ	3716	0	3686	25	0
11	FO	3663	0	3628	23	0
11	FP	3716	0	3686	31	0
11	FQ	3716	0	3686	25	0
All	All	346635	0	341925	2861	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 4.

All (2861) 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)
2:AD:157:TYR:HH	4:AH:1081:TRP:CD1	2.15	0.65
2:BD:783:ILE:C	2:BD:783:ILE:HD12	2.22	0.65
2:ED:783:ILE:C	2:ED:783:ILE:HD12	2.22	0.65
2:DD:783:ILE:C	2:DD:783:ILE:HD12	2.22	0.64
2:FD:783:ILE:C	2:FD:783:ILE:HD12	2.22	0.64
2:AD:783:ILE:C	2:AD:783:ILE:HD12	2.22	0.64
2:DD:157:TYR:HH	4:DH:1081:TRP:CD1	2.16	0.64
2:CD:783:ILE:C	2:CD:783:ILE:HD12	2.22	0.64
11:CO:476:LYS:HZ3	11:DO:16:SER:HB2	1.64	0.62
10:AN:14:ASP:CG	11:AP:411:LYS:HE2	2.27	0.60
4:DH:739:ARG:HA	4:DH:744:SER:O	2.02	0.60
2:ED:157:TYR:HH	4:EH:1081:TRP:CD1	2.20	0.60
5:CJ:31:THR:HG23	8:EK:45:ALA:HB2	1.84	0.60
10:FN:14:ASP:CG	11:FP:411:LYS:HE2	2.27	0.60
10:BN:14:ASP:CG	11:BP:411:LYS:HE2	2.27	0.60
10:BN:93:LEU:O	10:BN:101:VAL:N	2.35	0.60
2:BD:157:TYR:HH	4:BH:1081:TRP:CD1	2.20	0.59
10:AN:93:LEU:O	10:AN:101:VAL:N	2.35	0.59
4:BH:739:ARG:HA	4:BH:744:SER:O	2.02	0.59
2:CD:157:TYR:HH	4:CH:1081:TRP:CD1	2.20	0.59
4:FH:739:ARG:HA	4:FH:744:SER:O	2.02	0.59
10:EN:14:ASP:CG	11:EP:411:LYS:HE2	2.27	0.59
8:AK:45:ALA:HB2	5:EJ:31:THR:HG23	1.84	0.59
4:EH:739:ARG:HA	4:EH:744:SER:O	2.02	0.59
4:CH:739:ARG:HA	4:CH:744:SER:O	2.02	0.59
10:DN:14:ASP:CG	11:DP:411:LYS:HE2	2.27	0.59
4:AH:739:ARG:HA	4:AH:744:SER:O	2.02	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:AJ:31:THR:HG23	8:CK:45:ALA:HB2	1.84	0.58
4:CH:740:ARG:CG	4:CH:746:PHE:CE2	2.86	0.58
2:FD:157:TYR:HH	4:FH:1081:TRP:CD1	2.20	0.58
4:FH:740:ARG:CG	4:FH:746:PHE:CE2	2.86	0.58
4:BH:740:ARG:CG	4:BH:746:PHE:CE2	2.86	0.58
11:BO:476:LYS:HZ3	11:EO:16:SER:HB2	1.67	0.58
4:DH:740:ARG:CG	4:DH:746:PHE:CE2	2.86	0.58
10:CN:14:ASP:CG	11:CP:411:LYS:HE2	2.27	0.58
10:FN:93:LEU:O	10:FN:101:VAL:N	2.35	0.58
4:AH:740:ARG:CG	4:AH:746:PHE:CE2	2.86	0.58
11:CO:16:SER:HB2	11:FO:476:LYS:HZ3	1.67	0.58
8:AK:52:ASP:HB3	8:BK:161:VAL:O	2.04	0.58
8:BK:52:ASP:HB3	8:EK:161:VAL:O	2.04	0.58
4:FH:194:SER:C	4:FH:196:ARG:H	2.12	0.58
8:CK:52:ASP:HB3	8:DK:161:VAL:O	2.04	0.58
8:AK:161:VAL:O	8:DK:52:ASP:HB3	2.04	0.58
2:DD:1076:ILE:HG13	2:DD:1085:LEU:HD23	1.86	0.58
4:EH:740:ARG:CG	4:EH:746:PHE:CE2	2.86	0.58
11:AP:457:ARG:HA	11:AQ:472:PHE:O	2.04	0.57
11:BP:457:ARG:HA	11:BQ:472:PHE:O	2.04	0.57
8:CK:161:VAL:O	8:FK:52:ASP:HB3	2.04	0.57
1:DC:413:PHE:CZ	1:DC:466:TYR:HA	2.39	0.57
11:AP:446:GLU:CG	11:BQ:22:ILE:HD13	2.35	0.57
4:CH:194:SER:C	4:CH:196:ARG:H	2.12	0.57
4:EH:194:SER:C	4:EH:196:ARG:H	2.12	0.57
8:EK:52:ASP:HB3	8:FK:161:VAL:O	2.04	0.57
1:FC:413:PHE:CZ	1:FC:466:TYR:HA	2.40	0.57
4:BH:1145:SER:HB2	2:ED:303:TYR:HE2	1.69	0.57
4:CH:1145:SER:HB2	2:DD:303:TYR:HE2	1.69	0.57
8:CK:172:LYS:HB3	8:DK:108:HIS:CE1	2.40	0.57
1:AC:413:PHE:CZ	1:AC:466:TYR:HA	2.40	0.57
8:AK:172:LYS:HB3	8:BK:108:HIS:CE1	2.40	0.57
11:AQ:22:ILE:HD13	11:DP:446:GLU:CG	2.35	0.57
7:BI:114:ALA:HB1	11:BO:377:ARG:HH12	1.69	0.57
1:CC:413:PHE:CZ	1:CC:466:TYR:HA	2.40	0.57
4:CH:740:ARG:HG2	4:CH:746:PHE:CE2	2.40	0.57
7:EI:114:ALA:HB1	11:EO:377:ARG:HH12	1.69	0.57
1:BC:413:PHE:CZ	1:BC:466:TYR:HA	2.40	0.57
10:CN:93:LEU:O	10:CN:101:VAL:N	2.35	0.57
11:EP:457:ARG:HA	11:EQ:472:PHE:O	2.04	0.57
2:BD:1076:ILE:HG13	2:BD:1085:LEU:HD23	1.86	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:DP:457:ARG:HA	11:DQ:472:PHE:O	2.05	0.57
2:AD:303:TYR:HE2	4:DH:1145:SER:HB2	1.69	0.57
1:BA:22:ASN:HD21	1:BC:16:PRO:N	2.03	0.57
11:BP:446:GLU:CG	11:EQ:22:ILE:HD13	2.35	0.57
11:CP:446:GLU:CG	11:DQ:22:ILE:HD13	2.35	0.57
1:EA:22:ASN:HD21	1:EC:16:PRO:N	2.03	0.57
4:EH:740:ARG:HG2	4:EH:746:PHE:CE2	2.40	0.57
4:EH:1145:SER:HB2	2:FD:303:TYR:HE2	1.70	0.57
1:FA:22:ASN:HD21	1:FC:16:PRO:N	2.03	0.57
1:FB:163:LEU:HD21	4:FH:11:PRO:HG3	1.87	0.57
4:AH:740:ARG:HG2	4:AH:746:PHE:CE2	2.40	0.57
7:AI:114:ALA:HB1	11:AO:377:ARG:HH12	1.69	0.57
4:BH:740:ARG:HG2	4:BH:746:PHE:CE2	2.40	0.57
1:EC:413:PHE:CZ	1:EC:466:TYR:HA	2.39	0.57
2:ED:740:THR:HG22	2:ED:741:ASP:H	1.70	0.57
4:AH:194:SER:C	4:AH:196:ARG:H	2.12	0.57
4:BH:194:SER:C	4:BH:196:ARG:H	2.12	0.57
2:CD:303:TYR:HE2	4:FH:1145:SER:HB2	1.70	0.57
2:CD:1076:ILE:HG13	2:CD:1085:LEU:HD23	1.86	0.57
11:CP:457:ARG:HA	11:CQ:472:PHE:O	2.04	0.57
1:DA:551:ILE:HD11	1:DA:797:ILE:HG22	1.87	0.57
7:DI:114:ALA:HB1	11:DO:377:ARG:HH12	1.69	0.57
1:AA:413:PHE:CZ	1:AA:466:TYR:HA	2.40	0.56
2:AD:740:THR:HG22	2:AD:741:ASP:H	1.70	0.56
4:AH:1145:SER:HB2	2:BD:303:TYR:HE2	1.69	0.56
1:BB:163:LEU:HD21	4:BH:11:PRO:HG3	1.87	0.56
1:CA:413:PHE:CZ	1:CA:466:TYR:HA	2.40	0.56
1:EA:413:PHE:CZ	1:EA:466:TYR:HA	2.40	0.56
11:FQ:452:ASP:OD1	11:FQ:459:ILE:HD11	2.05	0.56
2:BD:723:LEU:HG	2:BD:723:LEU:O	2.06	0.56
4:BH:107:LEU:CD1	4:BH:207:ARG:NH1	2.69	0.56
1:DA:413:PHE:CZ	1:DA:466:TYR:HA	2.40	0.56
11:EO:476:LYS:HZ3	11:FO:16:SER:HB2	1.69	0.56
2:FD:740:THR:HG22	2:FD:741:ASP:H	1.70	0.56
11:FP:457:ARG:HA	11:FQ:472:PHE:O	2.04	0.56
1:AA:22:ASN:HD21	1:AC:16:PRO:N	2.03	0.56
2:AD:723:LEU:O	2:AD:723:LEU:HG	2.06	0.56
2:BD:740:THR:HG22	2:BD:741:ASP:H	1.70	0.56
1:CA:22:ASN:HD21	1:CC:16:PRO:N	2.03	0.56
2:CD:740:THR:HG22	2:CD:741:ASP:H	1.70	0.56
5:CJ:14:VAL:CG2	8:CK:109:LYS:HD3	2.36	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:CK:108:HIS:CE1	8:FK:172:LYS:HB3	2.40	0.56
11:CQ:22:ILE:HD13	11:FP:446:GLU:CG	2.35	0.56
2:DD:723:LEU:HG	2:DD:723:LEU:O	2.06	0.56
4:DH:194:SER:C	4:DH:196:ARG:H	2.12	0.56
10:DN:93:LEU:O	10:DN:101:VAL:N	2.35	0.56
1:EB:163:LEU:HD21	4:EH:11:PRO:HG3	1.87	0.56
1:EB:778:LEU:O	1:EB:781:PHE:O	2.24	0.56
5:EJ:14:VAL:CG2	8:EK:109:LYS:HD3	2.36	0.56
11:EQ:452:ASP:OD1	11:EQ:459:ILE:HD11	2.05	0.56
4:FH:740:ARG:HG2	4:FH:746:PHE:CE2	2.40	0.56
10:EN:93:LEU:O	10:EN:101:VAL:N	2.35	0.56
11:EP:446:GLU:CG	11:FQ:22:ILE:HD13	2.35	0.56
4:FH:107:LEU:CD1	4:FH:207:ARG:NH1	2.69	0.56
1:AA:551:ILE:HD11	1:AA:797:ILE:HG22	1.87	0.56
4:AH:107:LEU:CD1	4:AH:207:ARG:NH1	2.69	0.56
8:BK:172:LYS:HB3	8:EK:108:HIS:CE1	2.40	0.56
1:FB:413:PHE:CZ	1:FB:466:TYR:HA	2.41	0.56
1:AB:163:LEU:HD21	4:AH:11:PRO:HG3	1.87	0.56
1:AB:778:LEU:O	1:AB:781:PHE:O	2.24	0.56
1:BA:413:PHE:CZ	1:BA:466:TYR:HA	2.40	0.56
1:BB:778:LEU:O	1:BB:781:PHE:O	2.24	0.56
1:CB:163:LEU:HD21	4:CH:11:PRO:HG3	1.87	0.56
2:CD:723:LEU:HG	2:CD:723:LEU:O	2.06	0.56
7:CI:114:ALA:HB1	11:CO:377:ARG:HH12	1.69	0.56
4:DH:740:ARG:HG2	4:DH:746:PHE:CE2	2.40	0.56
2:FD:723:LEU:O	2:FD:723:LEU:HG	2.05	0.56
2:AD:1076:ILE:HG13	2:AD:1085:LEU:HD23	1.86	0.56
2:BD:204:VAL:HG11	2:BD:342:GLN:HE22	1.71	0.56
1:CA:57:ILE:HB	1:CA:64:ASN:OD1	2.06	0.56
2:ED:1076:ILE:HG13	2:ED:1085:LEU:HD23	1.86	0.56
1:FA:413:PHE:CZ	1:FA:466:TYR:HA	2.40	0.56
1:AB:163:LEU:CD2	4:AH:11:PRO:HG3	2.36	0.56
1:AB:413:PHE:CZ	1:AB:466:TYR:HA	2.41	0.56
4:AH:561:GLN:OE1	4:AH:683:PHE:HB3	2.06	0.56
5:AJ:14:VAL:CG2	8:AK:109:LYS:HD3	2.36	0.56
8:AK:108:HIS:CE1	8:DK:172:LYS:HB3	2.40	0.56
11:AO:16:SER:HB2	11:DO:476:LYS:HZ3	1.70	0.56
1:BB:413:PHE:CZ	1:BB:466:TYR:HA	2.41	0.56
11:BQ:452:ASP:OD1	11:BQ:459:ILE:HD11	2.05	0.56
1:CB:163:LEU:CD2	4:CH:11:PRO:HG3	2.36	0.56
1:DA:57:ILE:HB	1:DA:64:ASN:OD1	2.06	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:EA:213:ILE:O	1:EA:216:ILE:HG22	2.06	0.56
8:FK:232:THR:HG23	8:FK:232:THR:O	2.06	0.56
1:AA:57:ILE:HB	1:AA:64:ASN:OD1	2.06	0.56
11:AQ:452:ASP:OD1	11:AQ:459:ILE:HD11	2.05	0.56
11:CQ:452:ASP:OD1	11:CQ:459:ILE:HD11	2.05	0.56
1:DB:163:LEU:HD21	4:DH:11:PRO:HG3	1.87	0.56
2:DD:680:TYR:CD1	2:DD:807:TYR:CD1	2.94	0.56
4:DH:561:GLN:OE1	4:DH:683:PHE:HB3	2.06	0.56
2:ED:723:LEU:HG	2:ED:723:LEU:O	2.06	0.56
4:EH:107:LEU:CD1	4:EH:207:ARG:NH1	2.69	0.56
1:FA:57:ILE:HB	1:FA:64:ASN:OD1	2.06	0.56
1:BB:7:ILE:HG13	1:BB:7:ILE:O	2.06	0.56
2:BD:680:TYR:CD1	2:BD:807:TYR:CD1	2.94	0.56
4:CH:1095:GLN:NE2	4:CH:1196:ASP:O	2.39	0.56
1:DB:163:LEU:CD2	4:DH:11:PRO:HG3	2.36	0.56
1:DB:413:PHE:CZ	1:DB:466:TYR:HA	2.41	0.56
4:DH:107:LEU:CD1	4:DH:207:ARG:NH1	2.69	0.56
2:ED:204:VAL:HG11	2:ED:342:GLN:HE22	1.71	0.56
4:EH:1095:GLN:NE2	4:EH:1196:ASP:O	2.40	0.56
8:EK:232:THR:HG23	8:EK:232:THR:O	2.06	0.56
2:FD:1076:ILE:HG13	2:FD:1085:LEU:HD23	1.86	0.56
1:AB:162:LEU:O	2:AD:1216:TRP:HH2	1.89	0.55
2:AD:680:TYR:CD1	2:AD:807:TYR:CD1	2.95	0.55
1:BA:57:ILE:HB	1:BA:64:ASN:OD1	2.06	0.55
1:BB:163:LEU:CD2	4:BH:11:PRO:HG3	2.36	0.55
11:BP:446:GLU:OE2	11:EQ:22:ILE:HD11	2.07	0.55
1:DA:22:ASN:HD21	1:DC:16:PRO:N	2.03	0.55
4:BH:561:GLN:OE1	4:BH:683:PHE:HB3	2.06	0.55
1:CA:551:ILE:HD11	1:CA:797:ILE:HG22	1.87	0.55
4:CH:107:LEU:CD1	4:CH:207:ARG:NH1	2.69	0.55
1:DB:162:LEU:O	2:DD:1216:TRP:HH2	1.89	0.55
1:EA:57:ILE:HB	1:EA:64:ASN:OD1	2.06	0.55
8:EK:172:LYS:HB3	8:FK:108:HIS:CE1	2.40	0.55
11:EP:446:GLU:OE2	11:FQ:22:ILE:HD11	2.07	0.55
4:BH:1095:GLN:NE2	4:BH:1196:ASP:O	2.39	0.55
11:CP:446:GLU:OE2	11:DQ:22:ILE:HD11	2.07	0.55
1:EB:163:LEU:CD2	4:EH:11:PRO:HG3	2.36	0.55
1:FA:551:ILE:HD11	1:FA:797:ILE:HG22	1.87	0.55
1:FB:778:LEU:O	1:FB:781:PHE:O	2.24	0.55
2:AD:204:VAL:HG11	2:AD:342:GLN:HE22	1.71	0.55
4:BH:740:ARG:HB3	4:BH:741:PRO:HD2	1.89	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:CD:342:GLN:HG3	3:FG:16:LYS:O	2.07	0.55
11:CQ:22:ILE:HD11	11:FP:446:GLU:OE2	2.06	0.55
1:DA:4:THR:HG23	1:DA:363:THR:H	1.72	0.55
2:DD:204:VAL:HG11	2:DD:342:GLN:HE22	1.71	0.55
1:EA:551:ILE:HD11	1:EA:797:ILE:HG22	1.87	0.55
1:EB:7:ILE:HG13	1:EB:7:ILE:O	2.06	0.55
1:FA:213:ILE:O	1:FA:216:ILE:HG22	2.06	0.55
2:FD:204:VAL:HG11	2:FD:342:GLN:HE22	1.71	0.55
4:FH:1095:GLN:NE2	4:FH:1196:ASP:O	2.39	0.55
7:FI:114:ALA:HB1	11:FO:377:ARG:HH12	1.69	0.55
1:BA:409:LYS:HE2	1:BB:387:LEU:HA	1.88	0.55
1:CB:7:ILE:O	1:CB:7:ILE:HG13	2.06	0.55
2:CD:204:VAL:HG11	2:CD:342:GLN:HE22	1.71	0.55
2:CD:680:TYR:CD1	2:CD:807:TYR:CD1	2.94	0.55
1:DA:213:ILE:O	1:DA:216:ILE:HG22	2.06	0.55
4:DH:1095:GLN:NE2	4:DH:1196:ASP:O	2.39	0.55
1:EB:162:LEU:O	2:ED:1216:TRP:HH2	1.89	0.55
1:FB:163:LEU:CD2	4:FH:11:PRO:HG3	2.36	0.55
4:BH:746:PHE:HZ	4:BH:756:ASP:HB2	1.72	0.55
8:BK:232:THR:HG23	8:BK:232:THR:O	2.06	0.55
1:CB:413:PHE:CZ	1:CB:466:TYR:HA	2.41	0.55
8:CK:232:THR:O	8:CK:232:THR:HG23	2.06	0.55
2:DD:740:THR:HG22	2:DD:741:ASP:H	1.70	0.55
4:DH:740:ARG:HB3	4:DH:741:PRO:HD2	1.89	0.55
1:AA:409:LYS:HE2	1:AB:387:LEU:HA	1.88	0.55
2:AD:342:GLN:HG3	3:DG:16:LYS:O	2.07	0.55
4:AH:740:ARG:HB3	4:AH:741:PRO:HD2	1.89	0.55
1:BB:162:LEU:O	2:BD:1216:TRP:HH2	1.89	0.55
1:CA:4:THR:HG23	1:CA:363:THR:H	1.72	0.55
1:CB:162:LEU:O	2:CD:1216:TRP:HH2	1.89	0.55
1:CB:778:LEU:O	1:CB:781:PHE:O	2.24	0.55
1:DB:778:LEU:O	1:DB:781:PHE:O	2.24	0.55
11:DQ:452:ASP:OD1	11:DQ:459:ILE:HD11	2.05	0.55
1:EB:413:PHE:CZ	1:EB:466:TYR:HA	2.41	0.55
3:EE:34:LYS:HE3	3:EG:2:ASN:HB2	1.89	0.55
9:EM:105:ARG:NH2	9:EM:120:SER:HB3	2.22	0.55
1:FC:64:ASN:HD21	1:FC:86:LYS:HB3	1.72	0.55
4:FH:746:PHE:HZ	4:FH:756:ASP:HB2	1.72	0.55
1:AB:7:ILE:O	1:AB:7:ILE:HG13	2.06	0.55
3:AG:16:LYS:O	2:BD:342:GLN:HG3	2.07	0.55
1:CA:213:ILE:O	1:CA:216:ILE:HG22	2.06	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:DE:34:LYS:HE3	3:DG:2:ASN:HB2	1.89	0.55
1:EB:163:LEU:HD21	4:EH:11:PRO:CD	2.37	0.55
2:ED:680:TYR:CD1	2:ED:807:TYR:CD1	2.95	0.55
11:AQ:22:ILE:HD11	11:DP:446:GLU:OE2	2.07	0.55
1:BB:163:LEU:HD21	4:BH:11:PRO:CD	2.37	0.55
4:BH:800:VAL:HG13	4:BH:806:PRO:HG3	1.89	0.55
1:CC:64:ASN:HD21	1:CC:86:LYS:HB3	1.72	0.55
4:CH:740:ARG:HB3	4:CH:741:PRO:HD2	1.89	0.55
1:DC:471:THR:HG23	1:DC:476:ARG:HB2	1.89	0.55
4:DH:746:PHE:HZ	4:DH:756:ASP:HB2	1.72	0.55
4:EH:561:GLN:OE1	4:EH:683:PHE:HB3	2.06	0.55
1:AA:213:ILE:O	1:AA:216:ILE:HG22	2.06	0.55
2:AD:783:ILE:HD12	2:AD:784:GLN:HG3	1.89	0.55
1:BA:551:ILE:HD11	1:BA:797:ILE:HG22	1.87	0.55
1:BC:471:THR:HG23	1:BC:476:ARG:HB2	1.89	0.55
2:BD:783:ILE:HD12	2:BD:784:GLN:HG3	1.89	0.55
1:CB:416:ASP:OD2	1:CC:385:TYR:OH	2.25	0.55
4:CH:561:GLN:OE1	4:CH:683:PHE:HB3	2.06	0.55
1:DB:7:ILE:O	1:DB:7:ILE:HG13	2.06	0.55
3:EG:16:LYS:O	2:FD:342:GLN:HG3	2.07	0.55
4:EH:800:VAL:HG13	4:EH:806:PRO:HG3	1.89	0.55
4:FH:561:GLN:OE1	4:FH:683:PHE:HB3	2.06	0.55
1:AA:4:THR:HG23	1:AA:363:THR:H	1.72	0.54
11:AP:446:GLU:OE2	11:BQ:22:ILE:HD11	2.07	0.54
9:BM:105:ARG:NH2	9:BM:120:SER:HB3	2.22	0.54
10:BN:142:ASN:HB3	10:EN:70:ASN:HB2	1.90	0.54
2:ED:783:ILE:HD12	2:ED:784:GLN:HG3	1.89	0.54
4:EH:740:ARG:HB3	4:EH:741:PRO:HD2	1.89	0.54
4:FH:740:ARG:HB3	4:FH:741:PRO:HD2	1.89	0.54
9:FM:105:ARG:NH2	9:FM:120:SER:HB3	2.22	0.54
1:AB:163:LEU:HD21	4:AH:11:PRO:CD	2.37	0.54
10:AN:53:MET:HG3	9:BM:149:ASN:OD1	2.08	0.54
1:BA:213:ILE:O	1:BA:216:ILE:HG22	2.06	0.54
1:BC:64:ASN:HD21	1:BC:86:LYS:HB3	1.72	0.54
1:CA:409:LYS:HE2	1:CB:387:LEU:HA	1.88	0.54
3:CE:34:LYS:HE3	3:CG:2:ASN:HB2	1.89	0.54
4:CH:746:PHE:HZ	4:CH:756:ASP:HB2	1.72	0.54
2:DD:783:ILE:HD12	2:DD:784:GLN:HG3	1.89	0.54
2:FD:680:TYR:CD1	2:FD:807:TYR:CD1	2.94	0.54
4:AH:1095:GLN:NE2	4:AH:1196:ASP:O	2.39	0.54
9:CM:149:ASN:OD1	10:FN:53:MET:HG3	2.08	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:DH:753:VAL:HG12	4:DH:755:LEU:H	1.73	0.54
10:EN:142:ASN:HB3	10:FN:70:ASN:HB2	1.90	0.54
1:FA:409:LYS:HE2	1:FB:387:LEU:HA	1.88	0.54
1:FB:162:LEU:O	2:FD:1216:TRP:HH2	1.89	0.54
10:AN:70:ASN:HB2	10:DN:142:ASN:HB3	1.90	0.54
4:BH:753:VAL:HG12	4:BH:755:LEU:H	1.73	0.54
10:CN:70:ASN:HB2	10:FN:142:ASN:HB3	1.90	0.54
9:DM:105:ARG:NH2	9:DM:120:SER:HB3	2.22	0.54
1:EC:64:ASN:HD21	1:EC:86:LYS:HB3	1.72	0.54
1:EC:471:THR:HG23	1:EC:476:ARG:HB2	1.89	0.54
1:FB:7:ILE:O	1:FB:7:ILE:HG13	2.06	0.54
9:AM:149:ASN:OD1	10:DN:53:MET:HG3	2.08	0.54
1:DB:163:LEU:HD21	4:DH:11:PRO:CD	2.37	0.54
1:EA:4:THR:HG23	1:EA:363:THR:H	1.72	0.54
1:FA:854:VAL:O	1:FA:857:LYS:HG3	2.08	0.54
1:FB:163:LEU:HD21	4:FH:11:PRO:CD	2.37	0.54
3:FE:34:LYS:HE3	3:FG:2:ASN:HB2	1.89	0.54
1:AC:64:ASN:HD21	1:AC:86:LYS:HB3	1.72	0.54
4:AH:746:PHE:HZ	4:AH:756:ASP:HB2	1.72	0.54
1:CA:854:VAL:O	1:CA:857:LYS:HG3	2.08	0.54
1:CB:163:LEU:HD21	4:CH:11:PRO:CD	2.37	0.54
1:CC:471:THR:HG23	1:CC:476:ARG:HB2	1.89	0.54
10:CN:142:ASN:HB3	10:DN:70:ASN:HB2	1.90	0.54
1:EA:854:VAL:O	1:EA:857:LYS:HG3	2.08	0.54
1:AB:416:ASP:OD2	1:AC:385:TYR:OH	2.25	0.54
10:AN:142:ASN:HB3	10:BN:70:ASN:HB2	1.90	0.54
11:AQ:279:ILE:HD11	11:DP:343:VAL:HG12	1.90	0.54
1:BA:4:THR:HG23	1:BA:363:THR:H	1.72	0.54
3:BG:16:LYS:O	2:ED:342:GLN:HG3	2.07	0.54
11:BQ:298:SER:OG	11:BQ:299:PRO:HD3	2.08	0.54
3:CG:16:LYS:O	2:DD:342:GLN:HG3	2.07	0.54
10:CN:53:MET:HG3	9:DM:149:ASN:OD1	2.08	0.54
11:CP:343:VAL:HG12	11:DQ:279:ILE:HD11	1.90	0.54
1:DA:854:VAL:O	1:DA:857:LYS:HG3	2.08	0.54
8:DK:232:THR:HG23	8:DK:232:THR:O	2.06	0.54
3:AE:64:MET:HE2	3:AE:66:SER:O	2.08	0.54
8:AK:232:THR:HG23	8:AK:232:THR:O	2.06	0.54
3:BE:34:LYS:HE3	3:BG:2:ASN:HB2	1.89	0.54
4:CH:545:ASP:OD1	4:CH:546:ILE:N	2.40	0.54
1:EA:409:LYS:HE2	1:EB:387:LEU:HA	1.88	0.54
2:FD:455:ALA:HB2	2:FD:492:GLN:HG3	1.89	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:FH:800:VAL:HG13	4:FH:806:PRO:HG3	1.89	0.54
11:AQ:298:SER:OG	11:AQ:299:PRO:HD3	2.08	0.54
9:CM:105:ARG:NH2	9:CM:120:SER:HB3	2.22	0.54
4:FH:753:VAL:HG12	4:FH:755:LEU:H	1.73	0.54
1:AA:854:VAL:O	1:AA:857:LYS:HG3	2.08	0.54
2:AD:455:ALA:HB2	2:AD:492:GLN:HG3	1.89	0.54
4:AH:800:VAL:HG13	4:AH:806:PRO:HG3	1.89	0.54
9:AM:105:ARG:NH2	9:AM:120:SER:HB3	2.22	0.54
1:BA:854:VAL:O	1:BA:857:LYS:HG3	2.08	0.54
4:CH:753:VAL:HG12	4:CH:755:LEU:H	1.73	0.54
1:DA:409:LYS:HE2	1:DB:387:LEU:HA	1.88	0.54
1:FA:4:THR:HG23	1:FA:363:THR:H	1.72	0.54
2:FD:783:ILE:HD12	2:FD:784:GLN:HG3	1.89	0.54
11:FQ:298:SER:OG	11:FQ:299:PRO:HD3	2.08	0.54
1:AB:512:HIS:HE2	1:AB:885:ASP:CG	2.16	0.53
1:AC:471:THR:HG23	1:AC:476:ARG:HB2	1.89	0.53
3:AE:34:LYS:HE3	3:AG:2:ASN:HB2	1.89	0.53
8:AK:134:ASP:HB2	8:AK:156:THR:HB	1.91	0.53
10:BN:53:MET:HG3	9:EM:149:ASN:OD1	2.08	0.53
4:CH:417:ARG:HD3	4:CH:417:ARG:N	2.23	0.53
1:DC:64:ASN:HD21	1:DC:86:LYS:HB3	1.72	0.53
2:ED:455:ALA:HB2	2:ED:492:GLN:HG3	1.89	0.53
4:EH:740:ARG:HG3	4:EH:746:PHE:CE2	2.44	0.53
4:EH:746:PHE:HZ	4:EH:756:ASP:HB2	1.72	0.53
11:EQ:298:SER:OG	11:EQ:299:PRO:HD3	2.08	0.53
2:FD:18:LEU:HD21	2:FD:63:GLY:HA3	1.90	0.53
1:BB:416:ASP:OD2	1:BC:385:TYR:OH	2.25	0.53
1:BB:512:HIS:HE2	1:BB:885:ASP:CG	2.16	0.53
4:CH:740:ARG:HG3	4:CH:746:PHE:CE2	2.44	0.53
2:DD:18:LEU:HD21	2:DD:63:GLY:HA3	1.91	0.53
2:DD:455:ALA:HB2	2:DD:492:GLN:HG3	1.89	0.53
3:DE:64:MET:HE2	3:DE:66:SER:O	2.08	0.53
2:ED:18:LEU:HD21	2:ED:63:GLY:HA3	1.91	0.53
2:ED:723:LEU:HD23	2:ED:783:ILE:CD1	2.39	0.53
10:EN:53:MET:HG3	9:FM:149:ASN:OD1	2.08	0.53
4:FH:740:ARG:HG3	4:FH:746:PHE:CE2	2.44	0.53
2:AD:18:LEU:HD21	2:AD:63:GLY:HA3	1.90	0.53
2:AD:723:LEU:HD23	2:AD:783:ILE:CD1	2.39	0.53
5:AJ:404:GLN:OE1	4:CH:961:PRO:HD3	2.08	0.53
3:BE:64:MET:HE2	3:BE:66:SER:O	2.08	0.53
2:CD:41:ASP:HB2	7:CI:11:THR:O	2.09	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:CE:64:MET:HE2	3:CE:66:SER:O	2.08	0.53
1:DB:512:HIS:HE2	1:DB:885:ASP:CG	2.16	0.53
4:DH:740:ARG:HG3	4:DH:746:PHE:CE2	2.44	0.53
2:AD:41:ASP:HB2	7:AI:11:THR:O	2.09	0.53
4:BH:417:ARG:HD3	4:BH:417:ARG:N	2.23	0.53
2:CD:783:ILE:HD12	2:CD:784:GLN:HG3	1.89	0.53
4:CH:800:VAL:HG13	4:CH:806:PRO:HG3	1.89	0.53
4:DH:417:ARG:HD3	4:DH:417:ARG:N	2.23	0.53
4:EH:417:ARG:HD3	4:EH:417:ARG:N	2.23	0.53
4:EH:753:VAL:HG12	4:EH:755:LEU:H	1.73	0.53
11:EP:343:VAL:HG12	11:FQ:279:ILE:HD11	1.90	0.53
3:FE:64:MET:HE2	3:FE:66:SER:O	2.08	0.53
1:BA:385:TYR:OH	1:BC:416:ASP:OD2	2.27	0.53
1:BC:2:THR:OG1	1:BC:3:THR:N	2.42	0.53
2:BD:41:ASP:HB2	7:BI:11:THR:O	2.09	0.53
8:BK:134:ASP:HB2	8:BK:156:THR:HB	1.91	0.53
2:CD:11:LYS:HD3	8:FK:230:GLU:OE1	2.08	0.53
2:CD:18:LEU:HD21	2:CD:63:GLY:HA3	1.90	0.53
2:CD:680:TYR:CD1	2:CD:807:TYR:HD1	2.27	0.53
8:CK:134:ASP:HB2	8:CK:156:THR:HB	1.91	0.53
1:DA:610:PHE:O	1:DA:610:PHE:HD1	1.92	0.53
11:EO:116:ALA:HB1	11:EO:300:LEU:HD21	1.91	0.53
1:FA:610:PHE:O	1:FA:610:PHE:HD1	1.92	0.53
2:FD:680:TYR:CD1	2:FD:807:TYR:HD1	2.27	0.53
4:BH:740:ARG:HG3	4:BH:746:PHE:CE2	2.44	0.53
11:BP:343:VAL:HG12	11:EQ:279:ILE:HD11	1.90	0.53
2:CD:79:GLN:NE2	11:CO:257:GLY:O	2.42	0.53
11:CQ:279:ILE:HD11	11:FP:343:VAL:HG12	1.90	0.53
1:DA:385:TYR:OH	1:DC:416:ASP:OD2	2.27	0.53
2:DD:79:GLN:NE2	11:DO:257:GLY:O	2.42	0.53
4:DH:800:VAL:HG13	4:DH:806:PRO:HG3	1.89	0.53
8:DK:134:ASP:HB2	8:DK:156:THR:HB	1.91	0.53
10:DN:94:LEU:HD12	10:DN:94:LEU:N	2.24	0.53
10:EN:94:LEU:N	10:EN:94:LEU:HD12	2.24	0.53
1:AA:385:TYR:OH	1:AC:416:ASP:OD2	2.27	0.53
1:CA:385:TYR:OH	1:CC:416:ASP:OD2	2.27	0.53
1:CB:162:LEU:HD23	4:CH:8:PRO:HG2	1.91	0.53
1:CB:512:HIS:HE2	1:CB:885:ASP:CG	2.16	0.53
4:CH:291:VAL:HG12	4:CH:292:HIS:N	2.24	0.53
2:DD:723:LEU:HD23	2:DD:783:ILE:CD1	2.39	0.53
11:DQ:298:SER:OG	11:DQ:299:PRO:HD3	2.08	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:EA:610:PHE:O	1:EA:610:PHE:HD1	1.92	0.53
1:EB:512:HIS:HE2	1:EB:885:ASP:CG	2.16	0.53
2:ED:41:ASP:HB2	7:EI:11:THR:O	2.09	0.53
4:FH:417:ARG:HD3	4:FH:417:ARG:N	2.23	0.53
1:CA:610:PHE:O	1:CA:610:PHE:HD1	1.92	0.53
4:AH:417:ARG:HD3	4:AH:417:ARG:N	2.23	0.53
2:BD:18:LEU:HD21	2:BD:63:GLY:HA3	1.90	0.53
2:BD:723:LEU:HD23	2:BD:783:ILE:CD1	2.39	0.53
2:CD:723:LEU:HD23	2:CD:783:ILE:CD1	2.39	0.53
11:CQ:298:SER:OG	11:CQ:299:PRO:HD3	2.08	0.53
2:DD:680:TYR:CD1	2:DD:807:TYR:HD1	2.27	0.53
1:EA:385:TYR:OH	1:EC:416:ASP:OD2	2.27	0.53
2:ED:680:TYR:CD1	2:ED:807:TYR:HD1	2.27	0.53
8:EK:230:GLU:OE1	2:FD:11:LYS:HD3	2.08	0.53
2:FD:41:ASP:HB2	7:FI:11:THR:O	2.09	0.53
2:FD:166:ASP:OD1	2:FD:167:TYR:N	2.42	0.53
8:FK:134:ASP:HB2	8:FK:156:THR:HB	1.91	0.53
11:FO:116:ALA:HB1	11:FO:300:LEU:HD21	1.91	0.53
2:AD:519:ARG:NE	2:AD:558:GLU:OE1	2.40	0.53
4:AH:753:VAL:HG12	4:AH:755:LEU:H	1.73	0.53
4:AH:961:PRO:HD3	5:EJ:404:GLN:OE1	2.08	0.53
11:AO:404:ASN:HB2	11:AP:470:ALA:HB2	1.91	0.53
2:BD:455:ALA:HB2	2:BD:492:GLN:HG3	1.89	0.53
2:BD:680:TYR:CD1	2:BD:807:TYR:HD1	2.27	0.53
1:DB:162:LEU:HD23	4:DH:8:PRO:HG2	1.91	0.53
4:EH:681:GLU:OE1	4:EH:682:MET:N	2.39	0.53
5:EJ:14:VAL:HG22	8:EK:109:LYS:HD3	1.91	0.53
4:AH:740:ARG:HG3	4:AH:746:PHE:CE2	2.44	0.52
2:DD:41:ASP:HB2	7:DI:11:THR:O	2.09	0.52
3:EE:64:MET:HE2	3:EE:66:SER:O	2.08	0.52
8:EK:134:ASP:HB2	8:EK:156:THR:HB	1.91	0.52
1:FA:385:TYR:OH	1:FC:416:ASP:OD2	2.27	0.52
1:FB:162:LEU:HD23	4:FH:8:PRO:HG2	1.91	0.52
1:FB:416:ASP:OD2	1:FC:385:TYR:OH	2.25	0.52
1:FB:512:HIS:HE2	1:FB:885:ASP:CG	2.16	0.52
1:FC:471:THR:HG23	1:FC:476:ARG:HB2	1.89	0.52
2:AD:79:GLN:NE2	11:AO:257:GLY:O	2.42	0.52
2:AD:680:TYR:CD1	2:AD:807:TYR:HD1	2.27	0.52
4:AH:291:VAL:HG12	4:AH:292:HIS:N	2.24	0.52
10:BN:94:LEU:HD12	10:BN:94:LEU:N	2.24	0.52
2:CD:455:ALA:HB2	2:CD:492:GLN:HG3	1.89	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:CJ:404:GLN:OE1	4:EH:961:PRO:HD3	2.08	0.52
5:CJ:541:THR:O	5:CJ:542:LEU:HD23	2.10	0.52
8:CK:230:GLU:OE1	2:DD:11:LYS:HD3	2.09	0.52
2:ED:735:VAL:HG22	2:ED:749:LEU:CD2	2.39	0.52
2:FD:723:LEU:HD23	2:FD:783:ILE:CD1	2.39	0.52
10:FN:94:LEU:HD12	10:FN:94:LEU:N	2.24	0.52
1:AB:162:LEU:HD23	4:AH:8:PRO:HG2	1.91	0.52
2:AD:11:LYS:HD3	8:DK:230:GLU:OE1	2.08	0.52
1:BA:610:PHE:HD1	1:BA:610:PHE:O	1.92	0.52
2:BD:1230:ASP:OD1	2:BD:1232:PRO:HD2	2.10	0.52
8:BK:230:GLU:OE1	2:ED:11:LYS:HD3	2.08	0.52
11:BO:116:ALA:HB1	11:BO:300:LEU:HD21	1.91	0.52
2:CD:166:ASP:OD1	2:CD:167:TYR:N	2.42	0.52
2:CD:735:VAL:HG22	2:CD:749:LEU:CD2	2.39	0.52
5:CJ:14:VAL:HG22	8:CK:109:LYS:HD3	1.92	0.52
11:CO:404:ASN:HB2	11:CP:470:ALA:HB2	1.92	0.52
4:DH:545:ASP:OD1	4:DH:546:ILE:N	2.40	0.52
10:EN:50:MET:SD	10:FN:82:ASN:HB2	2.50	0.52
11:FO:404:ASN:HB2	11:FP:470:ALA:HB2	1.91	0.52
1:BC:492:THR:HB	1:BC:495:SER:HB2	1.92	0.52
2:BD:79:GLN:NE2	11:BO:257:GLY:O	2.42	0.52
2:BD:270:PHE:CZ	2:BD:388:ARG:HG2	2.44	0.52
1:EB:416:ASP:OD2	1:EC:385:TYR:OH	2.25	0.52
5:EJ:541:THR:O	5:EJ:542:LEU:HD23	2.10	0.52
2:FD:735:VAL:HG22	2:FD:749:LEU:CD2	2.39	0.52
5:AJ:14:VAL:HG22	8:AK:109:LYS:HD3	1.91	0.52
8:AK:230:GLU:OE1	2:BD:11:LYS:HD3	2.09	0.52
11:AO:476:LYS:HZ3	11:BO:16:SER:HB2	1.74	0.52
1:CB:39:THR:OG1	1:CC:40:ARG:NH1	2.42	0.52
2:CD:1230:ASP:OD1	2:CD:1232:PRO:HD2	2.10	0.52
2:DD:1230:ASP:OD1	2:DD:1232:PRO:HD2	2.10	0.52
11:DO:116:ALA:HB1	11:DO:300:LEU:HD21	1.91	0.52
2:ED:1230:ASP:OD1	2:ED:1232:PRO:HD2	2.10	0.52
1:FA:294:ASP:OD2	1:FA:415:TYR:OH	2.24	0.52
2:FD:1230:ASP:OD1	2:FD:1232:PRO:HD2	2.10	0.52
5:AJ:541:THR:O	5:AJ:542:LEU:HD23	2.10	0.52
2:CD:6:SER:HB3	7:FI:144:GLN:NE2	2.25	0.52
10:CN:138:LEU:HD23	10:CN:139:THR:N	2.25	0.52
10:DN:138:LEU:HD23	10:DN:139:THR:N	2.25	0.52
2:ED:166:ASP:OD1	2:ED:167:TYR:N	2.42	0.52
2:AD:270:PHE:CZ	2:AD:388:ARG:HG2	2.44	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:AD:735:VAL:HG22	2:AD:749:LEU:CD2	2.39	0.52
2:AD:1230:ASP:OD1	2:AD:1232:PRO:HD2	2.10	0.52
2:BD:735:VAL:HG22	2:BD:749:LEU:CD2	2.39	0.52
4:BH:545:ASP:OD1	4:BH:546:ILE:N	2.40	0.52
10:BN:50:MET:SD	10:EN:82:ASN:HB2	2.50	0.52
2:DD:735:VAL:HG22	2:DD:749:LEU:CD2	2.39	0.52
1:EB:39:THR:OG1	1:EC:40:ARG:NH1	2.42	0.52
7:EI:144:GLN:NE2	2:FD:6:SER:HB3	2.25	0.52
2:FD:519:ARG:NE	2:FD:558:GLU:OE1	2.40	0.52
1:AC:492:THR:HB	1:AC:495:SER:HB2	1.92	0.52
2:AD:1117:ILE:HD13	2:AD:1141:TYR:OH	2.10	0.52
4:AH:545:ASP:OD1	4:AH:546:ILE:N	2.40	0.52
10:AN:82:ASN:HB2	10:DN:50:MET:SD	2.50	0.52
2:BD:102:GLU:HG3	2:BD:120:LEU:HD12	1.92	0.52
1:CC:2:THR:OG1	1:CC:3:THR:N	2.42	0.52
10:CN:94:LEU:N	10:CN:94:LEU:HD12	2.24	0.52
1:DB:416:ASP:OD2	1:DC:385:TYR:OH	2.25	0.52
1:EB:162:LEU:HD23	4:EH:8:PRO:HG2	1.91	0.52
2:ED:79:GLN:NE2	11:EO:257:GLY:O	2.42	0.52
10:AN:138:LEU:HD23	10:AN:139:THR:N	2.25	0.52
7:CI:144:GLN:NE2	2:DD:6:SER:HB3	2.25	0.52
10:CN:50:MET:SD	10:DN:82:ASN:HB2	2.50	0.52
11:DO:404:ASN:HB2	11:DP:470:ALA:HB2	1.91	0.52
2:ED:270:PHE:CZ	2:ED:388:ARG:HG2	2.44	0.52
1:AA:610:PHE:O	1:AA:610:PHE:HD1	1.92	0.52
5:AJ:541:THR:C	5:AJ:542:LEU:HD23	2.36	0.52
7:AI:144:GLN:NE2	2:BD:6:SER:HB3	2.25	0.52
10:AN:50:MET:SD	10:BN:82:ASN:HB2	2.50	0.52
11:AP:343:VAL:HG12	11:BQ:279:ILE:HD11	1.90	0.52
4:BH:243:GLN:NE2	7:BI:26:VAL:H	2.08	0.52
4:CH:74:ASN:O	7:CI:24:ARG:CD	2.58	0.52
2:DD:270:PHE:CZ	2:DD:388:ARG:HG2	2.44	0.52
2:ED:813:VAL:HG12	2:ED:819:LEU:HA	1.92	0.52
2:AD:6:SER:HB3	7:DI:144:GLN:NE2	2.25	0.51
4:AH:243:GLN:NE2	7:AI:26:VAL:H	2.08	0.51
11:AO:116:ALA:HB1	11:AO:300:LEU:HD21	1.91	0.51
2:BD:166:ASP:OD1	2:BD:167:TYR:N	2.42	0.51
2:CD:695:ILE:HG22	2:CD:696:VAL:HG13	1.92	0.51
11:CO:116:ALA:HB1	11:CO:300:LEU:HD21	1.91	0.51
2:DD:1117:ILE:HD13	2:DD:1141:TYR:OH	2.10	0.51
4:DH:291:VAL:HG12	4:DH:292:HIS:N	2.24	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:ED:102:GLU:HG3	2:ED:120:LEU:HD12	1.92	0.51
2:ED:1117:ILE:HD13	2:ED:1141:TYR:OH	2.10	0.51
2:FD:813:VAL:HG12	2:FD:819:LEU:HA	1.92	0.51
10:FN:138:LEU:HD23	10:FN:139:THR:N	2.25	0.51
1:BB:162:LEU:HD23	4:BH:8:PRO:HG2	1.91	0.51
4:BH:74:ASN:O	7:BI:24:ARG:CD	2.58	0.51
10:CN:82:ASN:HB2	10:FN:50:MET:SD	2.50	0.51
2:DD:166:ASP:OD1	2:DD:167:TYR:N	2.42	0.51
2:DD:695:ILE:HG22	2:DD:696:VAL:HG13	1.92	0.51
11:DP:54:ILE:HD11	11:DQ:203:PRO:HG3	1.93	0.51
5:EJ:541:THR:C	5:EJ:542:LEU:HD23	2.35	0.51
1:FB:39:THR:OG1	1:FC:40:ARG:NH1	2.42	0.51
4:FH:291:VAL:HG12	4:FH:292:HIS:N	2.24	0.51
2:AD:166:ASP:OD1	2:AD:167:TYR:N	2.42	0.51
10:AN:94:LEU:HD12	10:AN:94:LEU:N	2.24	0.51
2:BD:1117:ILE:HD13	2:BD:1141:TYR:OH	2.10	0.51
1:CC:492:THR:HB	1:CC:495:SER:HB2	1.92	0.51
11:CP:54:ILE:HD11	11:CQ:203:PRO:HG3	1.93	0.51
1:EC:492:THR:HB	1:EC:495:SER:HB2	1.92	0.51
2:BD:779:SER:O	2:BD:783:ILE:HG23	2.11	0.51
11:BO:404:ASN:HB2	11:BP:470:ALA:HB2	1.91	0.51
2:CD:270:PHE:CZ	2:CD:388:ARG:HG2	2.44	0.51
2:DD:102:GLU:HG3	2:DD:120:LEU:HD12	1.92	0.51
4:EH:291:VAL:HG12	4:EH:292:HIS:N	2.24	0.51
10:EN:138:LEU:HD23	10:EN:139:THR:N	2.25	0.51
1:BB:389:SER:HB3	1:BB:390:PRO:HD2	1.93	0.51
4:CH:222:ARG:NH1	2:DD:377:GLN:HG2	2.26	0.51
1:DC:2:THR:OG1	1:DC:3:THR:N	2.42	0.51
2:ED:519:ARG:NE	2:ED:558:GLU:OE1	2.40	0.51
2:AD:102:GLU:HG3	2:AD:120:LEU:HD12	1.92	0.51
2:BD:813:VAL:HG12	2:BD:819:LEU:HA	1.92	0.51
2:CD:629:ASN:HB2	2:CD:1067:LEU:HB2	1.93	0.51
2:CD:1117:ILE:HD13	2:CD:1141:TYR:OH	2.10	0.51
5:CJ:541:THR:C	5:CJ:542:LEU:HD23	2.35	0.51
1:DB:39:THR:OG1	1:DC:40:ARG:NH1	2.42	0.51
4:DH:243:GLN:NE2	7:DI:26:VAL:H	2.08	0.51
4:EH:243:GLN:NE2	7:EI:26:VAL:H	2.08	0.51
11:EO:404:ASN:HB2	11:EP:470:ALA:HB2	1.91	0.51
1:FB:389:SER:HB3	1:FB:390:PRO:HD2	1.93	0.51
1:FC:2:THR:OG1	1:FC:3:THR:N	2.42	0.51
2:FD:270:PHE:CZ	2:FD:388:ARG:HG2	2.44	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:FD:779:SER:O	2:FD:783:ILE:HG23	2.11	0.51
10:FN:70:ASN:O	10:FN:74:LYS:HE2	2.11	0.51
1:AB:389:SER:HB3	1:AB:390:PRO:HD2	1.93	0.51
2:AD:779:SER:O	2:AD:783:ILE:HG23	2.11	0.51
4:AH:646:THR:HG22	4:AH:646:THR:O	2.11	0.51
4:BH:732:ALA:HB2	4:BH:752:TYR:HD1	1.76	0.51
4:DH:74:ASN:O	7:DI:24:ARG:CD	2.58	0.51
10:DN:70:ASN:O	10:DN:74:LYS:HE2	2.11	0.51
1:EB:389:SER:HB3	1:EB:390:PRO:HD2	1.93	0.51
2:ED:779:SER:O	2:ED:783:ILE:HG23	2.11	0.51
4:EH:545:ASP:OD1	4:EH:546:ILE:N	2.40	0.51
2:FD:695:ILE:HG22	2:FD:696:VAL:HG13	1.92	0.51
4:AH:74:ASN:O	7:AI:24:ARG:CD	2.58	0.51
1:BB:39:THR:OG1	1:BC:40:ARG:NH1	2.42	0.51
2:CD:377:GLN:HG2	4:FH:222:ARG:NH1	2.26	0.51
11:CP:87:THR:HG22	11:CP:93:LEU:HA	1.93	0.51
1:EA:27:ARG:HH22	1:EB:158:ARG:NH2	2.09	0.51
1:FA:27:ARG:HH22	1:FB:158:ARG:NH2	2.09	0.51
1:FC:492:THR:HB	1:FC:495:SER:HB2	1.92	0.51
11:FP:54:ILE:HD11	11:FQ:203:PRO:HG3	1.93	0.51
11:AP:446:GLU:HG3	11:BQ:22:ILE:HD13	1.93	0.51
2:BD:695:ILE:HG22	2:BD:696:VAL:HG13	1.92	0.51
4:BH:291:VAL:HG12	4:BH:292:HIS:N	2.24	0.51
7:BI:144:GLN:NE2	2:ED:6:SER:HB3	2.25	0.51
10:BN:138:LEU:HD23	10:BN:139:THR:N	2.25	0.51
2:CD:813:VAL:HG12	2:CD:819:LEU:HA	1.92	0.51
1:DC:492:THR:HB	1:DC:495:SER:HB2	1.92	0.51
2:DD:519:ARG:NE	2:DD:558:GLU:OE1	2.40	0.51
4:EH:222:ARG:NH1	2:FD:377:GLN:HG2	2.26	0.51
2:AD:377:GLN:HG2	4:DH:222:ARG:NH1	2.26	0.51
2:AD:629:ASN:HB2	2:AD:1067:LEU:HB2	1.93	0.51
11:AP:54:ILE:HD11	11:AQ:203:PRO:HG3	1.93	0.51
4:BH:681:GLU:OE1	4:BH:682:MET:N	2.39	0.51
1:CB:389:SER:HB3	1:CB:390:PRO:HD2	1.93	0.51
2:DD:629:ASN:HB2	2:DD:1067:LEU:HB2	1.93	0.51
4:EH:732:ALA:HB2	4:EH:752:TYR:HD1	1.76	0.51
10:EN:70:ASN:O	10:EN:74:LYS:HE2	2.11	0.51
4:FH:74:ASN:O	7:FI:24:ARG:CD	2.58	0.51
4:FH:243:GLN:NE2	7:FI:26:VAL:H	2.08	0.51
1:AB:162:LEU:O	2:AD:1216:TRP:CH2	2.64	0.50
11:AQ:22:ILE:HD13	11:DP:446:GLU:HG3	1.93	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:BD:629:ASN:HB2	2:BD:1067:LEU:HB2	1.93	0.50
3:BG:18:ARG:HG3	4:BH:1222:GLU:O	2.11	0.50
4:BH:646:THR:O	4:BH:646:THR:HG22	2.11	0.50
11:BP:446:GLU:HG3	11:EQ:22:ILE:HD13	1.93	0.50
2:CD:779:SER:O	2:CD:783:ILE:HG23	2.11	0.50
4:EH:74:ASN:O	7:EI:24:ARG:CD	2.58	0.50
3:AG:18:ARG:HG3	4:AH:1222:GLU:O	2.11	0.50
1:BA:27:ARG:HH22	1:BB:158:ARG:NH2	2.09	0.50
10:CN:70:ASN:O	10:CN:74:LYS:HE2	2.11	0.50
1:EB:162:LEU:O	2:ED:1216:TRP:CH2	2.64	0.50
1:CA:27:ARG:HH22	1:CB:158:ARG:NH2	2.09	0.50
2:CD:102:GLU:HG3	2:CD:120:LEU:HD12	1.92	0.50
3:CG:18:ARG:HG3	4:CH:1222:GLU:O	2.11	0.50
5:CJ:394:ILE:CG1	5:CJ:412:ILE:HD11	2.42	0.50
2:FD:1117:ILE:HD13	2:FD:1141:TYR:OH	2.10	0.50
11:FP:87:THR:HG22	11:FP:93:LEU:HA	1.93	0.50
4:AH:732:ALA:HB2	4:AH:752:TYR:HD1	1.76	0.50
5:AJ:394:ILE:CG1	5:AJ:412:ILE:HD11	2.42	0.50
4:CH:243:GLN:NE2	7:CI:26:VAL:H	2.08	0.50
1:DB:389:SER:HB3	1:DB:390:PRO:HD2	1.93	0.50
1:DB:898:THR:HG22	1:DB:900:SER:H	1.77	0.50
4:DH:646:THR:HG22	4:DH:646:THR:O	2.11	0.50
5:AJ:104:GLY:HA2	8:FK:46:GLN:NE2	2.27	0.50
1:BA:548:PHE:CD2	1:BA:549:GLN:HG2	2.47	0.50
10:BN:29:ASP:OD1	10:BN:57:SER:HB3	2.12	0.50
10:BN:70:ASN:O	10:BN:74:LYS:HE2	2.11	0.50
1:CB:898:THR:HG22	1:CB:900:SER:H	1.77	0.50
3:DG:18:ARG:HG3	4:DH:1222:GLU:O	2.11	0.50
11:DP:87:THR:HG22	11:DP:93:LEU:HA	1.93	0.50
11:FP:397:GLU:OE1	11:FQ:359:LYS:NZ	2.41	0.50
1:AB:39:THR:OG1	1:AC:40:ARG:NH1	2.42	0.50
1:AB:898:THR:HG22	1:AB:900:SER:H	1.77	0.50
5:AJ:361:ILE:HG22	6:CL:52:ARG:NH2	2.27	0.50
10:AN:70:ASN:O	10:AN:74:LYS:HE2	2.11	0.50
1:BC:384:VAL:O	1:BC:384:VAL:HG12	2.12	0.50
4:BH:222:ARG:NH1	2:ED:377:GLN:HG2	2.26	0.50
1:CB:162:LEU:O	2:CD:1216:TRP:CH2	2.64	0.50
10:CN:29:ASP:OD1	10:CN:57:SER:HB3	2.12	0.50
11:CP:446:GLU:HG3	11:DQ:22:ILE:HD13	1.93	0.50
8:DK:46:GLN:NE2	5:EJ:104:GLY:HA2	2.27	0.50
10:DN:29:ASP:OD1	10:DN:57:SER:HB3	2.12	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:EB:898:THR:HG22	1:EB:900:SER:H	1.77	0.50
2:ED:629:ASN:HB2	2:ED:1067:LEU:HB2	1.93	0.50
5:EJ:278:GLU:HB3	4:FH:959:PRO:HD2	1.94	0.50
1:FB:898:THR:HG22	1:FB:900:SER:H	1.77	0.50
2:FD:79:GLN:NE2	11:FO:257:GLY:O	2.42	0.50
2:FD:102:GLU:HG3	2:FD:120:LEU:HD12	1.92	0.50
2:FD:629:ASN:HB2	2:FD:1067:LEU:HB2	1.93	0.50
2:AD:813:VAL:HG12	2:AD:819:LEU:HA	1.92	0.50
5:AJ:394:ILE:HG12	5:AJ:412:ILE:HD11	1.94	0.50
1:BA:107:GLN:O	1:BA:107:GLN:HG3	2.12	0.50
1:BB:898:THR:HG22	1:BB:900:SER:H	1.77	0.50
11:BP:54:ILE:HD11	11:BQ:203:PRO:HG3	1.93	0.50
2:CD:519:ARG:NE	2:CD:558:GLU:OE1	2.40	0.50
1:DA:548:PHE:CD2	1:DA:549:GLN:HG2	2.47	0.50
11:EP:54:ILE:HD11	11:EQ:203:PRO:HG3	1.93	0.50
1:FA:107:GLN:HG3	1:FA:107:GLN:O	2.12	0.50
3:FG:18:ARG:HG3	4:FH:1222:GLU:O	2.11	0.50
1:AA:107:GLN:HG3	1:AA:107:GLN:O	2.12	0.50
2:AD:695:ILE:HG22	2:AD:696:VAL:HG13	1.92	0.50
4:AH:222:ARG:NH1	2:BD:377:GLN:HG2	2.26	0.50
4:CH:740:ARG:HB3	4:CH:741:PRO:CD	2.42	0.50
5:CJ:533:THR:O	5:CJ:534:LEU:HD23	2.12	0.50
10:CN:139:THR:HG22	10:CN:140:ILE:N	2.27	0.50
1:DA:27:ARG:HH22	1:DB:158:ARG:NH2	2.09	0.50
1:DB:162:LEU:O	2:DD:1216:TRP:CH2	2.64	0.50
1:EC:384:VAL:HG12	1:EC:384:VAL:O	2.12	0.50
2:ED:695:ILE:HG22	2:ED:696:VAL:HG13	1.92	0.50
4:AH:740:ARG:HB3	4:AH:741:PRO:CD	2.42	0.50
11:AP:17:LYS:HE2	11:DO:461:GLU:OE2	2.12	0.50
11:BP:116:ALA:HB1	11:BP:300:LEU:HD21	1.94	0.50
11:BQ:474:ILE:HD13	11:EQ:5:TYR:CZ	2.47	0.50
5:CJ:278:GLU:HB3	4:DH:959:PRO:HD2	1.94	0.50
2:DD:779:SER:O	2:DD:783:ILE:HG23	2.11	0.50
2:DD:813:VAL:HG12	2:DD:819:LEU:HA	1.92	0.50
4:DH:846:LEU:HD23	4:DH:915:ARG:HH22	1.77	0.50
1:EA:548:PHE:CD2	1:EA:549:GLN:HG2	2.47	0.50
5:EJ:533:THR:O	5:EJ:534:LEU:HD23	2.12	0.50
1:FA:16:PRO:HD3	1:FB:22:ASN:ND2	2.27	0.50
4:AH:846:LEU:HD23	4:AH:915:ARG:HH22	1.77	0.49
11:BQ:116:ALA:HB1	11:BQ:300:LEU:HD21	1.94	0.49
1:CA:16:PRO:HD3	1:CB:22:ASN:ND2	2.27	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:FN:29:ASP:OD1	10:FN:57:SER:HB3	2.12	0.49
1:AA:27:ARG:HH22	1:AB:158:ARG:NH2	2.09	0.49
1:AA:548:PHE:CD2	1:AA:549:GLN:HG2	2.47	0.49
11:AO:461:GLU:OE2	11:BP:17:LYS:HE2	2.12	0.49
1:BA:16:PRO:HD3	1:BB:22:ASN:ND2	2.27	0.49
4:BH:740:ARG:HB3	4:BH:741:PRO:CD	2.42	0.49
8:BK:46:GLN:NE2	5:CJ:104:GLY:HA2	2.27	0.49
10:BN:139:THR:HG22	10:BN:140:ILE:N	2.27	0.49
11:BP:87:THR:HG22	11:BP:93:LEU:HA	1.93	0.49
4:CH:732:ALA:HB2	4:CH:752:TYR:HD1	1.76	0.49
11:CP:116:ALA:HB1	11:CP:300:LEU:HD21	1.95	0.49
11:CQ:116:ALA:HB1	11:CQ:300:LEU:HD21	1.94	0.49
1:DB:305:ARG:NH2	1:DB:424:ALA:O	2.45	0.49
10:DN:108:ARG:HD2	11:DP:422:LEU:HD21	1.95	0.49
3:EG:18:ARG:HG3	4:EH:1222:GLU:O	2.11	0.49
10:EN:29:ASP:OD1	10:EN:57:SER:HB3	2.12	0.49
11:EP:87:THR:HG22	11:EP:93:LEU:HA	1.93	0.49
2:FD:747:PHE:HD2	2:FD:766:TYR:CE1	2.31	0.49
4:FH:732:ALA:HB2	4:FH:752:TYR:HD1	1.76	0.49
1:AA:16:PRO:HD3	1:AB:22:ASN:ND2	2.27	0.49
5:AJ:12:TYR:HE2	8:AK:12:GLN:O	1.96	0.49
6:AL:52:ARG:NH2	5:EJ:361:ILE:HG22	2.27	0.49
10:AN:139:THR:HG22	10:AN:140:ILE:N	2.27	0.49
2:BD:747:PHE:HD2	2:BD:766:TYR:CE1	2.31	0.49
11:BP:404:ASN:HB2	11:BQ:470:ALA:HB2	1.94	0.49
1:CB:567:ILE:HD12	1:CB:786:LEU:HD22	1.95	0.49
2:CD:747:PHE:HD2	2:CD:766:TYR:CE1	2.31	0.49
4:CH:681:GLU:OE1	4:CH:682:MET:N	2.39	0.49
4:CH:846:LEU:HD23	4:CH:915:ARG:HH22	1.77	0.49
4:CH:1149:LYS:NZ	4:CH:1153:GLU:OE2	2.46	0.49
5:CJ:394:ILE:HG12	5:CJ:412:ILE:HD11	1.94	0.49
10:CN:108:ARG:HD2	11:CP:422:LEU:HD21	1.95	0.49
2:DD:747:PHE:HD2	2:DD:766:TYR:CE1	2.30	0.49
11:DP:116:ALA:HB1	11:DP:300:LEU:HD21	1.94	0.49
11:EP:116:ALA:HB1	11:EP:300:LEU:HD21	1.95	0.49
11:EQ:474:ILE:HD13	11:FQ:5:TYR:CZ	2.47	0.49
10:FN:108:ARG:HD2	11:FP:422:LEU:HD21	1.95	0.49
11:FO:338:GLN:OE1	11:FO:354:ARG:NH1	2.39	0.49
4:AH:748:ALA:HB2	4:AH:752:TYR:HE1	1.77	0.49
8:AK:29:PRO:HG3	8:AK:65:LEU:HD11	1.95	0.49
11:AP:87:THR:HG22	11:AP:93:LEU:HA	1.93	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:AP:404:ASN:HB2	11:AQ:470:ALA:HB2	1.94	0.49
2:BD:390:GLU:CG	11:BO:90:ARG:HH12	2.26	0.49
2:BD:1192:VAL:HG11	2:BD:1210:THR:HG22	1.95	0.49
11:BO:461:GLU:OE2	11:EP:17:LYS:HE2	2.12	0.49
1:CA:548:PHE:CD2	1:CA:549:GLN:HG2	2.47	0.49
4:DH:748:ALA:HB2	4:DH:752:TYR:HE1	1.77	0.49
10:DN:31:GLU:HG3	10:DN:55:LYS:HB2	1.95	0.49
4:EH:639:ARG:HH22	4:EH:675:ASP:HB2	1.77	0.49
4:EH:646:THR:O	4:EH:646:THR:HG22	2.11	0.49
10:EN:139:THR:HG22	10:EN:140:ILE:N	2.27	0.49
11:EP:404:ASN:HB2	11:EQ:470:ALA:HB2	1.94	0.49
11:EQ:116:ALA:HB1	11:EQ:300:LEU:HD21	1.94	0.49
1:FB:162:LEU:O	2:FD:1216:TRP:CH2	2.64	0.49
4:FH:646:THR:O	4:FH:646:THR:HG22	2.11	0.49
11:FP:404:ASN:HB2	11:FQ:470:ALA:HB2	1.94	0.49
2:AD:747:PHE:HD2	2:AD:766:TYR:CE1	2.31	0.49
11:AQ:116:ALA:HB1	11:AQ:300:LEU:HD21	1.94	0.49
1:BA:252:TYR:HE1	1:BA:883:VAL:HG11	1.78	0.49
1:CB:305:ARG:NH2	1:CB:424:ALA:O	2.45	0.49
11:CP:17:LYS:HE2	11:FO:461:GLU:OE2	2.12	0.49
2:ED:390:GLU:CG	11:EO:90:ARG:HH12	2.26	0.49
11:EP:446:GLU:HG3	11:FQ:22:ILE:HD13	1.93	0.49
1:FC:384:VAL:O	1:FC:384:VAL:HG12	2.12	0.49
4:FH:740:ARG:HB3	4:FH:741:PRO:CD	2.42	0.49
11:FQ:116:ALA:HB1	11:FQ:300:LEU:HD21	1.94	0.49
1:AA:252:TYR:HE1	1:AA:883:VAL:HG11	1.78	0.49
1:AC:384:VAL:O	1:AC:384:VAL:HG12	2.12	0.49
2:AD:723:LEU:HD23	2:AD:783:ILE:HD11	1.95	0.49
4:AH:681:GLU:OE1	4:AH:682:MET:N	2.39	0.49
1:BA:166:ASP:OD2	1:BA:166:ASP:N	2.46	0.49
11:BP:397:GLU:OE1	11:BQ:359:LYS:NZ	2.41	0.49
10:DN:139:THR:HG22	10:DN:140:ILE:N	2.27	0.49
11:DQ:116:ALA:HB1	11:DQ:300:LEU:HD21	1.94	0.49
1:EA:16:PRO:HD3	1:EB:22:ASN:ND2	2.27	0.49
5:EJ:394:ILE:CG1	5:EJ:412:ILE:HD11	2.42	0.49
11:EO:461:GLU:OE2	11:FP:17:LYS:HE2	2.12	0.49
1:FA:548:PHE:CD2	1:FA:549:GLN:HG2	2.47	0.49
2:AD:390:GLU:CG	11:AO:90:ARG:HH12	2.26	0.49
4:AH:1149:LYS:NZ	4:AH:1153:GLU:OE2	2.46	0.49
5:AJ:533:THR:O	5:AJ:534:LEU:HD23	2.12	0.49
10:AN:31:GLU:HG3	10:AN:55:LYS:HB2	1.95	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:CH:646:THR:O	4:CH:646:THR:HG22	2.11	0.49
11:CO:461:GLU:OE2	11:DP:17:LYS:HE2	2.12	0.49
1:DB:362:ASP:O	1:DB:365:ARG:HG3	2.13	0.49
4:DH:740:ARG:HB3	4:DH:741:PRO:CD	2.42	0.49
1:EA:166:ASP:N	1:EA:166:ASP:OD2	2.46	0.49
1:EB:491:ILE:HD11	1:EB:530:ARG:HH12	1.78	0.49
1:EC:2:THR:OG1	1:EC:3:THR:N	2.42	0.49
2:ED:747:PHE:HD2	2:ED:766:TYR:CE1	2.31	0.49
10:EN:108:ARG:HD2	11:EP:422:LEU:HD21	1.95	0.49
1:FB:491:ILE:HD11	1:FB:530:ARG:HH12	1.78	0.49
4:FH:741:PRO:HG3	4:FH:755:LEU:HB3	1.95	0.49
11:FP:116:ALA:HB1	11:FP:300:LEU:HD21	1.94	0.49
4:AH:741:PRO:HG3	4:AH:755:LEU:HB3	1.95	0.49
11:AP:116:ALA:HB1	11:AP:300:LEU:HD21	1.95	0.49
11:AQ:5:TYR:CZ	11:DQ:474:ILE:HD13	2.47	0.49
1:BB:162:LEU:O	2:BD:1216:TRP:CH2	2.64	0.49
1:BB:362:ASP:O	1:BB:365:ARG:HG3	2.13	0.49
2:BD:723:LEU:HD23	2:BD:783:ILE:HD11	1.95	0.49
2:CD:1192:VAL:HG11	2:CD:1210:THR:HG22	1.95	0.49
10:CN:31:GLU:HG3	10:CN:55:LYS:HB2	1.95	0.49
2:DD:783:ILE:C	2:DD:783:ILE:CD1	2.86	0.49
1:EB:9:ASN:O	1:EC:173:ASN:HA	2.13	0.49
10:EN:94:LEU:HA	10:EN:99:GLU:O	2.13	0.49
1:FB:567:ILE:HD12	1:FB:786:LEU:HD22	1.95	0.49
1:AB:213:ILE:O	1:AB:216:ILE:HG22	2.13	0.49
1:BB:491:ILE:HD11	1:BB:530:ARG:HH12	1.78	0.49
10:BN:108:ARG:HD2	11:BP:422:LEU:HD21	1.95	0.49
5:CJ:361:ILE:HG22	6:EL:52:ARG:NH2	2.27	0.49
1:DB:567:ILE:HD12	1:DB:786:LEU:HD22	1.95	0.49
1:DC:384:VAL:O	1:DC:384:VAL:HG12	2.12	0.49
4:DH:748:ALA:HB2	4:DH:752:TYR:CE1	2.48	0.49
2:ED:1192:VAL:HG11	2:ED:1210:THR:HG22	1.95	0.49
3:EG:19:LEU:HD13	4:EH:1224:LEU:HB2	1.95	0.49
1:FA:166:ASP:OD2	1:FA:166:ASP:N	2.46	0.49
2:FD:390:GLU:CG	11:FO:90:ARG:HH12	2.26	0.49
2:FD:723:LEU:HD23	2:FD:783:ILE:HD11	1.95	0.49
4:FH:846:LEU:HD23	4:FH:915:ARG:HH22	1.77	0.49
10:FN:94:LEU:HA	10:FN:99:GLU:O	2.13	0.49
1:AB:305:ARG:NH2	1:AB:424:ALA:O	2.45	0.49
1:AB:491:ILE:HD11	1:AB:530:ARG:HH12	1.78	0.49
2:AD:1192:VAL:HG11	2:AD:1210:THR:HG22	1.95	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:AH:748:ALA:HB2	4:AH:752:TYR:CE1	2.48	0.49
10:AN:94:LEU:HA	10:AN:99:GLU:O	2.13	0.49
11:AQ:474:ILE:HD13	11:BQ:5:TYR:CZ	2.47	0.49
10:BN:31:GLU:HG3	10:BN:55:LYS:HB2	1.95	0.49
1:CA:107:GLN:HG3	1:CA:107:GLN:O	2.12	0.49
1:CB:909:ILE:HD11	1:CB:911:LEU:HD23	1.95	0.49
9:CM:42:THR:HG1	9:CM:57:LEU:C	2.17	0.49
11:CP:404:ASN:HB2	11:CQ:470:ALA:HB2	1.94	0.49
2:DD:723:LEU:HD23	2:DD:783:ILE:HD11	1.95	0.49
3:DG:64:MET:HE3	3:DG:66:SER:HB2	1.95	0.49
4:DH:732:ALA:HB2	4:DH:752:TYR:HD1	1.76	0.49
10:DN:94:LEU:HA	10:DN:99:GLU:O	2.13	0.49
11:DP:404:ASN:HB2	11:DQ:470:ALA:HB2	1.94	0.49
1:EB:163:LEU:CD2	4:EH:11:PRO:HD3	2.43	0.49
2:ED:723:LEU:HD23	2:ED:783:ILE:HD11	1.95	0.49
4:EH:741:PRO:HG3	4:EH:755:LEU:HB3	1.95	0.49
5:EJ:12:TYR:HE2	8:EK:12:GLN:O	1.96	0.49
8:EK:29:PRO:HG3	8:EK:65:LEU:HD11	1.95	0.49
3:FG:19:LEU:HD13	4:FH:1224:LEU:HB2	1.95	0.49
4:FH:1149:LYS:NZ	4:FH:1153:GLU:OE2	2.46	0.49
1:AA:294:ASP:OD2	1:AA:415:TYR:OH	2.24	0.48
3:AG:19:LEU:HD13	4:AH:1224:LEU:HB2	1.95	0.48
5:AJ:272:HIS:CD2	5:AJ:274:GLY:H	2.31	0.48
10:AN:29:ASP:OD1	10:AN:57:SER:HB3	2.12	0.48
4:BH:846:LEU:HD23	4:BH:915:ARG:HH22	1.77	0.48
1:CA:294:ASP:OD2	1:CA:415:TYR:OH	2.24	0.48
2:CD:723:LEU:HD22	2:CD:751:ILE:HD13	1.95	0.48
4:CH:748:ALA:HB2	4:CH:752:TYR:HE1	1.77	0.48
5:CJ:12:TYR:HE2	8:CK:12:GLN:O	1.96	0.48
1:DA:16:PRO:HD3	1:DB:22:ASN:ND2	2.27	0.48
3:EG:64:MET:HE3	3:EG:66:SER:HB2	1.95	0.48
1:FB:909:ILE:HD11	1:FB:911:LEU:HD23	1.95	0.48
2:FD:723:LEU:HD22	2:FD:751:ILE:HD13	1.95	0.48
4:FH:639:ARG:HH22	4:FH:675:ASP:HB2	1.77	0.48
1:AC:2:THR:OG1	1:AC:3:THR:N	2.42	0.48
1:BB:163:LEU:CD2	4:BH:11:PRO:HD3	2.43	0.48
3:BG:19:LEU:HD13	4:BH:1224:LEU:HB2	1.95	0.48
4:BH:748:ALA:HB2	4:BH:752:TYR:CE1	2.48	0.48
1:CA:196:GLN:O	1:CA:200:SER:OG	2.27	0.48
1:CB:491:ILE:HD11	1:CB:530:ARG:HH12	1.78	0.48
3:CE:48:THR:HB	2:DD:172:CYS:SG	2.53	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:DH:1149:LYS:NZ	4:DH:1153:GLU:OE2	2.46	0.48
8:DK:29:PRO:HG3	8:DK:65:LEU:HD11	1.95	0.48
4:EH:1149:LYS:NZ	4:EH:1153:GLU:OE2	2.46	0.48
1:FB:9:ASN:O	1:FC:173:ASN:HA	2.13	0.48
3:AG:64:MET:HE3	3:AG:66:SER:HB2	1.95	0.48
8:AK:174:SER:C	8:AK:176:ASP:H	2.22	0.48
10:AN:108:ARG:HD2	11:AP:422:LEU:HD21	1.95	0.48
1:BB:163:LEU:HD21	4:BH:11:PRO:CG	2.43	0.48
1:BB:213:ILE:O	1:BB:216:ILE:HG22	2.13	0.48
4:BH:639:ARG:HH22	4:BH:675:ASP:HB2	1.77	0.48
11:BO:338:GLN:OE1	11:BO:354:ARG:NH1	2.39	0.48
1:CB:586:VAL:O	1:CB:590:THR:HG23	2.14	0.48
2:CD:8:SER:OG	2:CD:9:LYS:N	2.47	0.48
2:CD:172:CYS:SG	3:FE:48:THR:HB	2.53	0.48
1:DA:252:TYR:HE1	1:DA:883:VAL:HG11	1.78	0.48
1:DB:213:ILE:O	1:DB:216:ILE:HG22	2.13	0.48
1:DB:491:ILE:HD11	1:DB:530:ARG:HH12	1.78	0.48
1:EA:252:TYR:HE1	1:EA:883:VAL:HG11	1.78	0.48
1:EB:213:ILE:O	1:EB:216:ILE:HG22	2.13	0.48
5:EJ:394:ILE:HG12	5:EJ:412:ILE:HD11	1.94	0.48
1:FB:305:ARG:NH2	1:FB:424:ALA:O	2.45	0.48
3:FG:64:MET:HE3	3:FG:66:SER:HB2	1.95	0.48
4:FH:748:ALA:HB2	4:FH:752:TYR:HE1	1.78	0.48
10:FN:31:GLU:HG3	10:FN:55:LYS:HB2	1.95	0.48
10:FN:139:THR:HG22	10:FN:140:ILE:N	2.27	0.48
2:AD:783:ILE:C	2:AD:783:ILE:CD1	2.86	0.48
5:AJ:278:GLU:HB3	4:BH:959:PRO:HD2	1.94	0.48
8:BK:29:PRO:HG3	8:BK:65:LEU:HD11	1.95	0.48
10:BN:14:ASP:OD1	11:BP:411:LYS:HE2	2.13	0.48
4:CH:741:PRO:HG3	4:CH:755:LEU:HB3	1.95	0.48
10:CN:94:LEU:HA	10:CN:99:GLU:O	2.13	0.48
11:CQ:5:TYR:CZ	11:FQ:474:ILE:HD13	2.47	0.48
1:DA:425:ASP:OD1	1:DA:425:ASP:N	2.46	0.48
1:DB:163:LEU:HD21	4:DH:11:PRO:CG	2.43	0.48
1:EA:107:GLN:HG3	1:EA:107:GLN:O	2.12	0.48
1:EC:541:LYS:HB2	1:EC:829:TYR:CZ	2.49	0.48
4:EH:740:ARG:HB3	4:EH:741:PRO:CD	2.42	0.48
10:EN:31:GLU:HG3	10:EN:55:LYS:HB2	1.95	0.48
1:FB:586:VAL:O	1:FB:590:THR:HG23	2.14	0.48
2:FD:687:ILE:HB	2:FD:696:VAL:HG23	1.96	0.48
2:AD:172:CYS:SG	3:DE:48:THR:HB	2.53	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BA:413:PHE:HZ	1:BA:466:TYR:HA	1.79	0.48
1:BB:586:VAL:O	1:BB:590:THR:HG23	2.14	0.48
2:BD:783:ILE:C	2:BD:783:ILE:CD1	2.86	0.48
3:BG:13:PHE:HD2	3:BG:19:LEU:HD21	1.79	0.48
3:BG:64:MET:HE3	3:BG:66:SER:HB2	1.95	0.48
4:BH:741:PRO:HG3	4:BH:755:LEU:HB3	1.95	0.48
10:BN:94:LEU:HA	10:BN:99:GLU:O	2.13	0.48
1:CB:163:LEU:CD2	4:CH:11:PRO:HD3	2.43	0.48
1:CB:213:ILE:O	1:CB:216:ILE:HG22	2.13	0.48
1:CB:362:ASP:O	1:CB:365:ARG:HG3	2.13	0.48
2:CD:632:LEU:HB2	2:CD:645:SER:HB3	1.95	0.48
2:CD:687:ILE:HB	2:CD:696:VAL:HG23	1.95	0.48
5:CJ:272:HIS:CD2	5:CJ:274:GLY:H	2.31	0.48
11:CQ:22:ILE:HD13	11:FP:446:GLU:HG3	1.93	0.48
11:CQ:474:ILE:HD13	11:DQ:5:TYR:CZ	2.47	0.48
1:DC:541:LYS:HB2	1:DC:829:TYR:CZ	2.49	0.48
3:DF:64:MET:HE3	3:DF:66:SER:HB2	1.95	0.48
4:DH:681:GLU:OE1	4:DH:682:MET:N	2.39	0.48
1:EA:37:ARG:O	1:EA:41:VAL:HG22	2.14	0.48
1:EB:362:ASP:O	1:EB:365:ARG:HG3	2.13	0.48
1:EC:96:VAL:HG11	1:EC:179:PHE:CE2	2.49	0.48
2:ED:687:ILE:HB	2:ED:696:VAL:HG23	1.96	0.48
11:EP:449:THR:HG22	11:EP:452:ASP:CG	2.39	0.48
1:FB:163:LEU:HD21	4:FH:11:PRO:CG	2.43	0.48
4:FH:545:ASP:OD1	4:FH:546:ILE:N	2.40	0.48
11:FP:449:THR:HG22	11:FP:452:ASP:CG	2.39	0.48
1:AB:163:LEU:HD21	4:AH:11:PRO:CG	2.43	0.48
1:BB:9:ASN:O	1:BC:173:ASN:HA	2.13	0.48
1:BC:96:VAL:HG11	1:BC:179:PHE:CE2	2.49	0.48
1:CC:157:GLN:HA	1:CC:170:LYS:HG2	1.95	0.48
3:CG:64:MET:HE3	3:CG:66:SER:HB2	1.95	0.48
1:DA:107:GLN:HG3	1:DA:107:GLN:O	2.12	0.48
1:DA:413:PHE:HZ	1:DA:466:TYR:HA	1.79	0.48
1:DB:9:ASN:O	1:DC:173:ASN:HA	2.13	0.48
1:DC:536:ASP:HB2	1:DC:824:THR:HG22	1.96	0.48
2:DD:1192:VAL:HG11	2:DD:1210:THR:HG22	1.95	0.48
3:DG:19:LEU:HD13	4:DH:1224:LEU:HB2	1.95	0.48
1:EB:163:LEU:HD21	4:EH:11:PRO:CG	2.43	0.48
4:EH:846:LEU:HD23	4:EH:915:ARG:HH22	1.77	0.48
10:EN:14:ASP:OD1	11:EP:411:LYS:HE2	2.13	0.48
11:EP:397:GLU:OE1	11:EQ:359:LYS:NZ	2.41	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:FD:632:LEU:HB2	2:FD:645:SER:HB3	1.95	0.48
2:AD:687:ILE:HB	2:AD:696:VAL:HG23	1.96	0.48
6:AL:45:ILE:HD11	6:EL:9:VAL:HG12	1.96	0.48
1:BB:305:ARG:NH2	1:BB:424:ALA:O	2.45	0.48
1:BB:567:ILE:HD12	1:BB:786:LEU:HD22	1.95	0.48
10:BN:9:PHE:HB2	10:EN:121:GLY:O	2.14	0.48
2:CD:723:LEU:HD23	2:CD:783:ILE:HD11	1.95	0.48
3:CG:19:LEU:HD13	4:CH:1224:LEU:HB2	1.95	0.48
1:DC:157:GLN:HA	1:DC:170:LYS:HG2	1.95	0.48
2:DD:390:GLU:CG	11:DO:90:ARG:HH12	2.26	0.48
4:EH:748:ALA:HB2	4:EH:752:TYR:HE1	1.77	0.48
1:FC:96:VAL:HG11	1:FC:179:PHE:HE2	1.78	0.48
1:AC:96:VAL:HG11	1:AC:179:PHE:CE2	2.49	0.48
3:AG:13:PHE:HD2	3:AG:19:LEU:HD21	1.79	0.48
10:AN:9:PHE:HB2	10:BN:121:GLY:O	2.14	0.48
10:AN:121:GLY:O	10:DN:9:PHE:HB2	2.14	0.48
1:BC:541:LYS:HB2	1:BC:829:TYR:CZ	2.49	0.48
1:CB:163:LEU:HD21	4:CH:11:PRO:CG	2.43	0.48
1:CC:536:ASP:HB2	1:CC:824:THR:HG22	1.96	0.48
1:CC:541:LYS:HB2	1:CC:829:TYR:CZ	2.49	0.48
2:CD:390:GLU:CG	11:CO:90:ARG:HH12	2.26	0.48
11:CO:338:GLN:OE1	11:CO:354:ARG:NH1	2.39	0.48
4:DH:639:ARG:HH22	4:DH:675:ASP:HB2	1.77	0.48
1:EA:595:PHE:HZ	1:EA:607:ASP:HB3	1.79	0.48
3:EF:64:MET:HE3	3:EF:66:SER:HB2	1.95	0.48
4:EH:748:ALA:HB2	4:EH:752:TYR:CE1	2.48	0.48
11:EO:338:GLN:OE1	11:EO:354:ARG:NH1	2.39	0.48
1:FC:536:ASP:HB2	1:FC:824:THR:HG22	1.96	0.48
2:FD:783:ILE:C	2:FD:783:ILE:CD1	2.86	0.48
2:FD:1192:VAL:HG11	2:FD:1210:THR:HG22	1.95	0.48
3:FG:13:PHE:CD2	3:FG:19:LEU:HD21	2.49	0.48
1:AB:362:ASP:O	1:AB:365:ARG:HG3	2.13	0.48
1:AB:586:VAL:O	1:AB:590:THR:HG23	2.14	0.48
2:AD:8:SER:OG	2:AD:9:LYS:N	2.47	0.48
2:AD:632:LEU:HB2	2:AD:645:SER:HB3	1.95	0.48
2:AD:723:LEU:HD22	2:AD:751:ILE:HD13	1.95	0.48
3:AE:48:THR:HB	2:BD:172:CYS:SG	2.53	0.48
3:AF:64:MET:HE3	3:AF:66:SER:HB2	1.95	0.48
1:BA:37:ARG:O	1:BA:41:VAL:HG22	2.14	0.48
2:BD:723:LEU:HD22	2:BD:751:ILE:HD13	1.95	0.48
3:BG:13:PHE:CD2	3:BG:19:LEU:HD21	2.49	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:BH:743:LYS:H	4:BH:743:LYS:HD3	1.79	0.48
4:BH:1149:LYS:NZ	4:BH:1153:GLU:OE2	2.46	0.48
4:CH:639:ARG:HH22	4:CH:675:ASP:HB2	1.77	0.48
1:DC:845:ASP:O	1:DC:849:GLN:HG3	2.14	0.48
2:DD:8:SER:OG	2:DD:9:LYS:N	2.47	0.48
2:DD:632:LEU:HB2	2:DD:645:SER:HB3	1.95	0.48
3:DG:13:PHE:CD2	3:DG:19:LEU:HD21	2.49	0.48
4:DH:74:ASN:O	7:DI:24:ARG:HD3	2.14	0.48
10:DN:14:ASP:OD1	11:DP:411:LYS:HE2	2.14	0.48
1:EB:305:ARG:NH2	1:EB:424:ALA:O	2.45	0.48
1:EC:536:ASP:HB2	1:EC:824:THR:HG22	1.96	0.48
2:ED:723:LEU:HD22	2:ED:751:ILE:HD13	1.95	0.48
4:EH:743:LYS:H	4:EH:743:LYS:HD3	1.79	0.48
1:FA:37:ARG:O	1:FA:41:VAL:HG22	2.14	0.48
1:FB:163:LEU:CD2	4:FH:11:PRO:HD3	2.43	0.48
1:FC:96:VAL:HG11	1:FC:179:PHE:CE2	2.49	0.48
1:FC:157:GLN:HA	1:FC:170:LYS:HG2	1.95	0.48
3:FG:13:PHE:HD2	3:FG:19:LEU:HD21	1.79	0.48
4:FH:74:ASN:O	7:FI:24:ARG:HD3	2.14	0.48
7:FI:86:TYR:OH	8:FK:162:GLU:OE2	2.30	0.48
8:FK:29:PRO:HG3	8:FK:65:LEU:HD11	1.95	0.48
1:AC:536:ASP:HB2	1:AC:824:THR:HG22	1.96	0.48
4:AH:619:TYR:O	4:AH:624:ILE:HD11	2.14	0.48
4:AH:639:ARG:HH22	4:AH:675:ASP:HB2	1.77	0.48
1:BC:536:ASP:HB2	1:BC:824:THR:HG22	1.96	0.48
1:BC:845:ASP:O	1:BC:849:GLN:HG3	2.14	0.48
2:BD:8:SER:OG	2:BD:9:LYS:N	2.47	0.48
3:BE:48:THR:HB	2:ED:172:CYS:SG	2.53	0.48
8:BK:174:SER:C	8:BK:176:ASP:H	2.22	0.48
4:CH:738:TYR:CD1	4:CH:752:TYR:CE1	3.02	0.48
4:CH:743:LYS:HD3	4:CH:743:LYS:H	1.79	0.48
8:CK:29:PRO:HG3	8:CK:65:LEU:HD11	1.95	0.48
1:DB:586:VAL:O	1:DB:590:THR:HG23	2.14	0.48
1:DB:909:ILE:HD11	1:DB:911:LEU:HD23	1.95	0.48
4:DH:75:PHE:CE2	7:DI:20:GLU:O	2.67	0.48
1:EC:845:ASP:O	1:EC:849:GLN:HG3	2.14	0.48
3:EG:13:PHE:CD2	3:EG:19:LEU:HD21	2.49	0.48
3:EG:13:PHE:HD2	3:EG:19:LEU:HD21	1.78	0.48
7:EI:86:TYR:OH	8:EK:162:GLU:OE2	2.30	0.48
3:FF:64:MET:HE3	3:FF:66:SER:HB2	1.95	0.48
4:FH:743:LYS:HD3	4:FH:743:LYS:H	1.79	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AC:157:GLN:HA	1:AC:170:LYS:HG2	1.95	0.47
2:AD:360:GLU:C	2:AD:361:LEU:HD12	2.39	0.47
4:AH:74:ASN:O	7:AI:24:ARG:HD3	2.14	0.47
4:AH:75:PHE:CE2	7:AI:20:GLU:O	2.67	0.47
1:BB:909:ILE:HD11	1:BB:911:LEU:HD23	1.95	0.47
11:BP:449:THR:HG22	11:BP:452:ASP:CG	2.39	0.47
1:CC:96:VAL:HG11	1:CC:179:PHE:CE2	2.49	0.47
1:CC:96:VAL:HG11	1:CC:179:PHE:HE2	1.78	0.47
1:DC:96:VAL:HG11	1:DC:179:PHE:HE2	1.78	0.47
4:DH:619:TYR:O	4:DH:624:ILE:HD11	2.14	0.47
1:EB:586:VAL:O	1:EB:590:THR:HG23	2.14	0.47
2:ED:1087:GLY:HA2	2:ED:1138:ALA:HB2	1.96	0.47
1:FB:362:ASP:O	1:FB:365:ARG:HG3	2.13	0.47
4:FH:75:PHE:CE2	7:FI:20:GLU:O	2.67	0.47
4:FH:738:TYR:CD1	4:FH:752:TYR:CE1	3.02	0.47
4:FH:748:ALA:HB2	4:FH:752:TYR:CE1	2.48	0.47
9:FM:42:THR:HG1	9:FM:57:LEU:C	2.19	0.47
1:AC:118:LEU:HD11	1:AC:180:LEU:HG	1.97	0.47
6:AL:9:VAL:HG12	6:CL:45:ILE:HD11	1.96	0.47
11:AP:404:ASN:CG	11:AQ:470:ALA:HB2	2.39	0.47
1:BB:868:GLU:HA	1:BB:871:THR:HG22	1.96	0.47
2:BD:1087:GLY:HA2	2:BD:1138:ALA:HB2	1.96	0.47
4:BH:748:ALA:HB2	4:BH:752:TYR:HE1	1.77	0.47
1:CA:413:PHE:HZ	1:CA:466:TYR:HA	1.79	0.47
1:CB:9:ASN:O	1:CC:173:ASN:HA	2.13	0.47
1:CC:118:LEU:HD11	1:CC:180:LEU:HG	1.97	0.47
1:CC:384:VAL:O	1:CC:384:VAL:HG12	2.12	0.47
2:CD:360:GLU:C	2:CD:361:LEU:HD12	2.39	0.47
1:DC:118:LEU:HD11	1:DC:180:LEU:HG	1.97	0.47
2:DD:723:LEU:HD22	2:DD:751:ILE:HD13	1.95	0.47
1:EC:157:GLN:HA	1:EC:170:LYS:HG2	1.95	0.47
4:EH:74:ASN:O	7:EI:24:ARG:HD3	2.14	0.47
4:EH:738:TYR:CD1	4:EH:752:TYR:CE1	3.02	0.47
4:FH:106:PHE:HD1	4:FH:114:SER:HB2	1.79	0.47
1:AA:37:ARG:O	1:AA:41:VAL:HG22	2.14	0.47
1:AA:608:GLN:O	1:AA:611:ASN:HB2	2.15	0.47
1:AB:9:ASN:O	1:AC:173:ASN:HA	2.13	0.47
1:AB:59:GLN:HG3	1:AB:60:PRO:HD2	1.97	0.47
1:AC:845:ASP:O	1:AC:849:GLN:HG3	2.14	0.47
4:BH:75:PHE:CE2	7:BI:20:GLU:O	2.67	0.47
3:CE:35:ARG:NH2	3:CG:2:ASN:O	2.47	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:CH:619:TYR:O	4:CH:624:ILE:HD11	2.14	0.47
9:CM:134:ALA:HA	9:CM:159:ASN:O	2.14	0.47
11:CP:449:THR:HG22	11:CP:452:ASP:CG	2.39	0.47
1:DA:37:ARG:O	1:DA:41:VAL:HG22	2.14	0.47
1:DB:163:LEU:CD2	4:DH:11:PRO:HD3	2.43	0.47
4:DH:741:PRO:HG3	4:DH:755:LEU:HB3	1.95	0.47
8:DK:174:SER:C	8:DK:176:ASP:H	2.22	0.47
1:EB:909:ILE:HD11	1:EB:911:LEU:HD23	1.95	0.47
2:ED:8:SER:OG	2:ED:9:LYS:N	2.47	0.47
5:EJ:272:HIS:CD2	5:EJ:274:GLY:H	2.31	0.47
1:FA:608:GLN:O	1:FA:611:ASN:HB2	2.15	0.47
1:FB:213:ILE:O	1:FB:216:ILE:HG22	2.13	0.47
1:AB:163:LEU:CD2	4:AH:11:PRO:HD3	2.43	0.47
1:AB:868:GLU:HA	1:AB:871:THR:HG22	1.96	0.47
1:AB:909:ILE:HD11	1:AB:911:LEU:HD23	1.95	0.47
4:AH:106:PHE:HD1	4:AH:114:SER:HB2	1.79	0.47
4:AH:1031:GLU:O	4:AH:1031:GLU:HG2	2.15	0.47
1:BA:595:PHE:HZ	1:BA:607:ASP:HB3	1.79	0.47
2:BD:360:GLU:C	2:BD:361:LEU:HD12	2.39	0.47
4:BH:74:ASN:O	7:BI:24:ARG:HD3	2.14	0.47
4:BH:738:TYR:CD1	4:BH:752:TYR:CE1	3.02	0.47
4:CH:75:PHE:CE2	7:CI:20:GLU:O	2.67	0.47
4:CH:748:ALA:HB2	4:CH:752:TYR:CE1	2.48	0.47
1:DA:608:GLN:O	1:DA:611:ASN:HB2	2.14	0.47
3:DG:13:PHE:HD2	3:DG:19:LEU:HD21	1.79	0.47
4:DH:1031:GLU:O	4:DH:1031:GLU:HG2	2.15	0.47
11:DP:449:THR:HG22	11:DP:452:ASP:CG	2.39	0.47
1:EA:294:ASP:OD2	1:EA:415:TYR:OH	2.24	0.47
1:EB:567:ILE:HD12	1:EB:786:LEU:HD22	1.95	0.47
4:EH:532:ARG:HD3	4:EH:536:HIS:CD2	2.50	0.47
1:FB:469:TYR:O	1:FB:472:TYR:HB3	2.14	0.47
1:FC:541:LYS:HB2	1:FC:829:TYR:CZ	2.49	0.47
2:FD:404:ALA:HB1	2:FD:492:GLN:NE2	2.30	0.47
4:FH:1031:GLU:O	4:FH:1031:GLU:HG2	2.15	0.47
2:AD:404:ALA:HB1	2:AD:492:GLN:NE2	2.30	0.47
10:AN:14:ASP:OD1	11:AP:411:LYS:HE2	2.13	0.47
11:AP:449:THR:HG22	11:AP:452:ASP:CG	2.39	0.47
2:BD:632:LEU:HB2	2:BD:645:SER:HB3	1.95	0.47
1:CA:37:ARG:O	1:CA:41:VAL:HG22	2.14	0.47
1:CC:845:ASP:O	1:CC:849:GLN:HG3	2.14	0.47
2:CD:783:ILE:C	2:CD:783:ILE:CD1	2.86	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:CF:64:MET:HE3	3:CF:66:SER:HB2	1.95	0.47
3:CG:13:PHE:CD2	3:CG:19:LEU:HD21	2.49	0.47
10:CN:14:ASP:OD1	11:CP:411:LYS:HE2	2.13	0.47
11:CO:442:ILE:HD12	11:CO:460:VAL:HG22	1.97	0.47
1:DB:868:GLU:HA	1:DB:871:THR:HG22	1.96	0.47
2:DD:687:ILE:HB	2:DD:696:VAL:HG23	1.96	0.47
11:DP:404:ASN:CG	11:DQ:470:ALA:HB2	2.40	0.47
2:ED:360:GLU:C	2:ED:361:LEU:HD12	2.39	0.47
5:EJ:212:GLU:HB2	5:EJ:302:LYS:HB3	1.97	0.47
1:FB:59:GLN:HG3	1:FB:60:PRO:HD2	1.97	0.47
4:FH:681:GLU:OE1	4:FH:682:MET:N	2.39	0.47
1:AA:166:ASP:OD2	1:AA:166:ASP:N	2.46	0.47
1:AA:216:ILE:HD11	1:AA:283:PRO:HG2	1.96	0.47
1:AC:541:LYS:HB2	1:AC:829:TYR:CZ	2.49	0.47
11:AP:397:GLU:OE1	11:AQ:359:LYS:NZ	2.41	0.47
1:BB:469:TYR:O	1:BB:472:TYR:HB3	2.15	0.47
2:BD:404:ALA:HB1	2:BD:492:GLN:NE2	2.30	0.47
4:BH:106:PHE:HD1	4:BH:114:SER:HB2	1.79	0.47
4:BH:639:ARG:NH2	4:BH:675:ASP:HB2	2.30	0.47
1:CA:560:LEU:HD11	1:CA:793:ARG:HD2	1.97	0.47
1:DA:560:LEU:HD11	1:DA:793:ARG:HD2	1.97	0.47
1:EA:216:ILE:HD11	1:EA:283:PRO:HG2	1.96	0.47
1:FA:560:LEU:HD11	1:FA:793:ARG:HD2	1.97	0.47
1:FC:118:LEU:HD11	1:FC:180:LEU:HG	1.97	0.47
4:FH:532:ARG:HD3	4:FH:536:HIS:CD2	2.50	0.47
8:FK:174:SER:C	8:FK:176:ASP:H	2.22	0.47
10:FN:14:ASP:OD1	11:FP:411:LYS:HE2	2.13	0.47
1:AA:560:LEU:HD11	1:AA:793:ARG:HD2	1.97	0.47
1:AA:592:LYS:HA	1:AA:595:PHE:HB2	1.97	0.47
1:AB:567:ILE:HD12	1:AB:786:LEU:HD22	1.95	0.47
1:AC:96:VAL:HG11	1:AC:179:PHE:HE2	1.78	0.47
1:AC:804:HIS:C	1:AC:806:PHE:H	2.23	0.47
2:AD:1087:GLY:HA2	2:AD:1138:ALA:HB2	1.96	0.47
3:AG:13:PHE:CD2	3:AG:19:LEU:HD21	2.49	0.47
4:AH:738:TYR:CD1	4:AH:752:TYR:CE1	3.02	0.47
4:AH:743:LYS:H	4:AH:743:LYS:HD3	1.79	0.47
1:BA:592:LYS:HA	1:BA:595:PHE:HB2	1.97	0.47
3:BF:64:MET:HE3	3:BF:66:SER:HB2	1.95	0.47
1:CA:595:PHE:HZ	1:CA:607:ASP:HB3	1.79	0.47
1:CB:59:GLN:HG3	1:CB:60:PRO:HD2	1.97	0.47
1:CC:804:HIS:C	1:CC:806:PHE:H	2.23	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:CD:404:ALA:HB1	2:CD:492:GLN:NE2	2.30	0.47
3:CE:91:LEU:HD21	3:CF:92:GLU:HA	1.97	0.47
3:CG:13:PHE:HD2	3:CG:19:LEU:HD21	1.79	0.47
4:CH:106:PHE:HD1	4:CH:114:SER:HB2	1.79	0.47
4:CH:532:ARG:HD3	4:CH:536:HIS:CD2	2.50	0.47
1:DA:595:PHE:HZ	1:DA:607:ASP:HB3	1.79	0.47
1:DC:96:VAL:HG11	1:DC:179:PHE:CE2	2.49	0.47
1:DC:804:HIS:C	1:DC:806:PHE:H	2.23	0.47
2:DD:404:ALA:HB1	2:DD:492:GLN:NE2	2.30	0.47
4:DH:436:GLN:OE1	4:DH:529:VAL:HG23	2.15	0.47
4:DH:532:ARG:HD3	4:DH:536:HIS:CD2	2.50	0.47
4:DH:743:LYS:H	4:DH:743:LYS:HD3	1.79	0.47
4:DH:1021:ILE:HD13	4:DH:1181:PRO:HB2	1.97	0.47
11:DO:442:ILE:HD12	11:DO:460:VAL:HG22	1.97	0.47
1:EA:413:PHE:HZ	1:EA:466:TYR:HA	1.79	0.47
1:EA:592:LYS:HA	1:EA:595:PHE:HB2	1.97	0.47
3:EE:48:THR:HB	2:FD:172:CYS:SG	2.53	0.47
3:EE:91:LEU:HD21	3:EF:92:GLU:HA	1.96	0.47
4:EH:639:ARG:NH2	4:EH:675:ASP:HB2	2.30	0.47
8:EK:174:SER:C	8:EK:176:ASP:H	2.22	0.47
8:EK:179:HIS:HB2	8:EK:226:PHE:HB2	1.97	0.47
11:EO:442:ILE:HD12	11:EO:460:VAL:HG22	1.97	0.47
1:FC:845:ASP:O	1:FC:849:GLN:HG3	2.14	0.47
4:FH:194:SER:C	4:FH:196:ARG:N	2.73	0.47
8:FK:179:HIS:HB2	8:FK:226:PHE:HB2	1.97	0.47
9:FM:134:ALA:HA	9:FM:159:ASN:O	2.14	0.47
1:AA:595:PHE:HZ	1:AA:607:ASP:HB3	1.79	0.47
4:AH:639:ARG:NH2	4:AH:675:ASP:HB2	2.30	0.47
1:BC:157:GLN:HA	1:BC:170:LYS:HG2	1.95	0.47
1:CA:166:ASP:OD2	1:CA:166:ASP:N	2.46	0.47
1:CA:252:TYR:HE1	1:CA:883:VAL:HG11	1.78	0.47
1:CA:608:GLN:O	1:CA:611:ASN:HB2	2.15	0.47
1:CB:469:TYR:O	1:CB:472:TYR:HB3	2.15	0.47
4:CH:436:GLN:OE1	4:CH:529:VAL:HG23	2.15	0.47
1:DA:216:ILE:HD11	1:DA:283:PRO:HG2	1.96	0.47
4:DH:634:LYS:HD2	4:DH:648:ALA:HB1	1.97	0.47
2:ED:783:ILE:C	2:ED:783:ILE:CD1	2.86	0.47
4:EH:1031:GLU:HG2	4:EH:1031:GLU:O	2.15	0.47
2:FD:1087:GLY:HA2	2:FD:1138:ALA:HB2	1.96	0.47
4:FH:243:GLN:HG2	4:FH:245:PHE:CE2	2.50	0.47
11:FO:442:ILE:HD12	11:FO:460:VAL:HG22	1.97	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:BH:532:ARG:HD3	4:BH:536:HIS:CD2	2.50	0.47
4:BH:619:TYR:O	4:BH:624:ILE:HD11	2.14	0.47
4:BH:1031:GLU:HG2	4:BH:1031:GLU:O	2.15	0.47
9:BM:134:ALA:HA	9:BM:159:ASN:O	2.14	0.47
1:CA:425:ASP:OD1	1:CA:425:ASP:N	2.46	0.47
1:CA:439:ILE:HG12	1:CA:509:ILE:HG12	1.97	0.47
2:CD:683:TYR:HB3	2:CD:708:ARG:HD3	1.97	0.47
4:CH:243:GLN:HG2	4:CH:245:PHE:CE2	2.50	0.47
4:CH:1031:GLU:O	4:CH:1031:GLU:HG2	2.15	0.47
6:CL:9:VAL:HG12	6:EL:45:ILE:HD11	1.96	0.47
10:CN:44:GLN:HE22	11:DP:425:ARG:HH11	1.63	0.47
10:CN:121:GLY:O	10:FN:9:PHE:HB2	2.14	0.47
11:CP:425:ARG:HH11	10:FN:44:GLN:HE22	1.63	0.47
1:DA:439:ILE:HG12	1:DA:509:ILE:HG12	1.97	0.47
1:DB:59:GLN:HG3	1:DB:60:PRO:HD2	1.97	0.47
2:DD:360:GLU:C	2:DD:361:LEU:HD12	2.39	0.47
9:DM:134:ALA:HA	9:DM:159:ASN:O	2.14	0.47
1:EA:608:GLN:O	1:EA:611:ASN:HB2	2.15	0.47
1:EC:118:LEU:HD11	1:EC:180:LEU:HG	1.97	0.47
4:EH:75:PHE:CE2	7:EI:20:GLU:O	2.67	0.47
4:EH:1211:ASN:OD1	2:FD:331:GLN:HG2	2.15	0.47
1:FA:595:PHE:HZ	1:FA:607:ASP:HB3	1.79	0.47
2:AD:681:TYR:O	2:AD:682:HIS:HD2	1.98	0.47
11:AO:442:ILE:HD12	11:AO:460:VAL:HG22	1.97	0.47
1:BA:560:LEU:HD11	1:BA:793:ARG:HD2	1.97	0.47
1:BA:608:GLN:O	1:BA:611:ASN:HB2	2.15	0.47
1:BC:96:VAL:HG11	1:BC:179:PHE:HE2	1.78	0.47
2:BD:687:ILE:HB	2:BD:696:VAL:HG23	1.96	0.47
11:BP:404:ASN:CG	11:BQ:470:ALA:HB2	2.39	0.47
4:CH:74:ASN:O	7:CI:24:ARG:HD3	2.14	0.47
4:CH:194:SER:C	4:CH:196:ARG:N	2.73	0.47
4:CH:1211:ASN:OD1	2:DD:331:GLN:HG2	2.15	0.47
2:DD:681:TYR:O	2:DD:682:HIS:HD2	1.98	0.47
3:DG:33:ASN:HD22	3:DG:36:ASP:HB2	1.80	0.47
1:EA:439:ILE:HG12	1:EA:509:ILE:HG12	1.97	0.47
1:EA:800:LEU:HG	1:EA:801:GLN:HE21	1.80	0.47
1:EC:804:HIS:C	1:EC:806:PHE:H	2.23	0.47
2:ED:632:LEU:HB2	2:ED:645:SER:HB3	1.95	0.47
2:ED:636:PHE:HE2	2:ED:1060:LEU:HD22	1.80	0.47
4:EH:106:PHE:HD1	4:EH:114:SER:HB2	1.79	0.47
1:FA:252:TYR:HE1	1:FA:883:VAL:HG11	1.78	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:FC:439:ILE:HG12	1:FC:509:ILE:HG12	1.97	0.47
1:FC:804:HIS:C	1:FC:806:PHE:H	2.23	0.47
2:FD:360:GLU:C	2:FD:361:LEU:HD12	2.39	0.47
2:FD:683:TYR:HB3	2:FD:708:ARG:HD3	1.97	0.47
11:FP:404:ASN:CG	11:FQ:470:ALA:HB2	2.39	0.47
1:AA:163:LEU:HD12	2:BD:331:GLN:HB2	1.97	0.46
1:AA:413:PHE:HZ	1:AA:466:TYR:HA	1.79	0.46
2:AD:331:GLN:HG2	4:DH:1211:ASN:OD1	2.15	0.46
4:AH:436:GLN:OE1	4:AH:529:VAL:HG23	2.15	0.46
4:AH:1211:ASN:OD1	2:BD:331:GLN:HG2	2.15	0.46
5:AJ:439:ASN:HD22	5:CJ:272:HIS:CE1	2.34	0.46
7:AI:119:LEU:HD12	7:AI:119:LEU:O	2.15	0.46
9:AM:134:ALA:HA	9:AM:159:ASN:O	2.14	0.46
11:AO:298:SER:HB2	11:AO:299:PRO:HD3	1.97	0.46
1:BA:800:LEU:HG	1:BA:801:GLN:HE21	1.80	0.46
1:BC:118:LEU:HD11	1:BC:180:LEU:HG	1.97	0.46
8:BK:179:HIS:HB2	8:BK:226:PHE:HB2	1.97	0.46
2:CD:331:GLN:HG2	4:FH:1211:ASN:OD1	2.15	0.46
11:CP:404:ASN:CG	11:CQ:470:ALA:HB2	2.39	0.46
4:DH:738:TYR:CD1	4:DH:752:TYR:CE1	3.02	0.46
7:DI:119:LEU:O	7:DI:119:LEU:HD12	2.15	0.46
11:DO:298:SER:HB2	11:DO:299:PRO:HD3	1.97	0.46
1:EA:560:LEU:HD11	1:EA:793:ARG:HD2	1.97	0.46
1:EB:59:GLN:HG3	1:EB:60:PRO:HD2	1.97	0.46
1:EB:868:GLU:HA	1:EB:871:THR:HG22	1.97	0.46
10:EN:9:PHE:HB2	10:FN:121:GLY:O	2.14	0.46
10:EN:42:LEU:HG	10:EN:44:GLN:H	1.80	0.46
1:FA:592:LYS:HA	1:FA:595:PHE:HB2	1.97	0.46
4:FH:513:GLU:HG2	4:FH:514:ARG:HG2	1.97	0.46
10:FN:124:ASN:OD1	10:FN:124:ASN:O	2.34	0.46
3:AG:33:ASN:HD22	3:AG:36:ASP:HB2	1.80	0.46
1:BA:163:LEU:HD12	2:ED:331:GLN:HB2	1.97	0.46
1:BC:804:HIS:C	1:BC:806:PHE:H	2.23	0.46
2:BD:636:PHE:HE2	2:BD:1060:LEU:HD22	1.80	0.46
11:BO:442:ILE:HD12	11:BO:460:VAL:HG22	1.97	0.46
3:CG:33:ASN:HD22	3:CG:36:ASP:HB2	1.80	0.46
4:CH:1021:ILE:HD13	4:CH:1181:PRO:HB2	1.97	0.46
1:DA:166:ASP:OD2	1:DA:166:ASP:N	2.46	0.46
1:DA:558:ASP:OD1	1:DA:558:ASP:N	2.48	0.46
3:DE:91:LEU:HD21	3:DF:92:GLU:HA	1.97	0.46
3:DF:33:ASN:HD22	3:DF:36:ASP:HB2	1.81	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:DH:106:PHE:HD1	4:DH:114:SER:HB2	1.79	0.46
10:DN:42:LEU:HG	10:DN:44:GLN:H	1.80	0.46
1:EA:503:ASP:OD1	1:EA:503:ASP:N	2.45	0.46
1:EB:469:TYR:O	1:EB:472:TYR:HB3	2.15	0.46
2:ED:404:ALA:HB1	2:ED:492:GLN:NE2	2.30	0.46
2:ED:683:TYR:HB3	2:ED:708:ARG:HD3	1.97	0.46
10:EN:124:ASN:OD1	10:EN:124:ASN:O	2.34	0.46
1:FA:216:ILE:HD11	1:FA:283:PRO:HG2	1.96	0.46
4:AH:1021:ILE:HD13	4:AH:1181:PRO:HB2	1.97	0.46
11:AP:425:ARG:HH11	10:DN:44:GLN:NE2	2.13	0.46
1:BA:439:ILE:HG12	1:BA:509:ILE:HG12	1.97	0.46
3:BE:91:LEU:HD21	3:BF:92:GLU:HA	1.97	0.46
1:CA:592:LYS:HA	1:CA:595:PHE:HB2	1.97	0.46
1:CB:868:GLU:HA	1:CB:871:THR:HG22	1.96	0.46
2:CD:1087:GLY:HA2	2:CD:1138:ALA:HB2	1.96	0.46
8:CK:174:SER:C	8:CK:176:ASP:H	2.22	0.46
10:CN:44:GLN:NE2	11:DP:425:ARG:HH11	2.13	0.46
10:CN:124:ASN:O	10:CN:124:ASN:OD1	2.34	0.46
1:DA:305:ARG:NH2	1:DA:324:GLN:OE1	2.49	0.46
1:DA:592:LYS:HA	1:DA:595:PHE:HB2	1.97	0.46
4:DH:194:SER:C	4:DH:196:ARG:N	2.73	0.46
4:DH:243:GLN:HG2	4:DH:245:PHE:CE2	2.50	0.46
4:EH:1021:ILE:HD13	4:EH:1181:PRO:HB2	1.97	0.46
11:EP:404:ASN:CG	11:EQ:470:ALA:HB2	2.40	0.46
5:AJ:212:GLU:HB2	5:AJ:302:LYS:HB3	1.97	0.46
5:AJ:272:HIS:CE1	5:EJ:439:ASN:HD22	2.34	0.46
1:BB:59:GLN:HG3	1:BB:60:PRO:HD2	1.97	0.46
2:BD:681:TYR:O	2:BD:682:HIS:HD2	1.98	0.46
4:BH:436:GLN:OE1	4:BH:529:VAL:HG23	2.15	0.46
10:BN:42:LEU:HG	10:BN:44:GLN:H	1.80	0.46
1:DC:439:ILE:HG12	1:DC:509:ILE:HG12	1.97	0.46
4:DH:639:ARG:NH2	4:DH:675:ASP:HB2	2.30	0.46
1:EC:96:VAL:HG11	1:EC:179:PHE:HE2	1.78	0.46
11:EO:247:ASP:O	11:EO:247:ASP:CG	2.59	0.46
1:AA:439:ILE:HG12	1:AA:509:ILE:HG12	1.97	0.46
3:AE:33:ASN:HD22	3:AE:36:ASP:HB2	1.81	0.46
4:AH:243:GLN:HG2	4:AH:245:PHE:CE2	2.50	0.46
4:AH:529:VAL:HG13	4:AH:529:VAL:O	2.16	0.46
1:BA:216:ILE:HD11	1:BA:283:PRO:HG2	1.96	0.46
3:BG:33:ASN:HD22	3:BG:36:ASP:HB2	1.80	0.46
4:BH:243:GLN:HG2	4:BH:245:PHE:CE2	2.50	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:BI:119:LEU:HD12	7:BI:119:LEU:O	2.15	0.46
10:BN:124:ASN:OD1	10:BN:124:ASN:O	2.34	0.46
11:BO:298:SER:HB2	11:BO:299:PRO:HD3	1.97	0.46
2:CD:681:TYR:O	2:CD:682:HIS:HD2	1.98	0.46
5:CJ:439:ASN:HD22	5:EJ:272:HIS:CE1	2.34	0.46
7:CI:86:TYR:OH	8:CK:162:GLU:OE2	2.30	0.46
2:DD:636:PHE:HE2	2:DD:1060:LEU:HD22	1.80	0.46
2:DD:683:TYR:HB3	2:DD:708:ARG:HD3	1.97	0.46
3:EG:33:ASN:HD22	3:EG:36:ASP:HB2	1.80	0.46
4:EH:436:GLN:OE1	4:EH:529:VAL:HG23	2.15	0.46
10:EN:44:GLN:HE22	11:FP:425:ARG:HH11	1.63	0.46
2:FD:747:PHE:HD2	2:FD:766:TYR:HE1	1.63	0.46
4:FH:436:GLN:OE1	4:FH:529:VAL:HG23	2.15	0.46
4:FH:639:ARG:NH2	4:FH:675:ASP:HB2	2.30	0.46
1:AB:469:TYR:O	1:AB:472:TYR:HB3	2.15	0.46
3:AE:91:LEU:HD21	3:AF:92:GLU:HA	1.97	0.46
3:AF:33:ASN:HD22	3:AF:36:ASP:HB2	1.81	0.46
10:AN:44:GLN:NE2	11:BP:425:ARG:HH11	2.13	0.46
1:BA:294:ASP:OD2	1:BA:415:TYR:OH	2.24	0.46
2:BD:1236:PHE:CD1	2:ED:361:LEU:HD11	2.51	0.46
3:BE:33:ASN:HD22	3:BE:36:ASP:HB2	1.81	0.46
4:BH:1021:ILE:HD13	4:BH:1181:PRO:HB2	1.97	0.46
4:BH:1132:SER:O	4:BH:1132:SER:OG	2.31	0.46
10:CN:9:PHE:HB2	10:DN:121:GLY:O	2.14	0.46
3:DE:33:ASN:HD22	3:DE:36:ASP:HB2	1.81	0.46
4:DH:513:GLU:HG2	4:DH:514:ARG:HG2	1.97	0.46
11:DP:397:GLU:OE1	11:DQ:359:LYS:NZ	2.41	0.46
1:EA:163:LEU:HD12	2:FD:331:GLN:HB2	1.97	0.46
1:EA:305:ARG:NH2	1:EA:324:GLN:OE1	2.49	0.46
2:ED:681:TYR:O	2:ED:682:HIS:HD2	1.98	0.46
2:ED:1236:PHE:CD1	2:FD:361:LEU:HD11	2.51	0.46
4:EH:513:GLU:HG2	4:EH:514:ARG:HG2	1.97	0.46
4:EH:529:VAL:O	4:EH:529:VAL:HG13	2.16	0.46
4:EH:619:TYR:O	4:EH:624:ILE:HD11	2.14	0.46
9:EM:134:ALA:HA	9:EM:159:ASN:O	2.14	0.46
4:FH:711:LYS:HE3	4:FH:711:LYS:HB3	1.81	0.46
4:AH:634:LYS:HD2	4:AH:648:ALA:HB1	1.97	0.46
11:AP:425:ARG:HH11	10:DN:44:GLN:HE22	1.63	0.46
4:BH:529:VAL:O	4:BH:529:VAL:HG13	2.16	0.46
10:BN:44:GLN:NE2	11:EP:425:ARG:HH11	2.13	0.46
2:CD:1236:PHE:CD1	2:DD:361:LEU:HD11	2.51	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:CE:2:ASN:OD1	3:CE:2:ASN:O	2.34	0.46
3:CE:51:LYS:HD2	3:CE:67:GLU:HA	1.98	0.46
3:CF:51:LYS:HD2	3:CF:67:GLU:HA	1.98	0.46
4:CH:529:VAL:HG13	4:CH:529:VAL:O	2.16	0.46
4:CH:895:ARG:O	4:CH:895:ARG:HG3	2.16	0.46
10:CN:42:LEU:HG	10:CN:44:GLN:H	1.80	0.46
2:DD:1087:GLY:HA2	2:DD:1138:ALA:HB2	1.96	0.46
3:DF:51:LYS:HD2	3:DF:67:GLU:HA	1.98	0.46
9:DM:42:THR:HG1	9:DM:57:LEU:C	2.19	0.46
4:EH:243:GLN:HG2	4:EH:245:PHE:CE2	2.50	0.46
4:EH:634:LYS:HD2	4:EH:648:ALA:HB1	1.97	0.46
1:FA:439:ILE:HG12	1:FA:509:ILE:HG12	1.96	0.46
2:FD:8:SER:OG	2:FD:9:LYS:N	2.47	0.46
4:FH:895:ARG:O	4:FH:895:ARG:HG3	2.16	0.46
1:AC:439:ILE:HG12	1:AC:509:ILE:HG12	1.98	0.46
4:AH:513:GLU:HG2	4:AH:514:ARG:HG2	1.97	0.46
7:BI:121:GLN:HE21	11:BO:476:LYS:HD2	1.81	0.46
2:CD:747:PHE:HD2	2:CD:766:TYR:HE1	1.63	0.46
4:CH:639:ARG:NH2	4:CH:675:ASP:HB2	2.30	0.46
6:CL:46:LEU:HG	6:CL:49:LYS:NZ	2.31	0.46
8:CK:179:HIS:HB2	8:CK:226:PHE:HB2	1.97	0.46
1:DB:469:TYR:O	1:DB:472:TYR:HB3	2.15	0.46
3:DE:2:ASN:O	3:DE:2:ASN:OD1	2.34	0.46
10:DN:124:ASN:OD1	10:DN:124:ASN:O	2.34	0.46
3:EF:51:LYS:HD2	3:EF:67:GLU:HA	1.98	0.46
4:EH:711:LYS:HE3	4:EH:711:LYS:HB3	1.81	0.46
7:EI:121:GLN:HE21	11:EO:476:LYS:HD2	1.81	0.46
8:EK:119:ASP:HB3	8:FK:147:LYS:CG	2.46	0.46
1:FA:800:LEU:HG	1:FA:801:GLN:HE21	1.80	0.46
4:FH:592:GLU:O	4:FH:596:LYS:HE2	2.16	0.46
7:FI:119:LEU:HD12	7:FI:119:LEU:O	2.15	0.46
10:FN:42:LEU:HG	10:FN:44:GLN:H	1.80	0.46
4:AH:532:ARG:HD3	4:AH:536:HIS:CD2	2.50	0.46
7:AI:121:GLN:HE21	11:AO:476:LYS:HD2	1.81	0.46
10:AN:124:ASN:OD1	10:AN:124:ASN:O	2.34	0.46
1:BA:558:ASP:OD1	1:BA:558:ASP:N	2.48	0.46
4:BH:513:GLU:HG2	4:BH:514:ARG:HG2	1.97	0.46
4:BH:846:LEU:HD23	4:BH:915:ARG:NH2	2.31	0.46
4:BH:1211:ASN:OD1	2:ED:331:GLN:HG2	2.15	0.46
8:BK:119:ASP:HB3	8:EK:147:LYS:CG	2.46	0.46
1:CA:38:LEU:HD22	1:CA:42:TYR:CE1	2.51	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:850:ALA:HB2	1:FC:844:ARG:O	2.16	0.46
4:CH:370:ASN:OD1	4:CH:370:ASN:N	2.48	0.46
7:CI:119:LEU:HD12	7:CI:119:LEU:O	2.15	0.46
2:DD:747:PHE:HD2	2:DD:766:TYR:HE1	1.63	0.46
1:FA:305:ARG:NH2	1:FA:324:GLN:OE1	2.49	0.46
4:FH:1021:ILE:HD13	4:FH:1181:PRO:HB2	1.97	0.46
1:AA:38:LEU:HD22	1:AA:42:TYR:CE1	2.51	0.46
1:AA:800:LEU:HG	1:AA:801:GLN:HE21	1.80	0.46
2:AD:636:PHE:HE2	2:AD:1060:LEU:HD22	1.80	0.46
1:BA:305:ARG:NH2	1:BA:324:GLN:OE1	2.49	0.46
10:BN:42:LEU:C	10:BN:44:GLN:H	2.24	0.46
1:CA:216:ILE:HD11	1:CA:283:PRO:HG2	1.96	0.46
1:CC:439:ILE:HG12	1:CC:509:ILE:HG12	1.98	0.46
1:CC:844:ARG:O	1:DA:850:ALA:HB2	2.16	0.46
5:CJ:212:GLU:HB2	5:CJ:302:LYS:HB3	1.97	0.46
7:CI:121:GLN:HE21	11:CO:476:LYS:HD2	1.81	0.46
11:CO:298:SER:HB2	11:CO:299:PRO:HD3	1.97	0.46
11:CP:425:ARG:HH11	10:FN:44:GLN:NE2	2.13	0.46
1:DB:100:LEU:HD11	1:DB:152:GLU:HG3	1.98	0.46
4:DH:592:GLU:O	4:DH:596:LYS:HE2	2.16	0.46
7:DI:121:GLN:HE21	11:DO:476:LYS:HD2	1.81	0.46
1:FB:868:GLU:HA	1:FB:871:THR:HG22	1.96	0.46
2:FD:681:TYR:O	2:FD:682:HIS:HD2	1.98	0.46
3:FE:91:LEU:HD21	3:FF:92:GLU:HA	1.97	0.46
7:FI:121:GLN:HE21	11:FO:476:LYS:HD2	1.81	0.46
11:FO:247:ASP:CG	11:FO:247:ASP:O	2.59	0.46
1:AA:305:ARG:NH2	1:AA:324:GLN:OE1	2.49	0.45
2:AD:465:SER:OG	2:AD:481:ARG:NH2	2.50	0.45
2:AD:683:TYR:HB3	2:AD:708:ARG:HD3	1.97	0.45
3:AF:51:LYS:HD2	3:AF:67:GLU:HA	1.98	0.45
8:AK:179:HIS:HB2	8:AK:226:PHE:HB2	1.97	0.45
1:BA:38:LEU:HD22	1:BA:42:TYR:CE1	2.51	0.45
1:BA:196:GLN:O	1:BA:200:SER:OG	2.27	0.45
3:BE:99:GLN:HB2	3:BG:98:LEU:HD11	1.98	0.45
3:BF:51:LYS:HD2	3:BF:67:GLU:HA	1.98	0.45
3:BG:19:LEU:HA	3:BG:23:TYR:CE2	2.52	0.45
4:BH:592:GLU:O	4:BH:596:LYS:HE2	2.16	0.45
4:BH:634:LYS:HD2	4:BH:648:ALA:HB1	1.97	0.45
11:BO:247:ASP:CG	11:BO:247:ASP:O	2.59	0.45
1:CA:608:GLN:NE2	1:CA:784:LYS:HA	2.31	0.45
3:DF:2:ASN:OD1	3:DF:2:ASN:O	2.34	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:EA:38:LEU:HD22	1:EA:42:TYR:CE1	2.51	0.45
4:EH:1132:SER:O	4:EH:1132:SER:OG	2.31	0.45
10:EN:44:GLN:NE2	11:FP:425:ARG:HH11	2.13	0.45
1:FA:503:ASP:OD1	1:FA:503:ASP:N	2.45	0.45
2:FD:636:PHE:HE2	2:FD:1060:LEU:HD22	1.80	0.45
3:FF:51:LYS:HD2	3:FF:67:GLU:HA	1.98	0.45
10:FN:89:LEU:HB3	10:FN:106:VAL:HB	1.98	0.45
2:AD:331:GLN:HB2	1:DA:163:LEU:HD12	1.97	0.45
11:AP:148:LEU:O	11:AP:151:VAL:HG12	2.17	0.45
2:BD:683:TYR:HB3	2:BD:708:ARG:HD3	1.97	0.45
11:BP:148:LEU:O	11:BP:151:VAL:HG12	2.17	0.45
1:CA:305:ARG:NH2	1:CA:324:GLN:OE1	2.49	0.45
3:CF:33:ASN:HD22	3:CF:36:ASP:HB2	1.81	0.45
3:CG:19:LEU:HA	3:CG:23:TYR:CE2	2.52	0.45
4:CH:729:LYS:HB2	4:CH:752:TYR:O	2.17	0.45
8:CK:147:LYS:CG	8:FK:119:ASP:HB3	2.46	0.45
2:DD:465:SER:OG	2:DD:481:ARG:NH2	2.50	0.45
3:DE:51:LYS:HD2	3:DE:67:GLU:HA	1.98	0.45
3:DG:19:LEU:HA	3:DG:23:TYR:CE2	2.52	0.45
4:DH:895:ARG:HG3	4:DH:895:ARG:O	2.16	0.45
11:DP:148:LEU:O	11:DP:151:VAL:HG12	2.17	0.45
11:DQ:148:LEU:O	11:DQ:151:VAL:HG12	2.17	0.45
1:EA:558:ASP:OD1	1:EA:558:ASP:N	2.48	0.45
1:EC:844:ARG:O	1:FA:850:ALA:HB2	2.16	0.45
2:ED:228:VAL:O	2:ED:232:ILE:HG12	2.17	0.45
4:EH:895:ARG:HG3	4:EH:895:ARG:O	2.16	0.45
11:EO:298:SER:HB2	11:EO:299:PRO:HD3	1.97	0.45
11:EP:148:LEU:O	11:EP:151:VAL:HG12	2.17	0.45
1:FA:38:LEU:HD22	1:FA:42:TYR:CE1	2.51	0.45
1:FA:608:GLN:NE2	1:FA:784:LYS:HA	2.31	0.45
2:FD:358:LYS:HE3	2:FD:363:ILE:CD1	2.47	0.45
3:FG:51:LYS:HD2	3:FG:67:GLU:HA	1.98	0.45
4:FH:634:LYS:HD2	4:FH:648:ALA:HB1	1.97	0.45
2:AD:682:HIS:CE1	2:AD:805:PHE:CG	3.05	0.45
3:AG:19:LEU:HA	3:AG:23:TYR:CE2	2.52	0.45
11:AO:338:GLN:OE1	11:AO:354:ARG:NH1	2.39	0.45
11:AQ:148:LEU:O	11:AQ:151:VAL:HG12	2.17	0.45
1:BA:167:ASP:OD2	1:BA:167:ASP:N	2.50	0.45
1:BA:608:GLN:NE2	1:BA:784:LYS:HA	2.31	0.45
1:BC:196:GLN:O	1:BC:200:SER:OG	2.25	0.45
2:BD:682:HIS:CE1	2:BD:805:PHE:CG	3.05	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:BE:35:ARG:NH2	3:BG:2:ASN:O	2.47	0.45
3:BF:33:ASN:HD22	3:BF:36:ASP:HB2	1.81	0.45
10:BN:89:LEU:HB3	10:BN:106:VAL:HB	1.98	0.45
11:BP:373:ASP:O	11:BP:377:ARG:HG3	2.17	0.45
1:CA:558:ASP:OD1	1:CA:558:ASP:N	2.48	0.45
2:CD:358:LYS:HE3	2:CD:363:ILE:CD1	2.47	0.45
3:CE:33:ASN:HD22	3:CE:36:ASP:HB2	1.81	0.45
3:CG:51:LYS:HD2	3:CG:67:GLU:HA	1.98	0.45
5:CJ:273:SER:HB2	5:EJ:400:ILE:HD13	1.99	0.45
11:CO:247:ASP:CG	11:CO:247:ASP:O	2.59	0.45
11:CQ:148:LEU:O	11:CQ:151:VAL:HG12	2.16	0.45
1:DA:800:LEU:HG	1:DA:801:GLN:HE21	1.80	0.45
4:DH:729:LYS:HB2	4:DH:752:TYR:O	2.17	0.45
4:DH:846:LEU:HD23	4:DH:915:ARG:NH2	2.31	0.45
1:EC:439:ILE:HG12	1:EC:509:ILE:HG12	1.98	0.45
3:EE:99:GLN:HB2	3:EG:98:LEU:HD11	1.98	0.45
4:EH:194:SER:C	4:EH:196:ARG:N	2.73	0.45
11:EP:373:ASP:O	11:EP:377:ARG:HG3	2.17	0.45
1:FA:413:PHE:HZ	1:FA:466:TYR:HA	1.79	0.45
2:FD:747:PHE:CD2	2:FD:766:TYR:HE1	2.35	0.45
2:FD:1130:ASN:OD1	2:FD:1137:PHE:HE1	2.00	0.45
3:FE:2:ASN:OD1	3:FE:2:ASN:O	2.34	0.45
3:FE:35:ARG:NH2	3:FG:2:ASN:O	2.47	0.45
4:FH:729:LYS:HB2	4:FH:752:TYR:O	2.17	0.45
1:AA:167:ASP:OD2	1:AA:167:ASP:N	2.50	0.45
1:AB:100:LEU:HD11	1:AB:152:GLU:HG3	1.98	0.45
1:AB:119:PHE:CD1	1:AB:126:ARG:HD2	2.52	0.45
3:AE:2:ASN:OD1	3:AE:2:ASN:O	2.34	0.45
3:AE:35:ARG:NH2	3:AG:2:ASN:O	2.47	0.45
3:AG:51:LYS:HD2	3:AG:67:GLU:HA	1.98	0.45
4:AH:592:GLU:O	4:AH:596:LYS:HE2	2.16	0.45
4:AH:846:LEU:HD23	4:AH:915:ARG:NH2	2.31	0.45
11:AQ:120:ASN:ND2	11:AQ:300:LEU:HD22	2.32	0.45
1:BC:844:ARG:O	1:EA:850:ALA:HB2	2.16	0.45
2:BD:465:SER:OG	2:BD:481:ARG:NH2	2.50	0.45
11:BP:120:ASN:ND2	11:BP:300:LEU:HD22	2.32	0.45
2:CD:636:PHE:HE2	2:CD:1060:LEU:HD22	1.80	0.45
2:CD:1130:ASN:OD1	2:CD:1137:PHE:HE1	2.00	0.45
4:CH:513:GLU:HG2	4:CH:514:ARG:HG2	1.97	0.45
4:DH:529:VAL:HG13	4:DH:529:VAL:O	2.16	0.45
11:DO:247:ASP:CG	11:DO:247:ASP:O	2.59	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:DQ:373:ASP:O	11:DQ:377:ARG:HG3	2.17	0.45
3:EF:2:ASN:OD1	3:EF:2:ASN:O	2.34	0.45
3:EG:51:LYS:HD2	3:EG:67:GLU:HA	1.98	0.45
8:EK:180:GLN:O	8:EK:181:ARG:NH1	2.44	0.45
11:EQ:120:ASN:ND2	11:EQ:300:LEU:HD22	2.32	0.45
3:FF:2:ASN:O	3:FF:2:ASN:OD1	2.34	0.45
3:FG:33:ASN:HD22	3:FG:36:ASP:HB2	1.80	0.45
4:FH:619:TYR:O	4:FH:624:ILE:HD11	2.14	0.45
1:AC:844:ARG:O	1:BA:850:ALA:HB2	2.16	0.45
3:AF:2:ASN:O	3:AF:2:ASN:OD1	2.34	0.45
4:AH:746:PHE:HE1	4:AH:752:TYR:CE2	2.35	0.45
8:AK:119:ASP:HB3	8:BK:147:LYS:CG	2.46	0.45
10:AN:42:LEU:HG	10:AN:44:GLN:H	1.80	0.45
1:BB:119:PHE:CD1	1:BB:126:ARG:HD2	2.52	0.45
1:BC:439:ILE:HG12	1:BC:509:ILE:HG12	1.97	0.45
2:BD:228:VAL:O	2:BD:232:ILE:HG12	2.17	0.45
2:BD:653:GLU:O	2:BD:656:GLN:HG2	2.17	0.45
11:BQ:120:ASN:ND2	11:BQ:300:LEU:HD22	2.32	0.45
1:CA:800:LEU:HG	1:CA:801:GLN:HE21	1.80	0.45
1:CB:100:LEU:HD11	1:CB:152:GLU:HG3	1.98	0.45
2:CD:220:GLU:HG3	2:CD:311:GLY:O	2.17	0.45
2:CD:361:LEU:HD11	2:FD:1236:PHE:CD1	2.51	0.45
2:CD:465:SER:OG	2:CD:481:ARG:NH2	2.50	0.45
4:CH:846:LEU:HD23	4:CH:915:ARG:NH2	2.31	0.45
1:DA:610:PHE:O	1:DA:610:PHE:CD1	2.70	0.45
1:DB:119:PHE:CD1	1:DB:126:ARG:HD2	2.52	0.45
1:DC:88:THR:HG23	1:DC:89:HIS:ND1	2.32	0.45
2:DD:682:HIS:CE1	2:DD:805:PHE:CG	3.05	0.45
2:ED:747:PHE:CD2	2:ED:766:TYR:HE1	2.35	0.45
4:EH:846:LEU:HD23	4:EH:915:ARG:NH2	2.31	0.45
6:EL:46:LEU:HG	6:EL:49:LYS:NZ	2.31	0.45
7:EI:119:LEU:HD12	7:EI:119:LEU:O	2.15	0.45
3:FG:19:LEU:HA	3:FG:23:TYR:CE2	2.52	0.45
2:AD:361:LEU:HD11	2:DD:1236:PHE:CD1	2.51	0.45
2:AD:653:GLU:O	2:AD:656:GLN:HG2	2.17	0.45
2:AD:1236:PHE:CD1	2:BD:361:LEU:HD11	2.51	0.45
4:AH:895:ARG:HG3	4:AH:895:ARG:O	2.16	0.45
5:AJ:273:SER:HB2	5:CJ:400:ILE:HD13	1.99	0.45
10:AN:44:GLN:HE22	11:BP:425:ARG:HH11	1.63	0.45
10:BN:44:GLN:HE22	11:EP:425:ARG:HH11	1.63	0.45
2:CD:331:GLN:HB2	1:FA:163:LEU:HD12	1.97	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:CD:747:PHE:CD2	2:CD:766:TYR:HE1	2.35	0.45
4:CH:634:LYS:HD2	4:CH:648:ALA:HB1	1.97	0.45
8:CK:119:ASP:HB3	8:DK:147:LYS:CG	2.46	0.45
10:CN:89:LEU:HB3	10:CN:106:VAL:HB	1.98	0.45
3:DE:99:GLN:HB2	3:DG:98:LEU:HD11	1.98	0.45
8:DK:179:HIS:HB2	8:DK:226:PHE:HB2	1.97	0.45
11:DQ:120:ASN:ND2	11:DQ:300:LEU:HD22	2.32	0.45
1:EB:548:PHE:HD2	1:EB:551:ILE:HD11	1.82	0.45
1:EC:21:THR:HG23	2:ED:1311:HIS:O	2.17	0.45
2:ED:404:ALA:HB1	2:ED:492:GLN:HE21	1.81	0.45
2:ED:682:HIS:CE1	2:ED:805:PHE:CG	3.05	0.45
2:ED:747:PHE:HD2	2:ED:766:TYR:HE1	1.63	0.45
3:EG:19:LEU:HA	3:EG:23:TYR:CE2	2.52	0.45
4:EH:592:GLU:O	4:EH:596:LYS:HE2	2.16	0.45
4:EH:729:LYS:HB2	4:EH:752:TYR:O	2.17	0.45
2:FD:220:GLU:HG3	2:FD:311:GLY:O	2.17	0.45
2:FD:465:SER:OG	2:FD:481:ARG:NH2	2.50	0.45
4:FH:529:VAL:HG13	4:FH:529:VAL:O	2.16	0.45
4:FH:846:LEU:HD23	4:FH:915:ARG:NH2	2.31	0.45
10:FN:42:LEU:C	10:FN:44:GLN:H	2.24	0.45
11:FQ:148:LEU:O	11:FQ:151:VAL:HG12	2.17	0.45
1:AA:608:GLN:NE2	1:AA:784:LYS:HA	2.31	0.45
1:AA:610:PHE:O	1:AA:610:PHE:CD1	2.70	0.45
1:AA:850:ALA:HB2	1:DC:844:ARG:O	2.16	0.45
2:AD:771:GLU:HA	2:AD:774:ASP:OD1	2.17	0.45
4:AH:729:LYS:HB2	4:AH:752:TYR:O	2.17	0.45
8:AK:147:LYS:CG	8:DK:119:ASP:HB3	2.46	0.45
11:AP:373:ASP:O	11:AP:377:ARG:HG3	2.17	0.45
11:AP:456:GLY:HA2	11:AQ:470:ALA:HA	1.98	0.45
11:AQ:373:ASP:O	11:AQ:377:ARG:HG3	2.17	0.45
3:BE:51:LYS:HD2	3:BE:67:GLU:HA	1.98	0.45
4:BH:746:PHE:HE1	4:BH:752:TYR:CE2	2.35	0.45
4:BH:895:ARG:HG3	4:BH:895:ARG:O	2.16	0.45
1:CA:404:ASN:O	1:CA:408:VAL:HG23	2.17	0.45
1:CC:21:THR:HG23	2:CD:1311:HIS:O	2.17	0.45
3:CE:99:GLN:HB2	3:CG:98:LEU:HD11	1.98	0.45
8:CK:180:GLN:O	8:CK:181:ARG:NH1	2.44	0.45
1:DA:404:ASN:O	1:DA:408:VAL:HG23	2.17	0.45
1:DC:21:THR:HG23	2:DD:1311:HIS:O	2.17	0.45
2:DD:771:GLU:HA	2:DD:774:ASP:OD1	2.17	0.45
3:DE:35:ARG:NH2	3:DG:2:ASN:O	2.47	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:EA:608:GLN:NE2	1:EA:784:LYS:HA	2.31	0.45
2:ED:465:SER:OG	2:ED:481:ARG:NH2	2.50	0.45
2:ED:1130:ASN:OD1	2:ED:1137:PHE:HE1	2.00	0.45
3:EE:33:ASN:HD22	3:EE:36:ASP:HB2	1.81	0.45
3:EE:35:ARG:NH2	3:EG:2:ASN:O	2.47	0.45
11:EP:120:ASN:ND2	11:EP:300:LEU:HD22	2.32	0.45
1:FA:425:ASP:OD1	1:FA:425:ASP:N	2.46	0.45
3:FE:99:GLN:HB2	3:FG:98:LEU:HD11	1.98	0.45
11:FO:298:SER:HB2	11:FO:299:PRO:HD3	1.97	0.45
11:FP:373:ASP:O	11:FP:377:ARG:HG3	2.17	0.45
2:AD:228:VAL:O	2:AD:232:ILE:HG12	2.17	0.45
3:AE:51:LYS:HD2	3:AE:67:GLU:HA	1.98	0.45
8:AK:147:LYS:HG3	8:DK:119:ASP:CB	2.47	0.45
11:AP:120:ASN:ND2	11:AP:300:LEU:HD22	2.32	0.45
1:BB:548:PHE:HD2	1:BB:551:ILE:HD11	1.82	0.45
2:BD:358:LYS:HE3	2:BD:363:ILE:CD1	2.47	0.45
2:BD:590:ALA:O	2:BD:594:THR:HG21	2.17	0.45
4:BH:729:LYS:HB2	4:BH:752:TYR:O	2.17	0.45
2:CD:221:THR:HG21	2:FD:538:SER:O	2.17	0.45
4:CH:592:GLU:O	4:CH:596:LYS:HE2	2.16	0.45
10:CN:42:LEU:C	10:CN:44:GLN:H	2.24	0.45
11:CP:148:LEU:O	11:CP:151:VAL:HG12	2.17	0.45
11:CQ:373:ASP:O	11:CQ:377:ARG:HG3	2.17	0.45
1:DA:608:GLN:NE2	1:DA:784:LYS:HA	2.31	0.45
2:DD:747:PHE:CD2	2:DD:766:TYR:HE1	2.35	0.45
11:DO:338:GLN:OE1	11:DO:354:ARG:NH1	2.39	0.45
11:DP:120:ASN:ND2	11:DP:300:LEU:HD22	2.32	0.45
2:ED:358:LYS:HE3	2:ED:363:ILE:CD1	2.47	0.45
1:FB:119:PHE:CD1	1:FB:126:ARG:HD2	2.52	0.45
3:FE:33:ASN:HD22	3:FE:36:ASP:HB2	1.81	0.45
11:FP:120:ASN:ND2	11:FP:300:LEU:HD22	2.32	0.45
11:FQ:120:ASN:ND2	11:FQ:300:LEU:HD22	2.32	0.45
2:AD:747:PHE:HD2	2:AD:766:TYR:HE1	1.63	0.45
2:AD:1130:ASN:OD1	2:AD:1137:PHE:HE1	2.00	0.45
3:AE:99:GLN:HB2	3:AG:98:LEU:HD11	1.98	0.45
6:AL:46:LEU:HG	6:AL:49:LYS:NZ	2.31	0.45
11:AO:247:ASP:CG	11:AO:247:ASP:O	2.59	0.45
1:BC:21:THR:HG23	2:BD:1311:HIS:O	2.17	0.45
2:BD:771:GLU:HA	2:BD:774:ASP:OD1	2.17	0.45
2:BD:1130:ASN:OD1	2:BD:1137:PHE:HE1	2.00	0.45
11:BQ:148:LEU:O	11:BQ:151:VAL:HG12	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CC:88:THR:HG23	1:CC:89:HIS:ND1	2.32	0.45
2:CD:771:GLU:HA	2:CD:774:ASP:OD1	2.17	0.45
4:CH:241:ASP:OD2	4:CH:241:ASP:N	2.50	0.45
11:CP:456:GLY:HA2	11:CQ:470:ALA:HA	1.99	0.45
1:DA:38:LEU:HD22	1:DA:42:TYR:CE1	2.51	0.45
1:DB:548:PHE:HD2	1:DB:551:ILE:HD11	1.82	0.45
2:DD:220:GLU:HG3	2:DD:311:GLY:O	2.17	0.45
2:DD:358:LYS:HE3	2:DD:363:ILE:CD1	2.47	0.45
9:DM:41:GLN:O	9:DM:59:VAL:HB	2.17	0.45
2:ED:653:GLU:O	2:ED:656:GLN:HG2	2.17	0.45
1:FA:404:ASN:O	1:FA:408:VAL:HG23	2.17	0.45
1:FA:558:ASP:OD1	1:FA:558:ASP:N	2.48	0.45
1:FB:548:PHE:HD2	1:FB:551:ILE:HD11	1.82	0.45
1:AA:404:ASN:O	1:AA:408:VAL:HG23	2.17	0.45
1:AC:88:THR:HG23	1:AC:89:HIS:ND1	2.32	0.45
3:AF:87:LEU:CD1	3:AG:59:HIS:HB3	2.47	0.45
8:AK:119:ASP:CB	8:BK:147:LYS:HG3	2.47	0.45
2:BD:404:ALA:HB1	2:BD:492:GLN:HE21	1.81	0.45
2:BD:747:PHE:HD2	2:BD:766:TYR:HE1	1.63	0.45
3:BE:2:ASN:O	3:BE:2:ASN:OD1	2.34	0.45
2:CD:590:ALA:O	2:CD:594:THR:HG21	2.17	0.45
8:CK:119:ASP:CB	8:DK:147:LYS:HG3	2.47	0.45
8:CK:147:LYS:HG3	8:FK:119:ASP:CB	2.47	0.45
11:CP:120:ASN:ND2	11:CP:300:LEU:HD22	2.32	0.45
3:DG:51:LYS:HD2	3:DG:67:GLU:HA	1.98	0.45
11:DP:373:ASP:O	11:DP:377:ARG:HG3	2.17	0.45
2:ED:677:TYR:OH	2:ED:822:GLU:OE2	2.28	0.45
3:EE:2:ASN:OD1	3:EE:2:ASN:O	2.34	0.45
3:EE:51:LYS:HD2	3:EE:67:GLU:HA	1.98	0.45
4:EH:241:ASP:OD2	4:EH:241:ASP:N	2.50	0.45
10:EN:42:LEU:C	10:EN:44:GLN:H	2.24	0.45
11:FP:148:LEU:O	11:FP:151:VAL:HG12	2.17	0.45
5:AJ:400:ILE:HD13	5:EJ:273:SER:HB2	1.99	0.44
10:AN:42:LEU:C	10:AN:44:GLN:H	2.24	0.44
1:BA:610:PHE:O	1:BA:610:PHE:CD1	2.70	0.44
1:CA:163:LEU:HD12	2:DD:331:GLN:HB2	1.97	0.44
2:CD:228:VAL:O	2:CD:232:ILE:HG12	2.17	0.44
2:CD:786:VAL:HA	2:CD:789:TYR:HD1	1.82	0.44
3:CE:59:HIS:HB3	3:CG:87:LEU:CD1	2.48	0.44
10:CN:118:ASP:O	10:FN:8:LYS:HD2	2.18	0.44
11:CQ:120:ASN:ND2	11:CQ:300:LEU:HD22	2.32	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:DD:404:ALA:HB1	2:DD:492:GLN:HE21	1.81	0.44
4:DH:746:PHE:HE1	4:DH:752:TYR:CE2	2.35	0.44
4:EH:284:ARG:HA	4:EH:285:PRO:HD3	1.87	0.44
10:EN:8:LYS:HD2	10:FN:118:ASP:O	2.18	0.44
1:FA:20:LEU:HD12	1:FA:21:THR:H	1.82	0.44
2:FD:404:ALA:HB1	2:FD:492:GLN:HE21	1.81	0.44
2:FD:783:ILE:HD12	2:FD:784:GLN:N	2.32	0.44
3:FE:51:LYS:HD2	3:FE:67:GLU:HA	1.98	0.44
4:FH:746:PHE:HE1	4:FH:752:TYR:CE2	2.35	0.44
4:AH:241:ASP:OD2	4:AH:241:ASP:N	2.50	0.44
4:AH:486:ASP:OD1	4:AH:486:ASP:N	2.50	0.44
10:AN:31:GLU:CG	10:AN:55:LYS:O	2.66	0.44
2:BD:747:PHE:CD2	2:BD:766:TYR:HE1	2.35	0.44
3:BG:51:LYS:HD2	3:BG:67:GLU:HA	1.98	0.44
1:CB:548:PHE:HD2	1:CB:551:ILE:HD11	1.82	0.44
3:CF:2:ASN:O	3:CF:2:ASN:OD1	2.34	0.44
4:CH:746:PHE:HE1	4:CH:752:TYR:CE2	2.35	0.44
11:CP:373:ASP:O	11:CP:377:ARG:HG3	2.17	0.44
1:EB:119:PHE:CD1	1:EB:126:ARG:HD2	2.52	0.44
4:EH:746:PHE:HE1	4:EH:752:TYR:CE2	2.35	0.44
11:EQ:148:LEU:O	11:EQ:151:VAL:HG12	2.16	0.44
2:FD:771:GLU:HA	2:FD:774:ASP:OD1	2.17	0.44
10:FN:31:GLU:CG	10:FN:55:LYS:O	2.66	0.44
11:FP:456:GLY:HA2	11:FQ:470:ALA:HA	1.98	0.44
2:AD:404:ALA:HB1	2:AD:492:GLN:HE21	1.81	0.44
9:AM:41:GLN:O	9:AM:59:VAL:HB	2.17	0.44
2:BD:605:LEU:HD12	2:BD:613:VAL:HG12	1.99	0.44
11:BP:456:GLY:HA2	11:BQ:470:ALA:HA	1.99	0.44
1:CB:119:PHE:CD1	1:CB:126:ARG:HD2	2.52	0.44
2:CD:783:ILE:CD1	2:CD:784:GLN:HG3	2.48	0.44
4:CH:167:LEU:HD12	4:CH:167:LEU:HA	1.73	0.44
2:DD:590:ALA:O	2:DD:594:THR:HG21	2.17	0.44
1:EA:404:ASN:O	1:EA:408:VAL:HG23	2.17	0.44
2:ED:538:SER:O	2:FD:221:THR:HG21	2.17	0.44
2:ED:771:GLU:HA	2:ED:774:ASP:OD1	2.17	0.44
3:EE:21:GLU:HG2	3:EG:15:ASN:OD1	2.18	0.44
10:EN:89:LEU:HB3	10:EN:106:VAL:HB	1.98	0.44
2:FD:228:VAL:O	2:FD:232:ILE:HG12	2.17	0.44
9:FM:41:GLN:O	9:FM:59:VAL:HB	2.17	0.44
2:AD:590:ALA:O	2:AD:594:THR:HG21	2.17	0.44
3:AE:59:HIS:HB3	3:AG:87:LEU:CD1	2.48	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:AH:1132:SER:O	4:AH:1132:SER:OG	2.31	0.44
8:AK:162:GLU:HG2	8:AK:165:ARG:HB3	1.99	0.44
1:BB:100:LEU:HD11	1:BB:152:GLU:HG3	1.98	0.44
2:BD:538:SER:O	2:ED:221:THR:HG21	2.17	0.44
3:BF:2:ASN:OD1	3:BF:2:ASN:O	2.34	0.44
10:BN:8:LYS:HD2	10:EN:118:ASP:O	2.18	0.44
2:CD:783:ILE:HD12	2:CD:784:GLN:N	2.32	0.44
2:CD:1088:THR:O	2:CD:1088:THR:HG22	2.17	0.44
2:DD:783:ILE:CD1	2:DD:784:GLN:HG3	2.48	0.44
1:EB:100:LEU:HD11	1:EB:152:GLU:HG3	1.98	0.44
10:EN:31:GLU:CG	10:EN:55:LYS:O	2.66	0.44
1:FB:100:LEU:HD11	1:FB:152:GLU:HG3	1.98	0.44
1:FC:21:THR:HG23	2:FD:1311:HIS:O	2.17	0.44
2:FD:682:HIS:CE1	2:FD:805:PHE:CG	3.05	0.44
1:AC:21:THR:HG23	2:AD:1311:HIS:O	2.17	0.44
2:AD:358:LYS:HE3	2:AD:363:ILE:CD1	2.47	0.44
2:AD:538:SER:O	2:BD:221:THR:HG21	2.17	0.44
4:AH:614:ASN:HB3	4:AH:617:GLU:HG3	2.00	0.44
4:AH:641:LYS:HG2	4:AH:688:LYS:HG2	2.00	0.44
10:AN:89:LEU:HB3	10:AN:106:VAL:HB	1.98	0.44
1:BA:22:ASN:OD1	2:BD:1325:LEU:HD23	2.18	0.44
1:BB:196:GLN:O	1:BB:200:SER:OG	2.27	0.44
1:BC:5:ILE:HG12	1:BC:363:THR:OG1	2.18	0.44
2:BD:220:GLU:HG3	2:BD:311:GLY:O	2.17	0.44
3:BE:21:GLU:HG2	3:BG:15:ASN:OD1	2.18	0.44
1:CA:22:ASN:OD1	2:CD:1325:LEU:HD23	2.18	0.44
2:CD:682:HIS:CE1	2:CD:805:PHE:CG	3.05	0.44
2:CD:747:PHE:CD2	2:CD:766:TYR:CE1	3.05	0.44
10:CN:8:LYS:HD2	10:DN:118:ASP:O	2.18	0.44
2:DD:228:VAL:O	2:DD:232:ILE:HG12	2.17	0.44
2:DD:747:PHE:CD2	2:DD:766:TYR:CE1	3.05	0.44
4:DH:614:ASN:HB3	4:DH:617:GLU:HG3	2.00	0.44
2:ED:590:ALA:O	2:ED:594:THR:HG21	2.17	0.44
4:EH:1025:GLN:O	4:EH:1033:LEU:HD12	2.18	0.44
9:EM:41:GLN:O	9:EM:59:VAL:HB	2.17	0.44
2:FD:747:PHE:CD2	2:FD:766:TYR:CE1	3.06	0.44
2:FD:783:ILE:CD1	2:FD:784:GLN:HG3	2.48	0.44
1:AA:20:LEU:HD12	1:AA:21:THR:H	1.82	0.44
1:BA:20:LEU:HD12	1:BA:21:THR:H	1.82	0.44
3:BE:59:HIS:HB3	3:BG:87:LEU:CD1	2.48	0.44
3:BF:87:LEU:CD1	3:BG:59:HIS:HB3	2.47	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:BQ:373:ASP:O	11:BQ:377:ARG:HG3	2.17	0.44
1:CC:88:THR:HA	1:CC:129:LEU:HD12	2.00	0.44
2:CD:336:TYR:CE1	4:FH:1207:ILE:HD11	2.53	0.44
2:CD:404:ALA:HB1	2:CD:492:GLN:HE21	1.81	0.44
8:CK:162:GLU:HG2	8:CK:165:ARG:HB3	2.00	0.44
11:CO:238:THR:HG22	11:CO:293:LEU:O	2.18	0.44
1:DA:20:LEU:HD12	1:DA:21:THR:H	1.82	0.44
1:DA:196:GLN:O	1:DA:200:SER:OG	2.27	0.44
2:DD:1130:ASN:OD1	2:DD:1137:PHE:HE1	2.00	0.44
2:ED:220:GLU:HG3	2:ED:311:GLY:O	2.17	0.44
3:EF:33:ASN:HD22	3:EF:36:ASP:HB2	1.81	0.44
4:EH:291:VAL:CG1	4:EH:292:HIS:N	2.81	0.44
4:EH:654:LEU:HD23	4:EH:654:LEU:HA	1.88	0.44
8:EK:119:ASP:CB	8:FK:147:LYS:HG3	2.47	0.44
1:FA:59:GLN:HB2	1:FA:62:ASP:HB2	2.00	0.44
2:FD:1088:THR:O	2:FD:1088:THR:HG22	2.17	0.44
4:FH:614:ASN:HB3	4:FH:617:GLU:HG3	2.00	0.44
7:FI:119:LEU:HD12	7:FI:119:LEU:C	2.43	0.44
1:AB:120:GLU:H	1:AB:120:GLU:CD	2.26	0.44
1:AB:548:PHE:HD2	1:AB:551:ILE:HD11	1.82	0.44
2:AD:221:THR:HG21	2:DD:538:SER:O	2.17	0.44
2:AD:747:PHE:CD2	2:AD:766:TYR:HE1	2.35	0.44
2:AD:783:ILE:HD12	2:AD:784:GLN:N	2.32	0.44
4:AH:1188:VAL:HG21	4:AH:1195:GLN:HB2	2.00	0.44
11:AO:238:THR:HG22	11:AO:293:LEU:O	2.18	0.44
1:BC:88:THR:HA	1:BC:129:LEU:HD12	2.00	0.44
1:BC:88:THR:HG23	1:BC:89:HIS:ND1	2.32	0.44
4:BH:641:LYS:HG2	4:BH:688:LYS:HG2	1.99	0.44
4:BH:1188:VAL:HG21	4:BH:1195:GLN:HB2	2.00	0.44
11:BO:238:THR:HG22	11:BO:293:LEU:O	2.18	0.44
1:CC:145:GLN:HG2	1:CC:182:PRO:HA	2.00	0.44
9:CM:41:GLN:O	9:CM:59:VAL:HB	2.17	0.44
1:DA:59:GLN:HB2	1:DA:62:ASP:HB2	2.00	0.44
1:DC:5:ILE:HG12	1:DC:363:THR:OG1	2.18	0.44
2:DD:786:VAL:HA	2:DD:789:TYR:HD1	1.82	0.44
4:DH:1025:GLN:O	4:DH:1033:LEU:HD12	2.18	0.44
11:DP:456:GLY:HA2	11:DQ:470:ALA:HA	1.99	0.44
5:EJ:210:LEU:HD22	5:EJ:301:VAL:HG13	2.00	0.44
1:FC:88:THR:HG23	1:FC:89:HIS:ND1	2.32	0.44
3:FE:21:GLU:HG2	3:FG:15:ASN:OD1	2.18	0.44
4:FH:291:VAL:CG1	4:FH:292:HIS:N	2.81	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:FQ:373:ASP:O	11:FQ:377:ARG:HG3	2.17	0.44
7:AI:119:LEU:HD12	7:AI:119:LEU:C	2.43	0.44
1:CA:804:HIS:C	1:CA:806:PHE:H	2.26	0.44
3:CF:87:LEU:CD1	3:CG:59:HIS:HB3	2.47	0.44
1:DA:22:ASN:OD1	2:DD:1325:LEU:HD23	2.18	0.44
2:DD:1088:THR:O	2:DD:1088:THR:HG22	2.17	0.44
1:EA:59:GLN:HB2	1:EA:62:ASP:HB2	2.00	0.44
1:EA:610:PHE:O	1:EA:610:PHE:CD1	2.70	0.44
1:EC:88:THR:HA	1:EC:129:LEU:HD12	2.00	0.44
1:EC:88:THR:HG23	1:EC:89:HIS:ND1	2.32	0.44
1:EC:145:GLN:HG2	1:EC:182:PRO:HA	1.99	0.44
2:ED:730:ALA:HA	2:ED:733:ASN:HD22	1.83	0.44
1:FA:22:ASN:OD1	2:FD:1325:LEU:HD23	2.18	0.44
3:FF:87:LEU:CD1	3:FG:59:HIS:HB3	2.47	0.44
4:FH:1025:GLN:O	4:FH:1033:LEU:HD12	2.18	0.44
4:FH:1229:LEU:HD12	4:FH:1229:LEU:HA	1.81	0.44
11:FO:238:THR:HG22	11:FO:293:LEU:O	2.18	0.44
1:AA:100:LEU:HG	1:AA:150:VAL:HG11	2.00	0.44
1:AB:90:TYR:HD1	1:AB:129:LEU:HD12	1.83	0.44
4:AH:110:ARG:NH2	4:AH:198:PRO:O	2.46	0.44
2:BD:783:ILE:HD12	2:BD:784:GLN:N	2.32	0.44
4:BH:614:ASN:HB3	4:BH:617:GLU:HG3	2.00	0.44
1:CA:100:LEU:HG	1:CA:150:VAL:HG11	2.00	0.44
1:CC:5:ILE:HG12	1:CC:363:THR:OG1	2.18	0.44
2:CD:653:GLU:O	2:CD:656:GLN:HG2	2.17	0.44
4:CH:614:ASN:HB3	4:CH:617:GLU:HG3	2.00	0.44
4:CH:1207:ILE:HD11	2:DD:336:TYR:CE1	2.53	0.44
4:CH:1229:LEU:HD12	4:CH:1229:LEU:HA	1.81	0.44
10:CN:44:GLN:HE22	11:DP:425:ARG:NH1	2.16	0.44
1:DA:100:LEU:HG	1:DA:150:VAL:HG11	2.00	0.44
1:DA:294:ASP:OD2	1:DA:415:TYR:OH	2.24	0.44
4:DH:241:ASP:OD2	4:DH:241:ASP:N	2.50	0.44
11:DO:238:THR:HG22	11:DO:293:LEU:O	2.18	0.44
2:ED:783:ILE:HD12	2:ED:784:GLN:N	2.32	0.44
2:ED:1088:THR:O	2:ED:1088:THR:HG22	2.17	0.44
4:EH:614:ASN:HB3	4:EH:617:GLU:HG3	2.00	0.44
7:EI:119:LEU:HD12	7:EI:119:LEU:C	2.43	0.44
11:EP:456:GLY:HA2	11:EQ:470:ALA:HA	1.99	0.44
2:FD:590:ALA:O	2:FD:594:THR:HG21	2.17	0.44
1:AA:59:GLN:HB2	1:AA:62:ASP:HB2	2.00	0.43
1:AC:5:ILE:HG12	1:AC:363:THR:OG1	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:AD:336:TYR:CE1	4:DH:1207:ILE:HD11	2.53	0.43
2:AD:605:LEU:HD12	2:AD:613:VAL:HG12	1.99	0.43
2:AD:747:PHE:CD2	2:AD:766:TYR:CE1	3.06	0.43
2:AD:783:ILE:CD1	2:AD:784:GLN:HG3	2.48	0.43
8:AK:180:GLN:O	8:AK:181:ARG:NH1	2.44	0.43
10:AN:118:ASP:O	10:DN:8:LYS:HD2	2.18	0.43
1:BA:59:GLN:HB2	1:BA:62:ASP:HB2	2.00	0.43
4:BH:291:VAL:CG1	4:BH:292:HIS:N	2.81	0.43
10:BN:31:GLU:CG	10:BN:55:LYS:O	2.66	0.43
1:CA:20:LEU:HD12	1:CA:21:THR:H	1.82	0.43
10:CN:31:GLU:CG	10:CN:55:LYS:O	2.66	0.43
3:DF:87:LEU:CD1	3:DG:59:HIS:HB3	2.47	0.43
7:DI:119:LEU:HD12	7:DI:119:LEU:C	2.43	0.43
2:ED:605:LEU:HD12	2:ED:613:VAL:HG12	2.00	0.43
2:ED:783:ILE:CD1	2:ED:784:GLN:HG3	2.48	0.43
4:EH:1229:LEU:HD12	4:EH:1229:LEU:HA	1.81	0.43
11:EQ:373:ASP:O	11:EQ:377:ARG:HG3	2.17	0.43
2:FD:653:GLU:O	2:FD:656:GLN:HG2	2.17	0.43
4:FH:241:ASP:N	4:FH:241:ASP:OD2	2.50	0.43
4:FH:869:ASP:OD2	4:FH:869:ASP:N	2.51	0.43
2:AD:1088:THR:O	2:AD:1088:THR:HG22	2.17	0.43
4:AH:80:THR:HB	4:AH:81:PRO:HD3	2.01	0.43
10:AN:8:LYS:HD2	10:BN:118:ASP:O	2.18	0.43
1:BA:100:LEU:HG	1:BA:150:VAL:HG11	2.00	0.43
1:BA:404:ASN:O	1:BA:408:VAL:HG23	2.17	0.43
1:BC:145:GLN:HG2	1:BC:182:PRO:HA	1.99	0.43
2:BD:730:ALA:HA	2:BD:733:ASN:HD22	1.83	0.43
2:BD:1088:THR:O	2:BD:1088:THR:HG22	2.17	0.43
8:BK:119:ASP:CB	8:EK:147:LYS:HG3	2.47	0.43
1:CA:59:GLN:HB2	1:CA:62:ASP:HB2	2.00	0.43
3:CE:21:GLU:HG2	3:CG:15:ASN:OD1	2.18	0.43
2:DD:653:GLU:O	2:DD:656:GLN:HG2	2.17	0.43
10:DN:89:LEU:HB3	10:DN:106:VAL:HB	1.98	0.43
1:EB:298:LEU:HD21	1:EB:422:CYS:HB3	2.01	0.43
1:EC:5:ILE:HG12	1:EC:363:THR:OG1	2.18	0.43
1:FA:167:ASP:OD2	1:FA:167:ASP:N	2.50	0.43
1:AA:22:ASN:OD1	2:AD:1325:LEU:HD23	2.18	0.43
1:AC:46:MET:HE3	1:AC:75:SER:HB2	2.01	0.43
3:AE:21:GLU:HG2	3:AG:15:ASN:OD1	2.18	0.43
1:BA:804:HIS:C	1:BA:806:PHE:H	2.26	0.43
1:BB:120:GLU:CD	1:BB:120:GLU:H	2.26	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BB:544:ASN:OD1	1:BB:544:ASN:N	2.52	0.43
2:BD:519:ARG:NE	2:BD:558:GLU:OE1	2.40	0.43
4:BH:241:ASP:OD2	4:BH:241:ASP:N	2.50	0.43
1:CB:90:TYR:HD1	1:CB:129:LEU:HD12	1.83	0.43
1:CB:104:SER:HB2	1:CB:368:LYS:HZ1	1.84	0.43
2:CD:538:SER:O	2:DD:221:THR:HG21	2.17	0.43
4:CH:641:LYS:HG2	4:CH:688:LYS:HG2	1.99	0.43
4:CH:1188:VAL:HG21	4:CH:1195:GLN:HB2	2.00	0.43
11:CP:425:ARG:NH1	10:FN:44:GLN:HE22	2.16	0.43
1:DA:804:HIS:C	1:DA:806:PHE:H	2.26	0.43
1:DC:24:ASP:O	1:DC:28:VAL:HG13	2.19	0.43
1:DC:145:GLN:HG2	1:DC:182:PRO:HA	2.00	0.43
2:DD:605:LEU:HD12	2:DD:613:VAL:HG12	1.99	0.43
3:DE:21:GLU:HG2	3:DG:15:ASN:OD1	2.18	0.43
10:DN:31:GLU:CG	10:DN:55:LYS:O	2.66	0.43
1:EA:100:LEU:HG	1:EA:150:VAL:HG11	2.00	0.43
1:EA:599:THR:OG1	1:EA:600:SER:N	2.51	0.43
2:ED:747:PHE:CD2	2:ED:766:TYR:CE1	3.05	0.43
6:EL:49:LYS:O	6:EL:49:LYS:HG2	2.18	0.43
11:EO:238:THR:HG22	11:EO:293:LEU:O	2.18	0.43
2:FD:605:LEU:HD12	2:FD:613:VAL:HG12	1.99	0.43
3:FF:33:ASN:HD22	3:FF:36:ASP:HB2	1.81	0.43
1:AB:544:ASN:OD1	1:AB:544:ASN:N	2.52	0.43
1:AC:24:ASP:O	1:AC:28:VAL:HG13	2.19	0.43
1:BC:46:MET:HE3	1:BC:75:SER:HB2	2.01	0.43
2:BD:783:ILE:CD1	2:BD:784:GLN:HG3	2.48	0.43
4:BH:1149:LYS:HD2	2:ED:307:LEU:HD13	2.01	0.43
9:BM:41:GLN:O	9:BM:59:VAL:HB	2.17	0.43
2:CD:358:LYS:HE3	2:CD:363:ILE:HD11	2.00	0.43
4:CH:291:VAL:CG1	4:CH:292:HIS:N	2.81	0.43
2:DD:358:LYS:HE3	2:DD:363:ILE:HD11	2.00	0.43
2:DD:783:ILE:HD12	2:DD:784:GLN:N	2.32	0.43
3:DE:59:HIS:HB3	3:DG:87:LEU:CD1	2.48	0.43
4:DH:80:THR:HB	4:DH:81:PRO:HD3	2.01	0.43
4:DH:654:LEU:HD23	4:DH:654:LEU:HA	1.88	0.43
1:EB:90:TYR:HD1	1:EB:129:LEU:HD12	1.83	0.43
1:EC:362:ASP:OD1	1:EC:364:ARG:HG2	2.19	0.43
11:EP:449:THR:HG23	11:EP:452:ASP:H	1.83	0.43
1:FA:610:PHE:O	1:FA:610:PHE:CD1	2.70	0.43
1:FA:804:HIS:C	1:FA:806:PHE:H	2.26	0.43
1:FB:90:TYR:HD1	1:FB:129:LEU:HD12	1.83	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:FD:41:ASP:CB	7:FI:11:THR:O	2.67	0.43
3:FE:59:HIS:HB3	3:FG:87:LEU:CD1	2.48	0.43
4:FH:1188:VAL:HG21	4:FH:1195:GLN:HB2	2.00	0.43
1:AA:599:THR:OG1	1:AA:600:SER:N	2.51	0.43
1:AC:362:ASP:OD1	1:AC:364:ARG:HG2	2.19	0.43
2:AD:786:VAL:HA	2:AD:789:TYR:HD1	1.82	0.43
1:BB:298:LEU:HD21	1:BB:422:CYS:HB3	2.01	0.43
1:BC:24:ASP:O	1:BC:28:VAL:HG13	2.19	0.43
2:BD:747:PHE:CD2	2:BD:766:TYR:CE1	3.05	0.43
4:BH:80:THR:HB	4:BH:81:PRO:HD3	2.01	0.43
1:CB:592:LYS:O	1:CB:597:ASP:HB2	2.19	0.43
2:CD:730:ALA:HA	2:CD:733:ASN:HD22	1.83	0.43
7:CI:119:LEU:HD12	7:CI:119:LEU:C	2.43	0.43
11:CO:404:ASN:OD1	11:CO:458:MET:HE2	2.19	0.43
2:DD:716:LEU:O	2:DD:720:LEU:N	2.52	0.43
4:DH:641:LYS:HG2	4:DH:688:LYS:HG2	2.00	0.43
1:EB:544:ASN:OD1	1:EB:544:ASN:N	2.52	0.43
3:EE:59:HIS:HB3	3:EG:87:LEU:CD1	2.48	0.43
4:EH:1207:ILE:HD11	2:FD:336:TYR:CE1	2.53	0.43
1:FB:298:LEU:HD21	1:FB:422:CYS:HB3	2.01	0.43
10:AN:44:GLN:HE22	11:BP:425:ARG:NH1	2.16	0.43
11:AP:425:ARG:NH1	10:DN:44:GLN:HE22	2.16	0.43
1:BC:362:ASP:OD1	1:BC:364:ARG:HG2	2.19	0.43
2:BD:358:LYS:HE3	2:BD:363:ILE:HD11	2.00	0.43
2:BD:786:VAL:HA	2:BD:789:TYR:HD1	1.82	0.43
4:BH:1025:GLN:O	4:BH:1033:LEU:HD12	2.18	0.43
7:BI:119:LEU:HD12	7:BI:119:LEU:C	2.43	0.43
11:BO:154:GLU:O	11:BO:190:ARG:NH2	2.52	0.43
1:CC:24:ASP:O	1:CC:28:VAL:HG13	2.19	0.43
4:CH:80:THR:HB	4:CH:81:PRO:HD3	2.01	0.43
1:DB:592:LYS:O	1:DB:597:ASP:HB2	2.19	0.43
1:DC:88:THR:HA	1:DC:129:LEU:HD12	2.00	0.43
1:DC:362:ASP:OD1	1:DC:364:ARG:HG2	2.19	0.43
2:ED:786:VAL:HA	2:ED:789:TYR:HD1	1.82	0.43
3:EF:87:LEU:CD1	3:EG:59:HIS:HB3	2.47	0.43
8:EK:162:GLU:HG2	8:EK:165:ARG:HB3	1.99	0.43
2:FD:786:VAL:HA	2:FD:789:TYR:HD1	1.82	0.43
4:FH:1132:SER:O	4:FH:1132:SER:OG	2.31	0.43
11:FP:449:THR:HG23	11:FP:452:ASP:H	1.83	0.43
1:AB:104:SER:HB2	1:AB:368:LYS:HZ1	1.83	0.43
1:AB:592:LYS:O	1:AB:597:ASP:HB2	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:AH:243:GLN:HG2	4:AH:245:PHE:CD2	2.54	0.43
5:AJ:210:LEU:HD22	5:AJ:301:VAL:HG13	2.00	0.43
6:AL:49:LYS:HG2	6:AL:49:LYS:O	2.18	0.43
9:AM:42:THR:HG1	9:AM:57:LEU:C	2.21	0.43
1:CA:237:THR:HG22	1:CA:243:VAL:O	2.19	0.43
1:CA:610:PHE:O	1:CA:610:PHE:CD1	2.70	0.43
2:CD:621:TYR:CE1	2:CD:1074:SER:HB2	2.54	0.43
4:CH:1025:GLN:O	4:CH:1033:LEU:HD12	2.18	0.43
5:CJ:210:LEU:HD22	5:CJ:301:VAL:HG13	2.00	0.43
1:DB:120:GLU:H	1:DB:120:GLU:CD	2.26	0.43
1:DC:46:MET:HE3	1:DC:75:SER:HB2	2.01	0.43
2:DD:41:ASP:CB	7:DI:11:THR:O	2.67	0.43
4:DH:15:ASP:N	4:DH:15:ASP:OD2	2.51	0.43
4:DH:459:VAL:O	4:DH:469:GLN:NE2	2.43	0.43
8:DK:162:GLU:HG2	8:DK:165:ARG:HB3	2.00	0.43
10:DN:42:LEU:C	10:DN:44:GLN:H	2.24	0.43
4:EH:110:ARG:NH2	4:EH:198:PRO:O	2.46	0.43
1:FC:5:ILE:HG12	1:FC:363:THR:OG1	2.18	0.43
1:FC:88:THR:HA	1:FC:129:LEU:HD12	2.00	0.43
2:FD:730:ALA:HA	2:FD:733:ASN:HD22	1.83	0.43
11:FO:404:ASN:OD1	11:FO:458:MET:HE2	2.19	0.43
1:AC:826:VAL:O	1:AC:885:ASP:HA	2.19	0.43
4:AH:194:SER:C	4:AH:196:ARG:N	2.73	0.43
4:AH:291:VAL:CG1	4:AH:292:HIS:N	2.81	0.43
4:AH:1149:LYS:HD2	2:BD:307:LEU:HD13	2.00	0.43
1:BB:90:TYR:HD1	1:BB:129:LEU:HD12	1.83	0.43
2:BD:469:ASP:OD2	2:BD:518:TYR:OH	2.37	0.43
8:BK:162:GLU:HG2	8:BK:165:ARG:HB3	2.00	0.43
1:CB:120:GLU:CD	1:CB:120:GLU:H	2.26	0.43
2:DD:621:TYR:CE1	2:DD:1074:SER:HB2	2.54	0.43
4:DH:291:VAL:CG1	4:DH:292:HIS:N	2.81	0.43
4:DH:1188:VAL:HG21	4:DH:1195:GLN:HB2	2.00	0.43
1:EA:20:LEU:HD12	1:EA:21:THR:H	1.83	0.43
1:EA:22:ASN:OD1	2:ED:1325:LEU:HD23	2.18	0.43
1:EB:120:GLU:CD	1:EB:120:GLU:H	2.26	0.43
2:ED:404:ALA:O	2:ED:492:GLN:NE2	2.39	0.43
4:EH:243:GLN:HG2	4:EH:245:PHE:CD2	2.54	0.43
4:EH:513:GLU:H	4:EH:513:GLU:CD	2.26	0.43
10:EN:31:GLU:HG3	10:EN:55:LYS:O	2.19	0.43
10:EN:44:GLN:HE22	11:FP:425:ARG:NH1	2.16	0.43
1:FA:100:LEU:HG	1:FA:150:VAL:HG11	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:FD:425:PRO:HA	2:FD:426:PRO:HD3	1.86	0.43
4:FH:748:ALA:HA	4:FH:752:TYR:OH	2.19	0.43
8:FK:162:GLU:HG2	8:FK:165:ARG:HB3	1.99	0.43
10:FN:31:GLU:HG3	10:FN:55:LYS:O	2.19	0.43
1:AA:610:PHE:CD1	1:AA:610:PHE:C	2.97	0.43
1:AB:298:LEU:HD21	1:AB:422:CYS:HB3	2.01	0.43
2:AD:11:LYS:CD	8:DK:230:GLU:OE1	2.67	0.43
4:AH:1207:ILE:HD11	2:BD:336:TYR:CE1	2.53	0.43
1:BA:237:THR:HG22	1:BA:243:VAL:O	2.19	0.43
1:CA:167:ASP:OD2	1:CA:167:ASP:N	2.50	0.43
1:CA:599:THR:OG1	1:CA:600:SER:N	2.51	0.43
2:CD:605:LEU:HD12	2:CD:613:VAL:HG12	1.99	0.43
4:CH:1149:LYS:HD2	2:DD:307:LEU:HD13	2.00	0.43
11:CO:154:GLU:O	11:CO:190:ARG:NH2	2.52	0.43
11:CO:458:MET:HE3	11:CO:458:MET:HB2	1.80	0.43
1:DA:599:THR:OG1	1:DA:600:SER:N	2.51	0.43
2:DD:730:ALA:HA	2:DD:733:ASN:HD22	1.83	0.43
11:DO:154:GLU:O	11:DO:190:ARG:NH2	2.52	0.43
1:EC:24:ASP:O	1:EC:28:VAL:HG13	2.19	0.43
2:ED:770:THR:HA	2:ED:773:VAL:HG12	2.01	0.43
4:EH:672:ASP:OD1	4:EH:672:ASP:N	2.52	0.43
4:EH:1188:VAL:HG21	4:EH:1195:GLN:HB2	2.00	0.43
1:FA:599:THR:OG1	1:FA:600:SER:N	2.51	0.43
1:FB:120:GLU:H	1:FB:120:GLU:CD	2.26	0.43
1:FC:145:GLN:HG2	1:FC:182:PRO:HA	2.00	0.43
1:AA:456:TYR:HD2	1:AA:510:GLU:CD	2.27	0.43
1:AC:58:TYR:CE2	1:AC:135:GLU:HB2	2.54	0.43
1:AC:120:GLU:OE2	1:AC:120:GLU:N	2.40	0.43
2:AD:621:TYR:CE1	2:AD:1074:SER:HB2	2.54	0.43
1:BB:592:LYS:O	1:BB:597:ASP:HB2	2.19	0.43
8:BK:230:GLU:OE1	2:ED:11:LYS:CD	2.67	0.43
1:CB:298:LEU:HD21	1:CB:422:CYS:HB3	2.01	0.43
1:CC:826:VAL:O	1:CC:885:ASP:HA	2.19	0.43
2:CD:41:ASP:CB	7:CI:11:THR:O	2.67	0.43
3:CF:13:PHE:O	3:CG:21:GLU:HG3	2.19	0.43
11:CP:220:SER:O	11:CP:220:SER:OG	2.36	0.43
1:DA:237:THR:HG22	1:DA:243:VAL:O	2.19	0.43
2:DD:770:THR:HA	2:DD:773:VAL:HG12	2.00	0.43
1:EA:804:HIS:C	1:EA:806:PHE:H	2.26	0.43
2:ED:716:LEU:O	2:ED:720:LEU:N	2.52	0.43
4:EH:641:LYS:HG2	4:EH:688:LYS:HG2	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:FB:592:LYS:O	1:FB:597:ASP:HB2	2.19	0.43
1:FC:328:GLN:C	1:FC:330:ALA:H	2.27	0.43
2:FD:469:ASP:OD2	2:FD:518:TYR:OH	2.37	0.43
2:FD:621:TYR:CE1	2:FD:1074:SER:HB2	2.54	0.43
4:FH:80:THR:HB	4:FH:81:PRO:HD3	2.01	0.43
4:FH:243:GLN:HG2	4:FH:245:PHE:CD2	2.54	0.43
4:FH:513:GLU:H	4:FH:513:GLU:CD	2.26	0.43
4:FH:608:ALA:HA	4:FH:771:ARG:NE	2.34	0.43
1:AC:145:GLN:HG2	1:AC:182:PRO:HA	2.00	0.42
2:AD:358:LYS:HE3	2:AD:363:ILE:HD11	2.00	0.42
2:AD:713:GLU:HB2	2:AD:714:PRO:HD3	2.01	0.42
3:AF:13:PHE:O	3:AG:21:GLU:HG3	2.19	0.42
4:AH:107:LEU:CD1	4:AH:207:ARG:HH11	2.32	0.42
1:BA:798:MET:O	1:BA:802:LEU:HD12	2.19	0.42
1:BB:163:LEU:HD21	4:BH:11:PRO:HD3	2.01	0.42
1:BC:120:GLU:OE2	1:BC:120:GLU:N	2.40	0.42
4:BH:1207:ILE:HD11	2:ED:336:TYR:CE1	2.53	0.42
11:BP:449:THR:HG23	11:BP:452:ASP:H	1.83	0.42
1:CA:124:ASN:OD1	1:CA:125:ASN:N	2.52	0.42
1:CA:503:ASP:OD1	1:CA:503:ASP:N	2.45	0.42
2:CD:11:LYS:CD	8:FK:230:GLU:OE1	2.67	0.42
2:CD:300:SER:HB3	4:FH:1152:GLU:OE1	2.19	0.42
11:CQ:220:SER:O	11:CQ:220:SER:OG	2.36	0.42
4:DH:608:ALA:HA	4:DH:771:ARG:NE	2.34	0.42
11:DO:404:ASN:OD1	11:DO:458:MET:HE2	2.19	0.42
1:EA:610:PHE:CD1	1:EA:610:PHE:C	2.97	0.42
1:EB:550:ASP:OD1	1:EB:550:ASP:N	2.49	0.42
1:EC:328:GLN:C	1:EC:330:ALA:H	2.27	0.42
4:EH:80:THR:HB	4:EH:81:PRO:HD3	2.01	0.42
1:FB:163:LEU:HD21	4:FH:11:PRO:HD3	2.01	0.42
1:FB:429:LEU:HD23	1:FB:429:LEU:HA	1.86	0.42
11:FO:154:GLU:O	11:FO:190:ARG:NH2	2.52	0.42
2:AD:307:LEU:HD13	4:DH:1149:LYS:HD2	2.01	0.42
2:AD:730:ALA:HA	2:AD:733:ASN:HD22	1.83	0.42
8:AK:81:LYS:HB2	8:AK:84:GLU:HG3	2.01	0.42
11:AP:45:ASN:HB3	11:AP:48:THR:HB	2.01	0.42
1:BA:599:THR:OG1	1:BA:600:SER:N	2.51	0.42
1:BB:824:THR:OG1	1:BB:890:TYR:O	2.32	0.42
1:BC:84:GLU:O	1:BC:84:GLU:HG3	2.20	0.42
2:BD:632:LEU:HD21	2:BD:655:ALA:HB1	2.02	0.42
2:BD:713:GLU:HB2	2:BD:714:PRO:HD3	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:BF:13:PHE:O	3:BG:21:GLU:HG3	2.19	0.42
4:BH:608:ALA:HA	4:BH:771:ARG:NE	2.34	0.42
10:BN:44:GLN:HE22	11:EP:425:ARG:NH1	2.16	0.42
1:CA:59:GLN:N	1:CA:62:ASP:O	2.42	0.42
1:CC:84:GLU:HG3	1:CC:84:GLU:O	2.20	0.42
6:CL:49:LYS:HG2	6:CL:49:LYS:O	2.18	0.42
1:DB:298:LEU:HD21	1:DB:422:CYS:HB3	2.01	0.42
2:DD:39:TRP:NE1	2:DD:46:ASP:OD2	2.52	0.42
2:ED:621:TYR:CE1	2:ED:1074:SER:HB2	2.54	0.42
1:FC:362:ASP:OD1	1:FC:364:ARG:HG2	2.19	0.42
4:FH:110:ARG:NH2	4:FH:198:PRO:O	2.46	0.42
1:AA:237:THR:HG22	1:AA:243:VAL:O	2.19	0.42
1:AA:804:HIS:C	1:AA:806:PHE:H	2.26	0.42
10:AN:75:TRP:CE2	10:AN:111:PRO:HD3	2.55	0.42
11:AP:449:THR:HG23	11:AP:452:ASP:H	1.83	0.42
4:BH:513:GLU:OE2	4:BH:513:GLU:N	2.44	0.42
1:CC:58:TYR:CE2	1:CC:135:GLU:HB2	2.54	0.42
4:CH:748:ALA:HA	4:CH:752:TYR:OH	2.19	0.42
4:DH:107:LEU:CD1	4:DH:207:ARG:HH11	2.32	0.42
11:DP:45:ASN:HB3	11:DP:48:THR:HB	2.01	0.42
1:EA:237:THR:HG22	1:EA:243:VAL:O	2.19	0.42
1:EC:46:MET:HE3	1:EC:75:SER:HB2	2.01	0.42
4:EH:1149:LYS:HD2	2:FD:307:LEU:HD13	2.00	0.42
1:FA:237:THR:HG22	1:FA:243:VAL:O	2.19	0.42
1:FA:610:PHE:CD1	1:FA:610:PHE:C	2.97	0.42
2:FD:770:THR:HA	2:FD:773:VAL:HG12	2.01	0.42
8:FK:180:GLN:O	8:FK:181:ARG:NH1	2.44	0.42
1:AA:22:ASN:OD1	2:AD:1325:LEU:CD2	2.68	0.42
1:AA:124:ASN:OD1	1:AA:125:ASN:N	2.52	0.42
1:AB:163:LEU:HD21	4:AH:11:PRO:HD3	2.01	0.42
1:AC:84:GLU:HG3	1:AC:84:GLU:O	2.20	0.42
2:AD:41:ASP:CB	7:AI:11:THR:O	2.67	0.42
2:AD:220:GLU:HG3	2:AD:311:GLY:O	2.17	0.42
2:AD:300:SER:HB3	4:DH:1152:GLU:OE1	2.19	0.42
4:AH:1025:GLN:O	4:AH:1033:LEU:HD12	2.18	0.42
11:AO:154:GLU:O	11:AO:190:ARG:NH2	2.52	0.42
1:BA:22:ASN:OD1	2:BD:1325:LEU:CD2	2.68	0.42
4:BH:513:GLU:H	4:BH:513:GLU:CD	2.26	0.42
10:BN:31:GLU:HG3	10:BN:55:LYS:O	2.19	0.42
2:CD:773:VAL:O	2:CD:777:VAL:HG23	2.19	0.42
4:CH:1152:GLU:OE1	2:DD:300:SER:HB3	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:CK:230:GLU:OE1	2:DD:11:LYS:CD	2.67	0.42
1:DA:124:ASN:OD1	1:DA:125:ASN:N	2.52	0.42
1:DA:167:ASP:OD2	1:DA:167:ASP:N	2.50	0.42
1:DA:800:LEU:HG	1:DA:801:GLN:NE2	2.34	0.42
1:DB:90:TYR:HD1	1:DB:129:LEU:HD12	1.83	0.42
2:DD:632:LEU:HD21	2:DD:655:ALA:HB1	2.01	0.42
11:DO:195:ASP:OD1	11:DO:296:PRO:HB2	2.20	0.42
1:EA:798:MET:O	1:EA:802:LEU:HD12	2.19	0.42
2:ED:358:LYS:HE3	2:ED:363:ILE:HD11	2.00	0.42
2:ED:632:LEU:HD21	2:ED:655:ALA:HB1	2.02	0.42
4:EH:1143:TYR:CZ	2:FD:218:GLN:OE1	2.73	0.42
11:EO:404:ASN:OD1	11:EO:458:MET:HE2	2.19	0.42
2:FD:773:VAL:O	2:FD:777:VAL:HG23	2.19	0.42
11:FO:458:MET:HE3	11:FO:458:MET:HB2	1.80	0.42
11:FP:45:ASN:HB3	11:FP:48:THR:HB	2.01	0.42
2:AD:425:PRO:HA	2:AD:426:PRO:HD3	1.86	0.42
10:AN:31:GLU:HG3	10:AN:55:LYS:O	2.19	0.42
1:BA:15:THR:OG1	1:BA:16:PRO:HD2	2.19	0.42
2:BD:41:ASP:CB	7:BI:11:THR:O	2.67	0.42
3:BG:57:TYR:O	3:BG:58:ASN:C	2.63	0.42
8:BK:81:LYS:HB2	8:BK:84:GLU:HG3	2.01	0.42
1:CC:362:ASP:OD1	1:CC:364:ARG:HG2	2.19	0.42
2:CD:39:TRP:NE1	2:CD:46:ASP:OD2	2.52	0.42
2:CD:248:THR:HG23	2:CD:390:GLU:HB3	2.01	0.42
2:CD:632:LEU:HD21	2:CD:655:ALA:HB1	2.02	0.42
4:CH:608:ALA:HA	4:CH:771:ARG:NE	2.34	0.42
10:CN:31:GLU:HG3	10:CN:55:LYS:O	2.19	0.42
11:CQ:45:ASN:HB3	11:CQ:48:THR:HB	2.02	0.42
1:DA:456:TYR:HD2	1:DA:510:GLU:CD	2.27	0.42
1:DC:328:GLN:C	1:DC:330:ALA:H	2.27	0.42
3:DF:13:PHE:O	3:DG:21:GLU:HG3	2.19	0.42
4:DH:110:ARG:NH2	4:DH:198:PRO:O	2.46	0.42
8:DK:81:LYS:HB2	8:DK:84:GLU:HG3	2.01	0.42
1:EA:124:ASN:OD1	1:EA:125:ASN:N	2.52	0.42
3:EF:13:PHE:O	3:EG:21:GLU:HG3	2.19	0.42
8:EK:230:GLU:OE1	2:FD:11:LYS:CD	2.67	0.42
11:EO:154:GLU:O	11:EO:190:ARG:NH2	2.52	0.42
3:FG:57:TYR:O	3:FG:58:ASN:C	2.63	0.42
4:FH:641:LYS:HG2	4:FH:688:LYS:HG2	2.00	0.42
1:AA:15:THR:OG1	1:AA:16:PRO:HD2	2.19	0.42
1:AA:798:MET:O	1:AA:802:LEU:HD12	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AC:88:THR:HA	1:AC:129:LEU:HD12	2.00	0.42
4:AH:748:ALA:HA	4:AH:752:TYR:OH	2.19	0.42
8:AK:119:ASP:HB3	8:BK:147:LYS:HG3	2.02	0.42
11:AO:338:GLN:HE22	11:AO:364:TRP:HD1	1.68	0.42
1:BA:121:GLN:HE21	1:BA:126:ARG:CZ	2.33	0.42
1:BA:456:TYR:HD2	1:BA:510:GLU:CD	2.27	0.42
1:BA:505:SER:O	1:BA:505:SER:OG	2.37	0.42
1:BC:83:ALA:C	1:BC:84:GLU:HG2	2.45	0.42
2:BD:390:GLU:HG3	11:BO:90:ARG:HH12	1.85	0.42
2:BD:716:LEU:O	2:BD:720:LEU:HB2	2.20	0.42
3:BF:57:TYR:O	3:BF:58:ASN:C	2.63	0.42
4:BH:243:GLN:HG2	4:BH:245:PHE:CD2	2.54	0.42
4:BH:459:VAL:O	4:BH:469:GLN:NE2	2.43	0.42
4:BH:1229:LEU:HD12	4:BH:1229:LEU:HA	1.81	0.42
11:BO:195:ASP:OD1	11:BO:296:PRO:HB2	2.20	0.42
1:CA:22:ASN:OD1	2:CD:1325:LEU:CD2	2.68	0.42
1:CA:800:LEU:HG	1:CA:801:GLN:NE2	2.34	0.42
1:CC:34:GLU:OE2	1:CC:37:ARG:NH2	2.52	0.42
2:CD:307:LEU:CD1	4:FH:1149:LYS:HB2	2.50	0.42
2:CD:770:THR:HA	2:CD:773:VAL:HG12	2.01	0.42
3:CE:19:LEU:HD23	3:CE:19:LEU:HA	1.83	0.42
1:DA:798:MET:O	1:DA:802:LEU:HD12	2.19	0.42
4:DH:243:GLN:HG2	4:DH:245:PHE:CD2	2.54	0.42
4:DH:748:ALA:HA	4:DH:752:TYR:OH	2.19	0.42
4:DH:1229:LEU:HD12	4:DH:1229:LEU:HA	1.81	0.42
1:EA:167:ASP:OD2	1:EA:167:ASP:N	2.50	0.42
2:ED:41:ASP:CB	7:EI:11:THR:O	2.67	0.42
2:ED:257:LYS:NZ	2:ED:284:ASP:OD1	2.53	0.42
2:ED:713:GLU:HB2	2:ED:714:PRO:HD3	2.01	0.42
4:EH:167:LEU:HD12	4:EH:167:LEU:HA	1.73	0.42
10:EN:75:TRP:CE2	10:EN:111:PRO:HD3	2.55	0.42
11:EO:102:ILE:HG13	11:EO:291:LEU:HD13	2.02	0.42
11:EP:45:ASN:HB3	11:EP:48:THR:HB	2.01	0.42
2:FD:248:THR:HG23	2:FD:390:GLU:HB3	2.01	0.42
2:FD:358:LYS:HE3	2:FD:363:ILE:HD11	2.00	0.42
11:FO:102:ILE:HG13	11:FO:291:LEU:HD13	2.02	0.42
1:AA:121:GLN:HE21	1:AA:126:ARG:CZ	2.33	0.42
2:AD:716:LEU:O	2:AD:720:LEU:N	2.52	0.42
3:AF:57:TYR:O	3:AF:58:ASN:C	2.63	0.42
8:AK:230:GLU:OE1	2:BD:11:LYS:CD	2.67	0.42
2:BD:257:LYS:NZ	2:BD:284:ASP:OD1	2.53	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:DD:300:SER:HA	2:DD:303:TYR:HB2	2.02	0.42
2:DD:469:ASP:OD2	2:DD:518:TYR:OH	2.37	0.42
4:DH:1132:SER:O	4:DH:1132:SER:OG	2.31	0.42
1:EC:58:TYR:CE2	1:EC:135:GLU:HB2	2.54	0.42
1:EC:84:GLU:HG3	1:EC:84:GLU:O	2.20	0.42
2:ED:716:LEU:O	2:ED:720:LEU:HB2	2.20	0.42
4:EH:608:ALA:HA	4:EH:771:ARG:NE	2.34	0.42
4:EH:716:ALA:HA	4:EH:759:PRO:HG2	2.02	0.42
4:EH:748:ALA:HA	4:EH:752:TYR:OH	2.19	0.42
1:FC:826:VAL:O	1:FC:885:ASP:HA	2.19	0.42
4:FH:15:ASP:OD2	4:FH:15:ASP:N	2.51	0.42
4:FH:724:VAL:HG11	4:FH:729:LYS:HD2	2.02	0.42
2:AD:300:SER:HA	2:AD:303:TYR:HB2	2.02	0.42
11:AO:102:ILE:HG13	11:AO:291:LEU:HD13	2.02	0.42
11:AO:404:ASN:OD1	11:AO:458:MET:HE2	2.19	0.42
11:BO:338:GLN:HE22	11:BO:364:TRP:HD1	1.68	0.42
3:CE:57:TYR:O	3:CE:58:ASN:C	2.63	0.42
3:CG:57:TYR:O	3:CG:58:ASN:C	2.63	0.42
4:CH:724:VAL:HG11	4:CH:729:LYS:HD2	2.02	0.42
11:CP:449:THR:HG23	11:CP:452:ASP:H	1.83	0.42
1:DC:58:TYR:CE2	1:DC:135:GLU:HB2	2.54	0.42
1:DC:84:GLU:HG3	1:DC:84:GLU:O	2.20	0.42
2:DD:248:THR:HG23	2:DD:390:GLU:HB3	2.01	0.42
2:DD:773:VAL:O	2:DD:777:VAL:HG23	2.19	0.42
11:DO:148:LEU:O	11:DO:151:VAL:HG12	2.20	0.42
3:EG:57:TYR:O	3:EG:58:ASN:C	2.63	0.42
4:EH:107:LEU:CD1	4:EH:207:ARG:HH11	2.32	0.42
8:EK:81:LYS:HB2	8:EK:84:GLU:HG3	2.01	0.42
1:FA:800:LEU:HG	1:FA:801:GLN:NE2	2.34	0.42
1:FB:544:ASN:OD1	1:FB:544:ASN:N	2.52	0.42
1:FC:58:TYR:CE2	1:FC:135:GLU:HB2	2.54	0.42
10:FN:75:TRP:CE2	10:FN:111:PRO:HD3	2.55	0.42
1:BC:328:GLN:C	1:BC:330:ALA:H	2.27	0.42
4:BH:163:GLN:HG2	4:BH:191:PRO:HG3	2.02	0.42
4:BH:1143:TYR:CZ	2:ED:218:GLN:OE1	2.73	0.42
11:BO:404:ASN:OD1	11:BO:458:MET:HE2	2.19	0.42
1:CA:610:PHE:CD1	1:CA:610:PHE:C	2.97	0.42
1:CC:46:MET:HE3	1:CC:75:SER:HB2	2.01	0.42
2:CD:218:GLN:OE1	4:FH:1143:TYR:CZ	2.73	0.42
4:CH:163:GLN:HG2	4:CH:191:PRO:HG3	2.02	0.42
4:CH:1149:LYS:HB2	2:DD:307:LEU:CD1	2.50	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:CJ:8:ARG:HH12	8:CK:164:ASN:ND2	2.18	0.42
1:DA:22:ASN:OD1	2:DD:1325:LEU:CD2	2.68	0.42
1:DC:220:GLN:OE1	1:DC:282:SER:HB2	2.20	0.42
4:DH:716:ALA:HA	4:DH:759:PRO:HG2	2.02	0.42
11:DO:102:ILE:HG13	11:DO:291:LEU:HD13	2.02	0.42
1:EA:22:ASN:OD1	2:ED:1325:LEU:CD2	2.68	0.42
1:EC:83:ALA:C	1:EC:84:GLU:HG2	2.45	0.42
2:ED:39:TRP:NE1	2:ED:46:ASP:OD2	2.52	0.42
4:EH:163:GLN:HG2	4:EH:191:PRO:HG3	2.02	0.42
1:FA:22:ASN:OD1	2:FD:1325:LEU:CD2	2.68	0.42
1:FA:456:TYR:HD2	1:FA:510:GLU:CD	2.27	0.42
1:FC:24:ASP:O	1:FC:28:VAL:HG13	2.19	0.42
1:FC:46:MET:HE3	1:FC:75:SER:HB2	2.01	0.42
4:FH:107:LEU:CD1	4:FH:207:ARG:HH11	2.32	0.42
1:AA:800:LEU:HG	1:AA:801:GLN:NE2	2.34	0.42
1:AB:163:LEU:HD12	1:AB:163:LEU:HA	1.92	0.42
1:AB:428:TYR:CE2	1:AB:459:ASN:HA	2.55	0.42
2:AD:39:TRP:NE1	2:AD:46:ASP:OD2	2.52	0.42
2:AD:158:THR:HG23	2:AD:202:ASP:OD2	2.20	0.42
4:AH:15:ASP:N	4:AH:15:ASP:OD2	2.51	0.42
4:AH:243:GLN:CG	4:AH:245:PHE:CD2	3.03	0.42
11:AP:220:SER:O	11:AP:220:SER:OG	2.36	0.42
1:BA:124:ASN:OD1	1:BA:125:ASN:N	2.52	0.42
1:BA:610:PHE:CD1	1:BA:610:PHE:C	2.97	0.42
2:BD:248:THR:HG23	2:BD:390:GLU:HB3	2.01	0.42
2:BD:621:TYR:CE1	2:BD:1074:SER:HB2	2.54	0.42
4:BH:748:ALA:HA	4:BH:752:TYR:OH	2.19	0.42
8:BK:119:ASP:HB3	8:EK:147:LYS:HG3	2.02	0.42
10:BN:75:TRP:CE2	10:BN:111:PRO:HD3	2.55	0.42
11:BO:148:LEU:O	11:BO:151:VAL:HG12	2.20	0.42
1:CA:189:LEU:HD23	1:CA:189:LEU:HA	1.90	0.42
1:CB:163:LEU:HD21	4:CH:11:PRO:HD3	2.01	0.42
1:CC:83:ALA:C	1:CC:84:GLU:HG2	2.45	0.42
1:CC:220:GLN:OE1	1:CC:282:SER:HB2	2.20	0.42
2:CD:307:LEU:HD13	4:FH:1149:LYS:HD2	2.00	0.42
2:CD:390:GLU:HG3	11:CO:90:ARG:HH12	1.85	0.42
2:CD:686:GLU:OE2	2:CD:694:SER:HB2	2.20	0.42
4:CH:746:PHE:CD2	4:CH:746:PHE:N	2.88	0.42
5:CJ:434:ILE:HG22	5:CJ:449:GLY:O	2.20	0.42
2:DD:713:GLU:HB2	2:DD:714:PRO:HD3	2.01	0.42
4:DH:243:GLN:CG	4:DH:245:PHE:CD2	3.03	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:EA:196:GLN:O	1:EA:200:SER:OG	2.27	0.42
1:EC:826:VAL:O	1:EC:885:ASP:HA	2.19	0.42
2:ED:390:GLU:HG3	11:EO:90:ARG:HH12	1.85	0.42
2:ED:643:LEU:HD23	2:ED:643:LEU:HA	1.90	0.42
2:ED:773:VAL:O	2:ED:777:VAL:HG23	2.19	0.42
4:EH:1152:GLU:OE1	2:FD:300:SER:HB3	2.19	0.42
11:EO:338:GLN:HE22	11:EO:364:TRP:HD1	1.68	0.42
1:FA:798:MET:O	1:FA:802:LEU:HD12	2.19	0.42
1:FC:84:GLU:HG3	1:FC:84:GLU:O	2.20	0.42
2:FD:257:LYS:NZ	2:FD:284:ASP:OD1	2.53	0.42
1:AA:425:ASP:OD1	1:AA:425:ASP:N	2.46	0.41
1:AC:328:GLN:C	1:AC:330:ALA:H	2.27	0.41
2:AD:716:LEU:O	2:AD:720:LEU:HB2	2.20	0.41
2:AD:770:THR:HA	2:AD:773:VAL:HG12	2.01	0.41
5:AJ:278:GLU:OE1	5:AJ:278:GLU:HA	2.20	0.41
1:BC:826:VAL:O	1:BC:885:ASP:HA	2.19	0.41
4:BH:732:ALA:CB	4:BH:752:TYR:HD1	2.33	0.41
4:BH:982:GLU:H	4:BH:982:GLU:CD	2.28	0.41
2:CD:257:LYS:NZ	2:CD:284:ASP:OD1	2.53	0.41
4:CH:718:THR:O	4:CH:718:THR:HG23	2.20	0.41
4:CH:1143:TYR:CZ	2:DD:218:GLN:OE1	2.73	0.41
11:CO:195:ASP:OD1	11:CO:296:PRO:HB2	2.20	0.41
4:DH:718:THR:HG23	4:DH:718:THR:O	2.20	0.41
4:DH:892:ASP:OD2	4:DH:892:ASP:N	2.53	0.41
10:DN:31:GLU:HG3	10:DN:55:LYS:O	2.19	0.41
11:DO:338:GLN:HE22	11:DO:364:TRP:HD1	1.68	0.41
11:DP:449:THR:HG23	11:DP:452:ASP:H	1.83	0.41
1:EA:121:GLN:HE21	1:EA:126:ARG:CZ	2.33	0.41
1:EB:592:LYS:O	1:EB:597:ASP:HB2	2.19	0.41
4:EH:746:PHE:CD2	4:EH:746:PHE:N	2.88	0.41
4:EH:1149:LYS:HB2	2:FD:307:LEU:CD1	2.50	0.41
5:EJ:416:ASP:OD1	5:EJ:421:ARG:NH1	2.53	0.41
11:EO:195:ASP:OD1	11:EO:296:PRO:HB2	2.20	0.41
1:FA:208:TRP:CE3	1:FA:216:ILE:HG13	2.55	0.41
2:FD:716:LEU:O	2:FD:720:LEU:HB2	2.20	0.41
3:FF:13:PHE:O	3:FG:21:GLU:HG3	2.19	0.41
4:FH:163:GLN:HG2	4:FH:191:PRO:HG3	2.02	0.41
4:FH:982:GLU:CD	4:FH:982:GLU:H	2.28	0.41
2:AD:773:VAL:O	2:AD:777:VAL:HG23	2.19	0.41
4:AH:718:THR:HG23	4:AH:718:THR:O	2.20	0.41
4:AH:732:ALA:CB	4:AH:752:TYR:HD1	2.34	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:AQ:8:PRO:HG3	11:DQ:471:GLU:OE1	2.20	0.41
11:AQ:45:ASN:HB3	11:AQ:48:THR:HB	2.02	0.41
2:BD:94:VAL:HG23	2:BD:95:LEU:HG	2.02	0.41
4:BH:107:LEU:HD11	4:BH:207:ARG:HD3	2.03	0.41
4:BH:194:SER:C	4:BH:196:ARG:N	2.73	0.41
4:BH:716:ALA:HA	4:BH:759:PRO:HG2	2.02	0.41
1:CA:15:THR:OG1	1:CA:16:PRO:HD2	2.19	0.41
1:CB:428:TYR:CE2	1:CB:459:ASN:HA	2.55	0.41
1:CC:328:GLN:C	1:CC:330:ALA:H	2.27	0.41
4:CH:243:GLN:HG2	4:CH:245:PHE:CD2	2.54	0.41
8:CK:81:LYS:HB2	8:CK:84:GLU:HG3	2.01	0.41
11:CO:148:LEU:O	11:CO:151:VAL:HG12	2.20	0.41
11:CQ:8:PRO:HG3	11:FQ:471:GLU:OE1	2.20	0.41
1:DA:487:ASN:OD1	1:DA:860:SER:OG	2.39	0.41
1:DA:802:LEU:HA	1:DA:802:LEU:HD23	1.86	0.41
1:DC:826:VAL:O	1:DC:885:ASP:HA	2.19	0.41
2:DD:94:VAL:HG23	2:DD:95:LEU:HG	2.02	0.41
2:DD:158:THR:HG23	2:DD:202:ASP:OD2	2.20	0.41
3:DE:57:TYR:O	3:DE:58:ASN:C	2.63	0.41
1:EA:800:LEU:HG	1:EA:801:GLN:NE2	2.34	0.41
5:EJ:8:ARG:HH12	8:EK:164:ASN:ND2	2.18	0.41
11:EP:446:GLU:HG2	11:FQ:22:ILE:HD13	2.02	0.41
4:FH:243:GLN:CG	4:FH:245:PHE:CD2	3.03	0.41
4:FH:716:ALA:HA	4:FH:759:PRO:HG2	2.02	0.41
8:FK:81:LYS:HB2	8:FK:84:GLU:HG3	2.01	0.41
11:FO:195:ASP:OD1	11:FO:296:PRO:HB2	2.20	0.41
11:FQ:45:ASN:HB3	11:FQ:48:THR:HB	2.02	0.41
1:AA:487:ASN:OD1	1:AA:860:SER:OG	2.39	0.41
2:AD:307:LEU:CD1	4:DH:1149:LYS:HB2	2.50	0.41
4:AH:370:ASN:OD1	4:AH:370:ASN:N	2.48	0.41
4:AH:1143:TYR:CZ	2:BD:218:GLN:OE1	2.73	0.41
4:AH:1149:LYS:HB2	2:BD:307:LEU:CD1	2.50	0.41
4:AH:1152:GLU:OE1	2:BD:300:SER:HB3	2.19	0.41
5:AJ:416:ASP:OD1	5:AJ:421:ARG:NH1	2.53	0.41
7:AI:145:GLU:OE1	8:AK:177:VAL:HA	2.21	0.41
11:AQ:220:SER:O	11:AQ:220:SER:OG	2.36	0.41
1:BC:58:TYR:CE2	1:BC:135:GLU:HB2	2.54	0.41
3:BE:57:TYR:O	3:BE:58:ASN:C	2.63	0.41
4:BH:1152:GLU:OE1	2:ED:300:SER:HB3	2.19	0.41
1:CA:27:ARG:HH22	1:CB:158:ARG:HH22	1.69	0.41
1:CA:456:TYR:HD2	1:CA:510:GLU:CD	2.27	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:505:SER:O	1:CA:505:SER:OG	2.37	0.41
4:CH:513:GLU:H	4:CH:513:GLU:CD	2.26	0.41
5:CJ:278:GLU:OE1	5:CJ:278:GLU:HA	2.20	0.41
5:CJ:416:ASP:OD1	5:CJ:421:ARG:NH1	2.53	0.41
11:CQ:471:GLU:OE1	11:DQ:8:PRO:HG3	2.20	0.41
1:DA:505:SER:O	1:DA:505:SER:OG	2.37	0.41
1:DC:83:ALA:C	1:DC:84:GLU:HG2	2.45	0.41
2:DD:686:GLU:OE2	2:DD:694:SER:HB2	2.20	0.41
4:DH:143:LEU:HG	4:DH:231:TYR:CD1	2.56	0.41
8:DK:46:GLN:HE22	5:EJ:104:GLY:CA	2.33	0.41
11:DO:120:ASN:ND2	11:DO:300:LEU:HD22	2.36	0.41
11:DQ:45:ASN:HB3	11:DQ:48:THR:HB	2.02	0.41
1:EA:456:TYR:HD2	1:EA:510:GLU:CD	2.27	0.41
4:EH:107:LEU:HD11	4:EH:207:ARG:HD3	2.03	0.41
4:EH:982:GLU:CD	4:EH:982:GLU:H	2.28	0.41
1:FA:124:ASN:OD1	1:FA:125:ASN:N	2.52	0.41
1:AC:83:ALA:C	1:AC:84:GLU:HG2	2.45	0.41
1:AC:220:GLN:OE1	1:AC:282:SER:HB2	2.20	0.41
2:AD:257:LYS:NZ	2:AD:284:ASP:OD1	2.53	0.41
3:AG:57:TYR:O	3:AG:58:ASN:C	2.63	0.41
4:AH:143:LEU:HG	4:AH:231:TYR:CD1	2.56	0.41
4:AH:608:ALA:HA	4:AH:771:ARG:NE	2.34	0.41
2:BD:158:THR:HG23	2:BD:202:ASP:OD2	2.20	0.41
2:BD:770:THR:HA	2:BD:773:VAL:HG12	2.01	0.41
2:BD:773:VAL:O	2:BD:777:VAL:HG23	2.19	0.41
4:BH:143:LEU:HG	4:BH:231:TYR:CD1	2.56	0.41
4:BH:1149:LYS:HB2	2:ED:307:LEU:CD1	2.50	0.41
1:CA:121:GLN:HE21	1:CA:126:ARG:CZ	2.33	0.41
1:CA:487:ASN:OD1	1:CA:860:SER:OG	2.39	0.41
2:CD:643:LEU:HD23	2:CD:643:LEU:HA	1.90	0.41
4:CH:143:LEU:HG	4:CH:231:TYR:CD1	2.55	0.41
4:CH:982:GLU:CD	4:CH:982:GLU:H	2.28	0.41
4:CH:1132:SER:O	4:CH:1132:SER:OG	2.31	0.41
11:CO:102:ILE:HG13	11:CO:291:LEU:HD13	2.02	0.41
1:DA:610:PHE:CD1	1:DA:610:PHE:C	2.97	0.41
2:DD:257:LYS:NZ	2:DD:284:ASP:OD1	2.53	0.41
3:DG:57:TYR:O	3:DG:58:ASN:C	2.63	0.41
4:DH:370:ASN:OD1	4:DH:370:ASN:N	2.48	0.41
10:DN:75:TRP:CE2	10:DN:111:PRO:HD3	2.55	0.41
1:EC:220:GLN:OE1	1:EC:282:SER:HB2	2.20	0.41
2:ED:158:THR:HG23	2:ED:202:ASP:OD2	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:ED:188:GLN:HG2	2:ED:586:TYR:CE2	2.56	0.41
2:ED:359:SER:O	2:ED:361:LEU:HD12	2.21	0.41
3:EF:57:TYR:O	3:EF:58:ASN:C	2.63	0.41
1:FA:15:THR:OG1	1:FA:16:PRO:HD2	2.19	0.41
1:FA:121:GLN:HE21	1:FA:126:ARG:CZ	2.33	0.41
2:FD:686:GLU:OE2	2:FD:694:SER:HB2	2.20	0.41
3:FE:57:TYR:O	3:FE:58:ASN:C	2.63	0.41
11:FO:120:ASN:ND2	11:FO:300:LEU:HD22	2.36	0.41
2:AD:218:GLN:OE1	4:DH:1143:TYR:CZ	2.73	0.41
3:AG:33:ASN:ND2	3:AG:36:ASP:HB2	2.36	0.41
5:AJ:12:TYR:CZ	8:AK:107:THR:HG22	2.56	0.41
5:AJ:104:GLY:CA	8:FK:46:GLN:HE22	2.33	0.41
8:AK:147:LYS:HG3	8:DK:119:ASP:HB3	2.02	0.41
1:BC:240:THR:O	1:BC:240:THR:OG1	2.35	0.41
11:BQ:45:ASN:HB3	11:BQ:48:THR:HB	2.02	0.41
1:CA:456:TYR:CD2	1:CA:510:GLU:CD	2.99	0.41
1:CA:609:LEU:HD23	1:CA:609:LEU:HA	1.95	0.41
2:CD:469:ASP:OD2	2:CD:518:TYR:OH	2.37	0.41
11:CP:45:ASN:HB3	11:CP:48:THR:HB	2.01	0.41
1:DA:15:THR:OG1	1:DA:16:PRO:HD2	2.19	0.41
1:DA:121:GLN:HE21	1:DA:126:ARG:CZ	2.33	0.41
1:DA:456:TYR:CD2	1:DA:510:GLU:CD	2.99	0.41
4:DH:163:GLN:HG2	4:DH:191:PRO:HG3	2.02	0.41
4:DH:630:PRO:HB2	4:DH:700:PHE:CE2	2.56	0.41
4:DH:724:VAL:HG11	4:DH:729:LYS:HD2	2.02	0.41
4:DH:746:PHE:CD2	4:DH:746:PHE:N	2.88	0.41
11:DP:194:MET:CE	11:DP:369:LEU:HD11	2.51	0.41
1:EA:208:TRP:CE3	1:EA:216:ILE:HG13	2.55	0.41
2:ED:686:GLU:OE2	2:ED:694:SER:HB2	2.20	0.41
3:EE:57:TYR:O	3:EE:58:ASN:C	2.63	0.41
3:EE:92:GLU:O	3:EE:95:VAL:HG12	2.21	0.41
4:EH:955:LYS:HA	4:EH:955:LYS:HD3	1.92	0.41
11:EO:148:LEU:O	11:EO:151:VAL:HG12	2.20	0.41
1:FA:456:TYR:CD2	1:FA:510:GLU:CD	2.99	0.41
1:FC:220:GLN:OE1	1:FC:282:SER:HB2	2.20	0.41
2:FD:390:GLU:HG3	11:FO:90:ARG:HH12	1.85	0.41
2:FD:716:LEU:O	2:FD:720:LEU:N	2.52	0.41
4:FH:459:VAL:O	4:FH:469:GLN:NE2	2.43	0.41
11:FO:148:LEU:O	11:FO:151:VAL:HG12	2.20	0.41
1:AB:73:ILE:HG22	1:AB:74:THR:O	2.21	0.41
2:AD:359:SER:O	2:AD:361:LEU:HD12	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:AD:686:GLU:OE2	2:AD:694:SER:HB2	2.20	0.41
4:AH:107:LEU:HD11	4:AH:207:ARG:HD3	2.03	0.41
4:AH:163:GLN:HG2	4:AH:191:PRO:HG3	2.02	0.41
5:AJ:434:ILE:HG22	5:AJ:449:GLY:O	2.20	0.41
11:AO:148:LEU:O	11:AO:151:VAL:HG12	2.20	0.41
11:AO:195:ASP:OD1	11:AO:296:PRO:HB2	2.20	0.41
1:BC:220:GLN:OE1	1:BC:282:SER:HB2	2.20	0.41
2:BD:643:LEU:HD23	2:BD:643:LEU:HA	1.90	0.41
3:BE:92:GLU:O	3:BE:95:VAL:HG12	2.21	0.41
4:BH:284:ARG:HA	4:BH:285:PRO:HD3	1.87	0.41
4:BH:746:PHE:CD2	4:BH:746:PHE:N	2.88	0.41
7:BI:145:GLU:OE1	8:BK:177:VAL:HA	2.21	0.41
8:BK:180:GLN:O	8:BK:181:ARG:NH1	2.44	0.41
11:BQ:217:ARG:NH1	11:BQ:348:LYS:O	2.54	0.41
1:CA:802:LEU:HA	1:CA:802:LEU:HD23	1.86	0.41
1:CB:73:ILE:HG22	1:CB:74:THR:O	2.21	0.41
2:CD:188:GLN:HG2	2:CD:586:TYR:CE2	2.56	0.41
4:CH:15:ASP:OD2	4:CH:15:ASP:N	2.52	0.41
5:CJ:309:ALA:HB1	5:CJ:333:ILE:HD13	2.03	0.41
8:CK:147:LYS:HG3	8:FK:119:ASP:HB3	2.02	0.41
11:CP:217:ARG:NH1	11:CP:348:LYS:O	2.54	0.41
1:DB:73:ILE:HG22	1:DB:74:THR:O	2.21	0.41
2:DD:390:GLU:HG3	11:DO:90:ARG:HH12	1.85	0.41
3:DF:33:ASN:ND2	3:DF:36:ASP:HB2	2.36	0.41
3:DF:57:TYR:O	3:DF:58:ASN:C	2.63	0.41
4:DH:591:GLN:HE21	4:DH:677:SER:HB3	1.86	0.41
7:DI:145:GLU:OE1	8:DK:177:VAL:HA	2.21	0.41
1:EA:456:TYR:CD2	1:EA:510:GLU:CD	2.99	0.41
1:EB:429:LEU:HD23	1:EB:429:LEU:HA	1.86	0.41
3:EG:33:ASN:ND2	3:EG:36:ASP:HB2	2.36	0.41
4:EH:143:LEU:HG	4:EH:231:TYR:CD1	2.56	0.41
4:EH:724:VAL:HG11	4:EH:729:LYS:HD2	2.02	0.41
5:EJ:309:ALA:HB1	5:EJ:333:ILE:HD13	2.03	0.41
5:EJ:434:ILE:HG22	5:EJ:449:GLY:O	2.20	0.41
11:EO:120:ASN:ND2	11:EO:300:LEU:HD22	2.36	0.41
11:EP:220:SER:O	11:EP:220:SER:OG	2.36	0.41
1:FA:27:ARG:HH22	1:FB:158:ARG:HH22	1.69	0.41
1:FB:428:TYR:CE2	1:FB:459:ASN:HA	2.55	0.41
2:FD:66:ASN:OD1	2:FD:457:LEU:HD21	2.21	0.41
11:FQ:194:MET:CE	11:FQ:369:LEU:HD11	2.51	0.41
3:AF:92:GLU:O	3:AF:95:VAL:HG12	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:AN:28:LEU:HD13	10:AN:104:TRP:CE2	2.56	0.41
1:BA:487:ASN:OD1	1:BA:860:SER:OG	2.39	0.41
1:BA:800:LEU:HG	1:BA:801:GLN:NE2	2.34	0.41
4:BH:243:GLN:CG	4:BH:245:PHE:CD2	3.03	0.41
4:BH:718:THR:O	4:BH:718:THR:HG23	2.20	0.41
11:BP:217:ARG:NH1	11:BP:348:LYS:O	2.54	0.41
11:BP:446:GLU:HG2	11:EQ:22:ILE:HD13	2.02	0.41
1:CA:208:TRP:CE3	1:CA:216:ILE:HG13	2.55	0.41
1:CA:798:MET:O	1:CA:802:LEU:HD12	2.19	0.41
2:CD:304:GLN:O	2:CD:308:GLN:HG2	2.21	0.41
2:CD:786:VAL:HA	2:CD:789:TYR:CD1	2.56	0.41
3:CF:33:ASN:ND2	3:CF:36:ASP:HB2	2.36	0.41
3:CG:92:GLU:O	3:CG:95:VAL:HG12	2.21	0.41
4:CH:436:GLN:OE1	4:CH:529:VAL:CG2	2.69	0.41
8:CK:172:LYS:CB	8:DK:108:HIS:CE1	3.04	0.41
1:DB:428:TYR:CE2	1:DB:459:ASN:HA	2.55	0.41
2:DD:188:GLN:HG2	2:DD:586:TYR:CE2	2.56	0.41
3:DE:33:ASN:ND2	3:DE:36:ASP:HB2	2.36	0.41
11:DP:217:ARG:NH1	11:DP:348:LYS:O	2.54	0.41
1:EA:15:THR:OG1	1:EA:16:PRO:HD2	2.20	0.41
1:EB:12:PRO:HD3	1:EB:27:ARG:HD3	2.03	0.41
1:EB:15:THR:HG23	1:EB:18:GLN:HB2	2.02	0.41
2:ED:469:ASP:OD2	2:ED:518:TYR:OH	2.37	0.41
3:EF:33:ASN:ND2	3:EF:36:ASP:HB2	2.36	0.41
4:EH:459:VAL:O	4:EH:469:GLN:NE2	2.43	0.41
4:EH:591:GLN:HE21	4:EH:677:SER:HB3	1.86	0.41
1:FA:487:ASN:OD1	1:FA:860:SER:OG	2.39	0.41
2:FD:632:LEU:HD21	2:FD:655:ALA:HB1	2.02	0.41
2:FD:713:GLU:HB2	2:FD:714:PRO:HD3	2.01	0.41
3:FE:92:GLU:O	3:FE:95:VAL:HG12	2.21	0.41
4:FH:143:LEU:HG	4:FH:231:TYR:CD1	2.56	0.41
4:FH:718:THR:O	4:FH:718:THR:HG23	2.20	0.41
1:AA:456:TYR:CD2	1:AA:510:GLU:CD	2.99	0.41
2:AD:682:HIS:CE1	2:AD:805:PHE:CD1	3.09	0.41
4:AH:591:GLN:HE21	4:AH:677:SER:HB3	1.86	0.41
4:AH:716:ALA:HA	4:AH:759:PRO:HG2	2.02	0.41
4:AH:746:PHE:CD2	4:AH:746:PHE:N	2.88	0.41
4:AH:955:LYS:HD3	4:AH:955:LYS:HA	1.92	0.41
8:AK:108:HIS:CE1	8:DK:172:LYS:CB	3.04	0.41
11:AP:194:MET:CE	11:AP:369:LEU:HD11	2.51	0.41
11:AQ:217:ARG:NH1	11:AQ:348:LYS:O	2.54	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BA:208:TRP:CE3	1:BA:216:ILE:HG13	2.55	0.41
1:BB:428:TYR:CE2	1:BB:459:ASN:HA	2.55	0.41
2:BD:359:SER:O	2:BD:361:LEU:HD12	2.21	0.41
2:BD:605:LEU:CD1	2:BD:613:VAL:HG12	2.51	0.41
2:BD:682:HIS:CE1	2:BD:805:PHE:CD1	3.09	0.41
3:BF:33:ASN:ND2	3:BF:36:ASP:HB2	2.36	0.41
11:BP:446:GLU:CG	11:EQ:22:ILE:CD1	2.99	0.41
3:CE:92:GLU:O	3:CE:95:VAL:HG12	2.21	0.41
4:CH:243:GLN:CG	4:CH:245:PHE:CD2	3.03	0.41
4:CH:591:GLN:HE21	4:CH:677:SER:HB3	1.86	0.41
4:CH:716:ALA:HA	4:CH:759:PRO:HG2	2.02	0.41
11:CO:120:ASN:ND2	11:CO:300:LEU:HD22	2.36	0.41
1:DC:23:LYS:O	1:DC:27:ARG:HG3	2.21	0.41
1:DC:196:GLN:O	1:DC:200:SER:OG	2.25	0.41
2:DD:491:THR:HG22	2:DD:492:GLN:H	1.86	0.41
3:DG:92:GLU:O	3:DG:95:VAL:HG12	2.21	0.41
4:DH:436:GLN:OE1	4:DH:529:VAL:CG2	2.69	0.41
4:DH:732:ALA:CB	4:DH:752:TYR:HD1	2.33	0.41
8:DK:180:GLN:O	8:DK:181:ARG:NH1	2.44	0.41
11:DQ:194:MET:CE	11:DQ:369:LEU:HD11	2.51	0.41
1:EB:20:LEU:CD1	2:ED:1330:LEU:HG	2.51	0.41
1:EB:428:TYR:CE2	1:EB:459:ASN:HA	2.55	0.41
1:EC:189:LEU:HD12	1:EC:189:LEU:HA	1.94	0.41
2:ED:786:VAL:HA	2:ED:789:TYR:CD1	2.56	0.41
4:EH:718:THR:HG23	4:EH:718:THR:O	2.20	0.41
4:EH:732:ALA:CB	4:EH:752:TYR:HD1	2.33	0.41
5:EJ:12:TYR:CZ	8:EK:107:THR:HG22	2.56	0.41
1:FB:15:THR:HG23	1:FB:18:GLN:HB2	2.02	0.41
1:FB:580:GLU:O	1:FB:584:ARG:NH1	2.54	0.41
4:FH:746:PHE:CD2	4:FH:746:PHE:N	2.88	0.41
1:AB:15:THR:HG23	1:AB:18:GLN:HB2	2.02	0.41
1:AC:377:LEU:HB2	1:AC:380:GLN:HG3	2.03	0.41
2:AD:304:GLN:O	2:AD:308:GLN:HG2	2.21	0.41
2:AD:307:LEU:HD13	4:DH:1149:LYS:HB2	2.03	0.41
2:AD:390:GLU:HG3	11:AO:90:ARG:HH12	1.85	0.41
2:AD:390:GLU:HG2	11:AO:90:ARG:HH12	1.86	0.41
2:AD:491:THR:HG22	2:AD:492:GLN:H	1.86	0.41
2:AD:605:LEU:CD1	2:AD:613:VAL:HG12	2.51	0.41
4:AH:436:GLN:OE1	4:AH:529:VAL:CG2	2.69	0.41
4:AH:513:GLU:H	4:AH:513:GLU:CD	2.26	0.41
4:AH:654:LEU:HD23	4:AH:654:LEU:HA	1.88	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:AH:724:VAL:HG11	4:AH:729:LYS:HD2	2.02	0.41
4:AH:869:ASP:OD2	4:AH:869:ASP:N	2.51	0.41
5:AJ:8:ARG:NH1	8:AK:164:ASN:ND2	2.69	0.41
5:AJ:8:ARG:HH12	8:AK:164:ASN:ND2	2.18	0.41
11:AO:120:ASN:ND2	11:AO:300:LEU:HD22	2.36	0.41
11:AP:393:LYS:O	11:AP:397:GLU:HG3	2.21	0.41
1:BB:12:PRO:HD3	1:BB:27:ARG:HD3	2.03	0.41
1:BB:20:LEU:CD1	2:BD:1330:LEU:HG	2.51	0.41
1:BB:498:LEU:HD13	1:BC:236:TYR:HE1	1.86	0.41
1:BB:580:GLU:O	1:BB:584:ARG:NH1	2.54	0.41
3:BF:92:GLU:O	3:BF:95:VAL:HG12	2.21	0.41
3:BG:92:GLU:O	3:BG:95:VAL:HG12	2.21	0.41
4:BH:1149:LYS:HB2	2:ED:307:LEU:HD13	2.03	0.41
10:BN:62:LYS:HG2	10:BN:130:SER:HB2	2.03	0.41
11:BQ:194:MET:CE	11:BQ:369:LEU:HD11	2.51	0.41
2:CD:66:ASN:OD1	2:CD:457:LEU:HD21	2.21	0.41
2:CD:158:THR:HG23	2:CD:202:ASP:OD2	2.20	0.41
2:CD:359:SER:O	2:CD:361:LEU:CD1	2.69	0.41
2:CD:713:GLU:HB2	2:CD:714:PRO:HD3	2.01	0.41
2:CD:716:LEU:O	2:CD:720:LEU:HB2	2.20	0.41
5:CJ:8:ARG:NH1	8:CK:164:ASN:ND2	2.69	0.41
5:CJ:12:TYR:CZ	8:CK:107:THR:HG22	2.56	0.41
10:CN:75:TRP:CE2	10:CN:111:PRO:HD3	2.55	0.41
11:CO:338:GLN:HE22	11:CO:364:TRP:HD1	1.68	0.41
11:CQ:22:ILE:HD13	11:FP:446:GLU:HG2	2.02	0.41
11:CQ:194:MET:CE	11:CQ:369:LEU:HD11	2.51	0.41
1:DA:27:ARG:HH22	1:DB:158:ARG:HH22	1.69	0.41
1:DC:377:LEU:HB2	1:DC:380:GLN:HG3	2.03	0.41
2:DD:37:LYS:HB2	4:DH:240:GLN:HB3	2.03	0.41
2:DD:226:GLU:HG3	2:DD:370:VAL:HG22	2.03	0.41
2:DD:716:LEU:O	2:DD:720:LEU:HB2	2.20	0.41
10:DN:62:LYS:HG2	10:DN:130:SER:HB2	2.03	0.41
1:EA:487:ASN:OD1	1:EA:860:SER:OG	2.39	0.41
1:EB:580:GLU:O	1:EB:584:ARG:NH1	2.54	0.41
1:EC:517:ASN:HD21	1:EC:829:TYR:CB	2.34	0.41
1:EC:569:ASP:N	1:EC:569:ASP:OD2	2.54	0.41
2:ED:66:ASN:OD1	2:ED:457:LEU:HD21	2.21	0.41
2:ED:94:VAL:HG23	2:ED:95:LEU:HG	2.02	0.41
2:ED:248:THR:HG23	2:ED:390:GLU:HB3	2.02	0.41
4:EH:436:GLN:OE1	4:EH:529:VAL:CG2	2.69	0.41
4:EH:892:ASP:OD2	4:EH:892:ASP:N	2.53	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:EJ:278:GLU:OE1	5:EJ:278:GLU:HA	2.20	0.41
10:EN:28:LEU:HD13	10:EN:104:TRP:CE2	2.56	0.41
11:EP:194:MET:CE	11:EP:369:LEU:HD11	2.51	0.41
11:EP:217:ARG:NH1	11:EP:348:LYS:O	2.54	0.41
1:FB:20:LEU:CD1	2:FD:1330:LEU:HG	2.51	0.41
1:FC:23:LYS:O	1:FC:27:ARG:HG3	2.21	0.41
1:FC:83:ALA:C	1:FC:84:GLU:HG2	2.45	0.41
2:FD:39:TRP:NE1	2:FD:46:ASP:OD2	2.52	0.41
2:FD:158:THR:HG23	2:FD:202:ASP:OD2	2.20	0.41
2:FD:188:GLN:HG2	2:FD:586:TYR:CE2	2.56	0.41
2:FD:300:SER:HA	2:FD:303:TYR:HB2	2.02	0.41
2:FD:1130:ASN:HB2	2:FD:1132:GLY:O	2.21	0.41
4:FH:107:LEU:HD11	4:FH:207:ARG:HD3	2.03	0.41
4:FH:436:GLN:OE1	4:FH:529:VAL:CG2	2.69	0.41
4:FH:955:LYS:HA	4:FH:955:LYS:HD3	1.93	0.41
11:FO:338:GLN:HE22	11:FO:364:TRP:HD1	1.68	0.41
1:AA:208:TRP:CE3	1:AA:216:ILE:HG13	2.55	0.41
1:AB:498:LEU:HD13	1:AC:236:TYR:HE1	1.86	0.41
1:AC:23:LYS:O	1:AC:27:ARG:HG3	2.21	0.41
2:AD:37:LYS:HB2	4:AH:240:GLN:HB3	2.03	0.41
2:AD:404:ALA:O	2:AD:492:GLN:NE2	2.39	0.41
2:AD:632:LEU:HD21	2:AD:655:ALA:HB1	2.02	0.41
3:AE:92:GLU:O	3:AE:95:VAL:HG12	2.21	0.41
3:AF:15:ASN:O	4:AH:1219:LEU:O	2.39	0.41
1:BA:456:TYR:CD2	1:BA:510:GLU:CD	2.99	0.41
2:BD:300:SER:HA	2:BD:303:TYR:HB2	2.02	0.41
3:BE:33:ASN:ND2	3:BE:36:ASP:HB2	2.36	0.41
3:BG:33:ASN:ND2	3:BG:36:ASP:HB2	2.36	0.41
4:BH:383:GLN:O	4:BH:386:LYS:NZ	2.50	0.41
4:BH:892:ASP:OD2	4:BH:892:ASP:N	2.53	0.41
8:BK:46:GLN:HE22	5:CJ:104:GLY:CA	2.33	0.41
11:BO:102:ILE:HG13	11:BO:291:LEU:HD13	2.02	0.41
11:BP:45:ASN:HB3	11:BP:48:THR:HB	2.01	0.41
3:CF:15:ASN:O	4:CH:1219:LEU:O	2.39	0.41
4:CH:743:LYS:HB2	4:CH:743:LYS:HE2	1.91	0.41
5:CJ:278:GLU:CB	4:DH:959:PRO:HG2	2.51	0.41
10:CN:50:MET:HA	10:CN:51:PRO:HD3	1.97	0.41
1:DA:595:PHE:CZ	1:DA:607:ASP:HB3	2.56	0.41
1:DB:163:LEU:HD21	4:DH:11:PRO:HD3	2.01	0.41
2:DD:304:GLN:O	2:DD:308:GLN:HG2	2.21	0.41
2:DD:359:SER:O	2:DD:361:LEU:HD12	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:DD:611:ASP:OD1	2:DD:611:ASP:N	2.49	0.41
2:DD:786:VAL:HA	2:DD:789:TYR:CD1	2.56	0.41
2:DD:1130:ASN:HB2	2:DD:1132:GLY:O	2.21	0.41
3:DF:15:ASN:O	4:DH:1219:LEU:O	2.39	0.41
4:DH:912:ILE:HA	4:DH:913:PRO:HD3	1.93	0.41
4:DH:982:GLU:CD	4:DH:982:GLU:H	2.28	0.41
1:EB:163:LEU:HD21	4:EH:11:PRO:HD3	2.01	0.41
1:EB:310:VAL:HG13	1:EB:311:SER:N	2.36	0.41
3:EE:33:ASN:ND2	3:EE:36:ASP:HB2	2.36	0.41
4:EH:630:PRO:HB2	4:EH:700:PHE:CE2	2.56	0.41
11:EQ:471:GLU:OE1	11:FQ:8:PRO:HG3	2.20	0.41
1:FA:59:GLN:N	1:FA:62:ASP:O	2.42	0.41
1:FB:12:PRO:HD3	1:FB:27:ARG:HD3	2.03	0.41
1:FC:240:THR:O	1:FC:240:THR:OG1	2.36	0.41
1:FC:517:ASN:HD21	1:FC:829:TYR:CB	2.34	0.41
2:FD:359:SER:O	2:FD:361:LEU:HD12	2.21	0.41
2:FD:786:VAL:HA	2:FD:789:TYR:CD1	2.56	0.41
3:FF:33:ASN:ND2	3:FF:36:ASP:HB2	2.36	0.41
11:FP:217:ARG:NH1	11:FP:348:LYS:O	2.54	0.41
1:AA:153:LEU:N	1:AA:153:LEU:HD12	2.36	0.40
2:AD:94:VAL:HG23	2:AD:95:LEU:HG	2.02	0.40
3:AE:57:TYR:O	3:AE:58:ASN:C	2.63	0.40
3:AG:92:GLU:O	3:AG:95:VAL:HG12	2.21	0.40
1:BB:73:ILE:HG22	1:BB:74:THR:O	2.21	0.40
1:BB:162:LEU:HG	4:BH:1036:LEU:HD21	2.04	0.40
1:BC:517:ASN:HD21	1:BC:829:TYR:CB	2.34	0.40
2:BD:39:TRP:NE1	2:BD:46:ASP:OD2	2.52	0.40
2:BD:359:SER:O	2:BD:361:LEU:CD1	2.69	0.40
4:BH:436:GLN:OE1	4:BH:529:VAL:CG2	2.69	0.40
4:BH:654:LEU:HD23	4:BH:654:LEU:HA	1.88	0.40
11:BO:120:ASN:ND2	11:BO:300:LEU:HD22	2.36	0.40
11:BP:393:LYS:O	11:BP:397:GLU:HG3	2.22	0.40
1:CC:417:ARG:NH1	1:CC:467:TRP:O	2.53	0.40
1:CC:569:ASP:N	1:CC:569:ASP:OD2	2.54	0.40
2:CD:94:VAL:HG23	2:CD:95:LEU:HG	2.02	0.40
2:CD:300:SER:HA	2:CD:303:TYR:HB2	2.02	0.40
3:CE:23:TYR:N	3:CE:23:TYR:CD1	2.89	0.40
4:CH:1027:ASP:OD2	4:CH:1030:GLN:NE2	2.46	0.40
7:CI:145:GLU:OE1	8:CK:177:VAL:HA	2.21	0.40
1:DA:59:GLN:N	1:DA:62:ASP:O	2.42	0.40
3:DF:92:GLU:O	3:DF:95:VAL:HG12	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:EB:532:ASN:OD1	1:EC:812:GLY:N	2.54	0.40
2:ED:96:THR:HB	2:ED:266:ARG:O	2.21	0.40
2:ED:678:LYS:HE3	2:ED:1118:ASP:OD1	2.21	0.40
4:EH:243:GLN:CG	4:EH:245:PHE:CD2	3.03	0.40
4:EH:1149:LYS:HB2	2:FD:307:LEU:HD13	2.03	0.40
11:EP:446:GLU:CG	11:FQ:22:ILE:CD1	2.99	0.40
11:EQ:45:ASN:HB3	11:EQ:48:THR:HB	2.02	0.40
11:EQ:194:MET:CE	11:EQ:369:LEU:HD11	2.51	0.40
1:FA:153:LEU:N	1:FA:153:LEU:HD12	2.36	0.40
1:FA:595:PHE:CZ	1:FA:607:ASP:HB3	2.56	0.40
3:FF:15:ASN:O	4:FH:1219:LEU:O	2.39	0.40
10:FN:42:LEU:HA	10:FN:43:PRO:HD3	1.96	0.40
11:FP:194:MET:CE	11:FP:369:LEU:HD11	2.51	0.40
11:FQ:217:ARG:NH1	11:FQ:348:LYS:O	2.54	0.40
1:AA:27:ARG:HH22	1:AB:158:ARG:HH22	1.69	0.40
1:AA:802:LEU:HA	1:AA:802:LEU:HD23	1.87	0.40
2:AD:66:ASN:OD1	2:AD:457:LEU:HD21	2.21	0.40
4:AH:1149:LYS:HB2	2:BD:307:LEU:HD13	2.03	0.40
8:AK:172:LYS:CB	8:BK:108:HIS:CE1	3.04	0.40
8:AK:232:THR:O	8:AK:232:THR:CG2	2.69	0.40
11:AP:217:ARG:NH1	11:AP:348:LYS:O	2.54	0.40
1:BA:153:LEU:N	1:BA:153:LEU:HD12	2.36	0.40
1:BB:15:THR:HG23	1:BB:18:GLN:HB2	2.02	0.40
1:BC:377:LEU:HB2	1:BC:380:GLN:HG3	2.03	0.40
2:BD:678:LYS:HE3	2:BD:1118:ASP:OD1	2.21	0.40
4:BH:414:GLU:O	4:BH:417:ARG:HD2	2.22	0.40
4:BH:630:PRO:HB2	4:BH:700:PHE:CE2	2.56	0.40
4:BH:724:VAL:HG11	4:BH:729:LYS:HD2	2.02	0.40
11:BQ:393:LYS:O	11:BQ:397:GLU:HG3	2.21	0.40
2:CD:96:THR:HB	2:CD:266:ARG:O	2.21	0.40
2:CD:359:SER:O	2:CD:361:LEU:HD12	2.21	0.40
3:CF:92:GLU:O	3:CF:95:VAL:HG12	2.21	0.40
3:CG:23:TYR:N	3:CG:23:TYR:CD1	2.89	0.40
4:CH:107:LEU:HD11	4:CH:207:ARG:HD3	2.03	0.40
4:CH:383:GLN:O	4:CH:386:LYS:NZ	2.50	0.40
4:CH:520:ARG:NH1	4:CH:522:GLU:OE2	2.55	0.40
8:CK:108:HIS:CE1	8:FK:172:LYS:CB	3.04	0.40
8:CK:232:THR:O	8:CK:232:THR:CG2	2.69	0.40
11:CP:446:GLU:HG2	11:DQ:22:ILE:HD13	2.02	0.40
1:DB:532:ASN:OD1	1:DC:812:GLY:N	2.54	0.40
2:DD:66:ASN:OD1	2:DD:457:LEU:HD21	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:DD:605:LEU:CD1	2:DD:613:VAL:HG12	2.51	0.40
2:DD:636:PHE:CE2	2:DD:1060:LEU:HD22	2.57	0.40
4:DH:520:ARG:NH1	4:DH:522:GLU:OE2	2.54	0.40
11:DP:393:LYS:O	11:DP:397:GLU:HG3	2.21	0.40
1:EA:153:LEU:N	1:EA:153:LEU:HD12	2.36	0.40
1:EC:38:LEU:HD23	1:EC:38:LEU:HA	1.82	0.40
2:ED:226:GLU:HG3	2:ED:370:VAL:HG22	2.03	0.40
11:EP:393:LYS:O	11:EP:397:GLU:HG3	2.21	0.40
1:FB:73:ILE:HG22	1:FB:74:THR:O	2.21	0.40
1:FB:498:LEU:HD13	1:FC:236:TYR:HE1	1.86	0.40
1:FB:550:ASP:OD1	1:FB:550:ASP:N	2.49	0.40
1:FC:569:ASP:N	1:FC:569:ASP:OD2	2.54	0.40
2:FD:37:LYS:HB2	4:FH:240:GLN:HB3	2.03	0.40
2:FD:96:THR:HB	2:FD:266:ARG:O	2.21	0.40
3:FF:57:TYR:O	3:FF:58:ASN:C	2.63	0.40
7:FI:15:PHE:HA	7:FI:16:PRO:HA	1.91	0.40
7:FI:145:GLU:OE1	8:FK:177:VAL:HA	2.21	0.40
8:FK:81:LYS:HA	8:FK:82:PRO:HD3	1.94	0.40
1:AA:853:GLU:OE1	1:AA:853:GLU:HA	2.22	0.40
1:AB:20:LEU:CD1	2:AD:1330:LEU:HG	2.51	0.40
2:AD:96:THR:HB	2:AD:266:ARG:O	2.21	0.40
2:AD:226:GLU:HG3	2:AD:370:VAL:HG22	2.03	0.40
2:AD:248:THR:HG23	2:AD:390:GLU:HB3	2.01	0.40
2:AD:611:ASP:OD1	2:AD:611:ASP:N	2.49	0.40
2:AD:636:PHE:CE2	2:AD:1060:LEU:HD22	2.57	0.40
2:AD:1130:ASN:HB2	2:AD:1132:GLY:O	2.21	0.40
3:AF:33:ASN:ND2	3:AF:36:ASP:HB2	2.36	0.40
11:AQ:471:GLU:OE1	11:BQ:8:PRO:HG3	2.20	0.40
1:BA:40:ARG:HE	1:BC:39:THR:HG1	1.67	0.40
1:BA:595:PHE:CZ	1:BA:607:ASP:HB3	2.56	0.40
1:BC:34:GLU:OE2	1:BC:37:ARG:NH2	2.52	0.40
2:BD:96:THR:HB	2:BD:266:ARG:O	2.21	0.40
2:BD:188:GLN:HG2	2:BD:586:TYR:CE2	2.56	0.40
2:BD:686:GLU:OE2	2:BD:694:SER:HB2	2.20	0.40
2:BD:747:PHE:CD1	2:BD:747:PHE:C	3.00	0.40
11:BP:194:MET:CE	11:BP:369:LEU:HD11	2.51	0.40
11:BQ:471:GLU:OE1	11:EQ:8:PRO:HG3	2.20	0.40
1:CC:196:GLN:O	1:CC:200:SER:OG	2.25	0.40
1:CC:517:ASN:HD21	1:CC:829:TYR:CB	2.34	0.40
2:CD:37:LYS:HB2	4:CH:240:GLN:HB3	2.03	0.40
3:CF:57:TYR:O	3:CF:58:ASN:C	2.63	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:CG:33:ASN:ND2	3:CG:36:ASP:HB2	2.36	0.40
8:CK:143:ASP:OD1	8:CK:144:GLN:N	2.54	0.40
11:CQ:217:ARG:NH1	11:CQ:348:LYS:O	2.54	0.40
1:DA:208:TRP:CE3	1:DA:216:ILE:HG13	2.55	0.40
1:DB:438:LYS:HE2	1:DB:483:TYR:O	2.22	0.40
2:DD:359:SER:O	2:DD:361:LEU:CD1	2.69	0.40
3:DE:23:TYR:N	3:DE:23:TYR:CD1	2.89	0.40
1:EB:73:ILE:HG22	1:EB:74:THR:O	2.21	0.40
2:ED:300:SER:HA	2:ED:303:TYR:HB2	2.02	0.40
2:ED:605:LEU:CD1	2:ED:613:VAL:HG12	2.51	0.40
3:EF:92:GLU:O	3:EF:95:VAL:HG12	2.21	0.40
3:EG:92:GLU:O	3:EG:95:VAL:HG12	2.21	0.40
4:EH:370:ASN:OD1	4:EH:370:ASN:N	2.48	0.40
11:EQ:217:ARG:NH1	11:EQ:348:LYS:O	2.54	0.40
1:FB:310:VAL:HG13	1:FB:311:SER:N	2.36	0.40
2:FD:304:GLN:O	2:FD:308:GLN:HG2	2.21	0.40
2:FD:359:SER:O	2:FD:361:LEU:CD1	2.69	0.40
4:FH:520:ARG:NH1	4:FH:522:GLU:OE2	2.55	0.40
10:FN:28:LEU:HD13	10:FN:104:TRP:CE2	2.56	0.40
10:FN:80:ALA:O	10:FN:81:LEU:C	2.64	0.40
11:FP:393:LYS:O	11:FP:397:GLU:HG3	2.21	0.40
1:AB:12:PRO:HD3	1:AB:27:ARG:HD3	2.03	0.40
1:AB:162:LEU:HG	4:AH:1036:LEU:HD21	2.04	0.40
1:AC:517:ASN:HD21	1:AC:829:TYR:CB	2.34	0.40
2:AD:747:PHE:CD1	2:AD:747:PHE:C	3.00	0.40
4:AH:609:THR:HA	4:AH:610:PRO:HD3	1.96	0.40
4:AH:842:ALA:HB2	4:AH:920:CYS:SG	2.62	0.40
4:AH:892:ASP:OD2	4:AH:892:ASP:N	2.53	0.40
10:AN:70:ASN:O	10:AN:74:LYS:HG3	2.22	0.40
11:AQ:393:LYS:O	11:AQ:397:GLU:HG3	2.21	0.40
4:BH:110:ARG:NH2	4:BH:198:PRO:O	2.46	0.40
4:BH:842:ALA:HB2	4:BH:920:CYS:SG	2.62	0.40
1:CB:310:VAL:HG13	1:CB:311:SER:N	2.37	0.40
1:CB:580:GLU:O	1:CB:584:ARG:NH1	2.54	0.40
1:CC:23:LYS:O	1:CC:27:ARG:HG3	2.21	0.40
2:CD:1067:LEU:HB3	2:CD:1068:ASP:H	1.74	0.40
4:CH:414:GLU:O	4:CH:417:ARG:HD2	2.22	0.40
4:CH:630:PRO:HB2	4:CH:700:PHE:CE2	2.56	0.40
4:CH:1149:LYS:HB2	2:DD:307:LEU:HD13	2.03	0.40
1:DB:163:LEU:HD12	1:DB:163:LEU:HA	1.92	0.40
2:DD:678:LYS:HE3	2:DD:1118:ASP:OD1	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:DQ:217:ARG:NH1	11:DQ:348:LYS:O	2.54	0.40
11:DQ:393:LYS:O	11:DQ:397:GLU:HG3	2.21	0.40
1:EA:595:PHE:CZ	1:EA:607:ASP:HB3	2.56	0.40
5:EJ:125:ASN:HA	5:EJ:162:GLN:O	2.22	0.40
8:EK:119:ASP:HB3	8:FK:147:LYS:HG3	2.02	0.40
3:FE:33:ASN:ND2	3:FE:36:ASP:HB2	2.36	0.40
3:FG:33:ASN:ND2	3:FG:36:ASP:HB2	2.36	0.40
4:FH:591:GLN:HE21	4:FH:677:SER:HB3	1.86	0.40
4:FH:892:ASP:OD2	4:FH:892:ASP:N	2.53	0.40
1:AA:67:VAL:HB	1:AA:85:THR:OG1	2.22	0.40
1:AA:558:ASP:OD1	1:AA:558:ASP:N	2.48	0.40
1:AA:595:PHE:CZ	1:AA:607:ASP:HB3	2.56	0.40
1:AB:580:GLU:O	1:AB:584:ARG:NH1	2.54	0.40
2:AD:469:ASP:OD2	2:AD:518:TYR:OH	2.37	0.40
10:AN:80:ALA:O	10:AN:81:LEU:C	2.64	0.40
10:AN:88:ASP:CG	11:AP:418:ASN:HD22	2.29	0.40
11:AQ:22:ILE:HD13	11:DP:446:GLU:HG2	2.02	0.40
1:BA:802:LEU:HA	1:BA:802:LEU:HD23	1.86	0.40
1:BA:853:GLU:HA	1:BA:853:GLU:OE1	2.22	0.40
1:BB:104:SER:HB2	1:BB:368:LYS:NZ	2.37	0.40
2:BD:37:LYS:HB2	4:BH:240:GLN:HB3	2.03	0.40
2:BD:304:GLN:O	2:BD:308:GLN:HG2	2.21	0.40
3:BF:23:TYR:N	3:BF:23:TYR:CD1	2.89	0.40
4:BH:15:ASP:OD2	4:BH:15:ASP:N	2.51	0.40
10:BN:28:LEU:HD13	10:BN:104:TRP:CE2	2.56	0.40
1:CB:15:THR:HG23	1:CB:18:GLN:HB2	2.02	0.40
1:CC:377:LEU:HB2	1:CC:380:GLN:HG3	2.03	0.40
2:CD:307:LEU:HD13	4:FH:1149:LYS:HB2	2.03	0.40
10:CN:80:ALA:O	10:CN:81:LEU:C	2.64	0.40
11:CQ:22:ILE:CD1	11:FP:446:GLU:CG	2.99	0.40
11:CQ:393:LYS:O	11:CQ:397:GLU:HG3	2.21	0.40
2:DD:96:THR:HB	2:DD:266:ARG:O	2.21	0.40
2:DD:660:ASP:OD1	2:DD:661:LYS:N	2.55	0.40
4:DH:107:LEU:HD11	4:DH:207:ARG:HD3	2.03	0.40
4:DH:414:GLU:O	4:DH:417:ARG:HD2	2.22	0.40
4:DH:711:LYS:HB3	4:DH:711:LYS:HE3	1.81	0.40
4:DH:842:ALA:HB2	4:DH:920:CYS:SG	2.62	0.40
1:EB:498:LEU:HD13	1:EC:236:TYR:HE1	1.86	0.40
4:EH:15:ASP:OD2	4:EH:15:ASP:N	2.51	0.40
5:EJ:8:ARG:NH1	8:EK:164:ASN:ND2	2.69	0.40
6:EL:49:LYS:O	6:EL:49:LYS:CG	2.69	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:EI:145:GLU:OE1	8:EK:177:VAL:HA	2.21	0.40
1:FB:438:LYS:HE2	1:FB:483:TYR:O	2.21	0.40
2:FD:636:PHE:CE2	2:FD:1060:LEU:HD22	2.57	0.40
3:FF:92:GLU:O	3:FF:95:VAL:HG12	2.21	0.40
8:FK:91:ASP:O	8:FK:95:VAL:HG22	2.22	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	AA	721/1476 (49%)	690 (96%)	31 (4%)	0	100	100
1	AB	712/1476 (48%)	686 (96%)	26 (4%)	0	100	100
1	AC	688/1476 (47%)	667 (97%)	21 (3%)	0	100	100
1	BA	721/1476 (49%)	690 (96%)	31 (4%)	0	100	100
1	BB	712/1476 (48%)	686 (96%)	26 (4%)	0	100	100
1	BC	688/1476 (47%)	667 (97%)	21 (3%)	0	100	100
1	CA	721/1476 (49%)	690 (96%)	31 (4%)	0	100	100
1	CB	712/1476 (48%)	686 (96%)	26 (4%)	0	100	100
1	CC	688/1476 (47%)	667 (97%)	21 (3%)	0	100	100
1	DA	721/1476 (49%)	690 (96%)	31 (4%)	0	100	100
1	DB	712/1476 (48%)	686 (96%)	26 (4%)	0	100	100
1	DC	688/1476 (47%)	667 (97%)	21 (3%)	0	100	100
1	EA	721/1476 (49%)	690 (96%)	31 (4%)	0	100	100
1	EB	712/1476 (48%)	686 (96%)	26 (4%)	0	100	100
1	EC	688/1476 (47%)	667 (97%)	21 (3%)	0	100	100
1	FA	721/1476 (49%)	690 (96%)	31 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	FB	712/1476 (48%)	686 (96%)	26 (4%)	0	100	100
1	FC	688/1476 (47%)	667 (97%)	21 (3%)	0	100	100
2	AD	1099/1335 (82%)	1075 (98%)	24 (2%)	0	100	100
2	BD	1099/1335 (82%)	1075 (98%)	24 (2%)	0	100	100
2	CD	1099/1335 (82%)	1075 (98%)	24 (2%)	0	100	100
2	DD	1099/1335 (82%)	1075 (98%)	24 (2%)	0	100	100
2	ED	1099/1335 (82%)	1075 (98%)	24 (2%)	0	100	100
2	FD	1099/1335 (82%)	1075 (98%)	24 (2%)	0	100	100
3	AE	98/154 (64%)	93 (95%)	5 (5%)	0	100	100
3	AF	98/154 (64%)	94 (96%)	4 (4%)	0	100	100
3	AG	98/154 (64%)	94 (96%)	4 (4%)	0	100	100
3	BE	98/154 (64%)	93 (95%)	5 (5%)	0	100	100
3	BF	98/154 (64%)	94 (96%)	4 (4%)	0	100	100
3	BG	98/154 (64%)	94 (96%)	4 (4%)	0	100	100
3	CE	98/154 (64%)	93 (95%)	5 (5%)	0	100	100
3	CF	98/154 (64%)	94 (96%)	4 (4%)	0	100	100
3	CG	98/154 (64%)	94 (96%)	4 (4%)	0	100	100
3	DE	98/154 (64%)	93 (95%)	5 (5%)	0	100	100
3	DF	98/154 (64%)	94 (96%)	4 (4%)	0	100	100
3	DG	98/154 (64%)	94 (96%)	4 (4%)	0	100	100
3	EE	98/154 (64%)	93 (95%)	5 (5%)	0	100	100
3	EF	98/154 (64%)	94 (96%)	4 (4%)	0	100	100
3	EG	98/154 (64%)	94 (96%)	4 (4%)	0	100	100
3	FE	98/154 (64%)	93 (95%)	5 (5%)	0	100	100
3	FF	98/154 (64%)	94 (96%)	4 (4%)	0	100	100
3	FG	98/154 (64%)	94 (96%)	4 (4%)	0	100	100
4	AH	1225/1231 (100%)	1186 (97%)	39 (3%)	0	100	100
4	BH	1225/1231 (100%)	1186 (97%)	39 (3%)	0	100	100
4	CH	1225/1231 (100%)	1186 (97%)	39 (3%)	0	100	100
4	DH	1225/1231 (100%)	1186 (97%)	39 (3%)	0	100	100
4	EH	1225/1231 (100%)	1185 (97%)	40 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
4	FH	1225/1231 (100%)	1186 (97%)	39 (3%)	0	100	100
5	AJ	583/589 (99%)	571 (98%)	12 (2%)	0	100	100
5	CJ	583/589 (99%)	571 (98%)	12 (2%)	0	100	100
5	EJ	583/589 (99%)	571 (98%)	12 (2%)	0	100	100
6	AL	33/50 (66%)	32 (97%)	1 (3%)	0	100	100
6	CL	33/50 (66%)	32 (97%)	1 (3%)	0	100	100
6	EL	33/50 (66%)	32 (97%)	1 (3%)	0	100	100
7	AI	134/149 (90%)	131 (98%)	3 (2%)	0	100	100
7	BI	134/149 (90%)	131 (98%)	3 (2%)	0	100	100
7	CI	134/149 (90%)	131 (98%)	3 (2%)	0	100	100
7	DI	134/149 (90%)	131 (98%)	3 (2%)	0	100	100
7	EI	134/149 (90%)	131 (98%)	3 (2%)	0	100	100
7	FI	134/149 (90%)	131 (98%)	3 (2%)	0	100	100
8	AK	230/234 (98%)	224 (97%)	6 (3%)	0	100	100
8	BK	230/234 (98%)	223 (97%)	7 (3%)	0	100	100
8	CK	230/234 (98%)	223 (97%)	7 (3%)	0	100	100
8	DK	230/234 (98%)	223 (97%)	7 (3%)	0	100	100
8	EK	230/234 (98%)	224 (97%)	6 (3%)	0	100	100
8	FK	230/234 (98%)	223 (97%)	7 (3%)	0	100	100
9	AM	149/167 (89%)	145 (97%)	4 (3%)	0	100	100
9	BM	149/167 (89%)	145 (97%)	4 (3%)	0	100	100
9	CM	149/167 (89%)	145 (97%)	4 (3%)	0	100	100
9	DM	149/167 (89%)	145 (97%)	4 (3%)	0	100	100
9	EM	149/167 (89%)	145 (97%)	4 (3%)	0	100	100
9	FM	149/167 (89%)	145 (97%)	4 (3%)	0	100	100
10	AN	140/143 (98%)	131 (94%)	9 (6%)	0	100	100
10	BN	140/143 (98%)	131 (94%)	9 (6%)	0	100	100
10	CN	140/143 (98%)	131 (94%)	9 (6%)	0	100	100
10	DN	140/143 (98%)	131 (94%)	9 (6%)	0	100	100
10	EN	140/143 (98%)	131 (94%)	9 (6%)	0	100	100
10	FN	140/143 (98%)	131 (94%)	9 (6%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
11	AO	469/484 (97%)	456 (97%)	13 (3%)	0	100	100
11	AP	478/484 (99%)	471 (98%)	7 (2%)	0	100	100
11	AQ	478/484 (99%)	472 (99%)	6 (1%)	0	100	100
11	BO	469/484 (97%)	456 (97%)	13 (3%)	0	100	100
11	BP	478/484 (99%)	471 (98%)	7 (2%)	0	100	100
11	BQ	478/484 (99%)	472 (99%)	6 (1%)	0	100	100
11	CO	469/484 (97%)	456 (97%)	13 (3%)	0	100	100
11	CP	478/484 (99%)	471 (98%)	7 (2%)	0	100	100
11	CQ	478/484 (99%)	472 (99%)	6 (1%)	0	100	100
11	DO	469/484 (97%)	456 (97%)	13 (3%)	0	100	100
11	DP	478/484 (99%)	471 (98%)	7 (2%)	0	100	100
11	DQ	478/484 (99%)	472 (99%)	6 (1%)	0	100	100
11	EO	469/484 (97%)	456 (97%)	13 (3%)	0	100	100
11	EP	478/484 (99%)	471 (98%)	7 (2%)	0	100	100
11	EQ	478/484 (99%)	472 (99%)	6 (1%)	0	100	100
11	FO	469/484 (97%)	456 (97%)	13 (3%)	0	100	100
11	FP	478/484 (99%)	471 (98%)	7 (2%)	0	100	100
11	FQ	478/484 (99%)	472 (99%)	6 (1%)	0	100	100
All	All	42750/59523 (72%)	41494 (97%)	1256 (3%)	0	100	100

There are no Ramachandran outliers to report.

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	AA	650/1306 (50%)	650 (100%)	0	100	100
1	AB	647/1306 (50%)	647 (100%)	0	100	100
1	AC	623/1306 (48%)	623 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	BA	650/1306 (50%)	650 (100%)	0	100	100
1	BB	647/1306 (50%)	647 (100%)	0	100	100
1	BC	623/1306 (48%)	623 (100%)	0	100	100
1	CA	650/1306 (50%)	650 (100%)	0	100	100
1	CB	647/1306 (50%)	647 (100%)	0	100	100
1	CC	623/1306 (48%)	623 (100%)	0	100	100
1	DA	650/1306 (50%)	650 (100%)	0	100	100
1	DB	647/1306 (50%)	647 (100%)	0	100	100
1	DC	623/1306 (48%)	623 (100%)	0	100	100
1	EA	650/1306 (50%)	650 (100%)	0	100	100
1	EB	647/1306 (50%)	647 (100%)	0	100	100
1	EC	623/1306 (48%)	623 (100%)	0	100	100
1	FA	650/1306 (50%)	650 (100%)	0	100	100
1	FB	647/1306 (50%)	647 (100%)	0	100	100
1	FC	623/1306 (48%)	623 (100%)	0	100	100
2	AD	1000/1195 (84%)	998 (100%)	2 (0%)	87	89
2	BD	1000/1195 (84%)	998 (100%)	2 (0%)	87	89
2	CD	1000/1195 (84%)	998 (100%)	2 (0%)	87	89
2	DD	1000/1195 (84%)	998 (100%)	2 (0%)	87	89
2	ED	1000/1195 (84%)	998 (100%)	2 (0%)	87	89
2	FD	1000/1195 (84%)	998 (100%)	2 (0%)	87	89
3	AE	95/143 (66%)	95 (100%)	0	100	100
3	AF	95/143 (66%)	95 (100%)	0	100	100
3	AG	95/143 (66%)	95 (100%)	0	100	100
3	BE	95/143 (66%)	95 (100%)	0	100	100
3	BF	95/143 (66%)	95 (100%)	0	100	100
3	BG	95/143 (66%)	95 (100%)	0	100	100
3	CE	95/143 (66%)	95 (100%)	0	100	100
3	CF	95/143 (66%)	95 (100%)	0	100	100
3	CG	95/143 (66%)	95 (100%)	0	100	100
3	DE	95/143 (66%)	95 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	DF	95/143 (66%)	95 (100%)	0	100	100
3	DG	95/143 (66%)	95 (100%)	0	100	100
3	EE	95/143 (66%)	95 (100%)	0	100	100
3	EF	95/143 (66%)	95 (100%)	0	100	100
3	EG	95/143 (66%)	95 (100%)	0	100	100
3	FE	95/143 (66%)	95 (100%)	0	100	100
3	FF	95/143 (66%)	95 (100%)	0	100	100
3	FG	95/143 (66%)	95 (100%)	0	100	100
4	AH	1071/1075 (100%)	1070 (100%)	1 (0%)	88	91
4	BH	1071/1075 (100%)	1070 (100%)	1 (0%)	88	91
4	CH	1071/1075 (100%)	1070 (100%)	1 (0%)	88	91
4	DH	1071/1075 (100%)	1070 (100%)	1 (0%)	88	91
4	EH	1071/1075 (100%)	1070 (100%)	1 (0%)	88	91
4	FH	1071/1075 (100%)	1070 (100%)	1 (0%)	88	91
5	AJ	471/475 (99%)	471 (100%)	0	100	100
5	CJ	471/475 (99%)	471 (100%)	0	100	100
5	EJ	471/475 (99%)	471 (100%)	0	100	100
6	AL	32/38 (84%)	32 (100%)	0	100	100
6	CL	32/38 (84%)	32 (100%)	0	100	100
6	EL	32/38 (84%)	32 (100%)	0	100	100
7	AI	123/132 (93%)	123 (100%)	0	100	100
7	BI	123/132 (93%)	123 (100%)	0	100	100
7	CI	123/132 (93%)	123 (100%)	0	100	100
7	DI	123/132 (93%)	123 (100%)	0	100	100
7	EI	123/132 (93%)	123 (100%)	0	100	100
7	FI	123/132 (93%)	123 (100%)	0	100	100
8	AK	209/211 (99%)	209 (100%)	0	100	100
8	BK	209/211 (99%)	209 (100%)	0	100	100
8	CK	209/211 (99%)	209 (100%)	0	100	100
8	DK	209/211 (99%)	209 (100%)	0	100	100
8	EK	209/211 (99%)	209 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
8	FK	209/211 (99%)	209 (100%)	0	100	100
9	AM	143/153 (94%)	143 (100%)	0	100	100
9	BM	143/153 (94%)	143 (100%)	0	100	100
9	CM	143/153 (94%)	143 (100%)	0	100	100
9	DM	143/153 (94%)	143 (100%)	0	100	100
9	EM	143/153 (94%)	143 (100%)	0	100	100
9	FM	143/153 (94%)	143 (100%)	0	100	100
10	AN	125/126 (99%)	125 (100%)	0	100	100
10	BN	125/126 (99%)	125 (100%)	0	100	100
10	CN	125/126 (99%)	125 (100%)	0	100	100
10	DN	125/126 (99%)	125 (100%)	0	100	100
10	EN	125/126 (99%)	125 (100%)	0	100	100
10	FN	125/126 (99%)	125 (100%)	0	100	100
11	AO	392/402 (98%)	392 (100%)	0	100	100
11	AP	398/402 (99%)	398 (100%)	0	100	100
11	AQ	398/402 (99%)	398 (100%)	0	100	100
11	BO	392/402 (98%)	392 (100%)	0	100	100
11	BP	398/402 (99%)	398 (100%)	0	100	100
11	BQ	398/402 (99%)	398 (100%)	0	100	100
11	CO	392/402 (98%)	392 (100%)	0	100	100
11	CP	398/402 (99%)	398 (100%)	0	100	100
11	CQ	398/402 (99%)	398 (100%)	0	100	100
11	DO	392/402 (98%)	392 (100%)	0	100	100
11	DP	398/402 (99%)	398 (100%)	0	100	100
11	DQ	398/402 (99%)	398 (100%)	0	100	100
11	EO	392/402 (98%)	392 (100%)	0	100	100
11	EP	398/402 (99%)	398 (100%)	0	100	100
11	EQ	398/402 (99%)	398 (100%)	0	100	100
11	FO	392/402 (98%)	392 (100%)	0	100	100
11	FP	398/402 (99%)	398 (100%)	0	100	100
11	FQ	398/402 (99%)	398 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
All	All	37893/52209 (73%)	37875 (100%)	18 (0%)	100	100

All (18) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	AD	303	TYR
2	AD	720	LEU
4	AH	999	VAL
2	BD	303	TYR
2	BD	720	LEU
4	BH	999	VAL
2	CD	303	TYR
2	CD	720	LEU
4	CH	999	VAL
2	DD	303	TYR
2	DD	720	LEU
4	DH	999	VAL
2	ED	303	TYR
2	ED	720	LEU
4	EH	999	VAL
2	FD	303	TYR
2	FD	720	LEU
4	FH	999	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (571) such sidechains are listed below:

Mol	Chain	Res	Type
1	AA	35	GLN
1	AA	107	GLN
1	AA	114	GLN
1	AA	131	ASN
1	AA	206	GLN
1	AA	260	GLN
1	AA	488	ASN
1	AA	490	ASN
1	AA	499	HIS
1	AA	556	GLN
1	AA	801	GLN
1	AA	808	GLN
1	AB	35	GLN
1	AB	114	GLN

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Mol	Chain	Res	Type
1	AB	131	ASN
1	AB	218	GLN
1	AB	276	ASN
1	AB	324	GLN
1	AB	397	GLN
1	AB	404	ASN
1	AB	809	ASN
1	AB	905	GLN
1	AC	114	GLN
1	AC	136	ASN
1	AC	154	GLN
1	AC	276	ASN
1	AC	289	ASN
1	AC	332	GLN
1	AC	388	ASN
1	AC	488	ASN
1	AC	490	ASN
1	AC	494	ASN
1	AC	499	HIS
1	AC	517	ASN
1	AC	779	ASN
1	AC	808	GLN
1	AC	815	HIS
2	AD	165	GLN
2	AD	298	HIS
2	AD	322	ASN
2	AD	342	GLN
2	AD	378	GLN
2	AD	456	GLN
2	AD	563	HIS
2	AD	682	HIS
2	AD	717	GLN
2	AD	733	ASN
2	AD	787	GLN
2	AD	825	HIS
2	AD	826	HIS
2	AD	848	GLN
2	AD	1311	HIS
2	AD	1320	ASN
3	AE	33	ASN
3	AF	33	ASN
3	AG	33	ASN

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Mol	Chain	Res	Type
4	AH	226	GLN
4	AH	243	GLN
4	AH	287	GLN
4	AH	381	GLN
4	AH	511	GLN
4	AH	731	GLN
4	AH	763	ASN
4	AH	1137	ASN
4	AH	1169	ASN
5	AJ	185	GLN
5	AJ	272	HIS
5	AJ	385	GLN
5	AJ	439	ASN
5	AJ	452	ASN
5	AJ	527	ASN
5	AJ	560	ASN
5	AJ	562	GLN
6	AL	47	GLN
7	AI	112	ASN
7	AI	121	GLN
8	AK	108	HIS
8	AK	136	GLN
8	AK	138	ASN
8	AK	163	GLN
8	AK	164	ASN
9	AM	102	HIS
10	AN	44	GLN
11	AO	47	HIS
11	AO	115	GLN
11	AO	183	GLN
11	AO	423	GLN
11	AO	479	HIS
11	AP	47	HIS
11	AP	108	HIS
11	AP	135	ASN
11	AP	188	GLN
11	AP	207	ASN
11	AP	423	GLN
11	AQ	47	HIS
11	AQ	108	HIS
11	AQ	135	ASN
11	AQ	207	ASN

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Mol	Chain	Res	Type
11	AQ	423	GLN
1	BA	35	GLN
1	BA	107	GLN
1	BA	114	GLN
1	BA	131	ASN
1	BA	206	GLN
1	BA	260	GLN
1	BA	488	ASN
1	BA	490	ASN
1	BA	499	HIS
1	BA	556	GLN
1	BA	801	GLN
1	BA	808	GLN
1	BA	809	ASN
1	BA	810	ASN
1	BB	35	GLN
1	BB	114	GLN
1	BB	131	ASN
1	BB	218	GLN
1	BB	226	ASN
1	BB	276	ASN
1	BB	324	GLN
1	BB	397	GLN
1	BB	404	ASN
1	BB	809	ASN
1	BB	905	GLN
1	BC	136	ASN
1	BC	154	GLN
1	BC	276	ASN
1	BC	289	ASN
1	BC	332	GLN
1	BC	388	ASN
1	BC	488	ASN
1	BC	490	ASN
1	BC	494	ASN
1	BC	499	HIS
1	BC	517	ASN
1	BC	779	ASN
1	BC	808	GLN
1	BC	815	HIS
2	BD	298	HIS
2	BD	342	GLN

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Mol	Chain	Res	Type
2	BD	378	GLN
2	BD	456	GLN
2	BD	472	GLN
2	BD	563	HIS
2	BD	620	HIS
2	BD	682	HIS
2	BD	717	GLN
2	BD	733	ASN
2	BD	787	GLN
2	BD	825	HIS
2	BD	826	HIS
2	BD	848	GLN
2	BD	1311	HIS
2	BD	1320	ASN
3	BE	33	ASN
3	BF	33	ASN
3	BG	33	ASN
4	BH	226	GLN
4	BH	243	GLN
4	BH	287	GLN
4	BH	381	GLN
4	BH	511	GLN
4	BH	731	GLN
4	BH	763	ASN
4	BH	1137	ASN
7	BI	59	ASN
7	BI	61	GLN
7	BI	112	ASN
7	BI	121	GLN
8	BK	46	GLN
8	BK	108	HIS
10	BN	44	GLN
11	BO	47	HIS
11	BO	115	GLN
11	BO	183	GLN
11	BO	207	ASN
11	BO	423	GLN
11	BO	479	HIS
11	BP	47	HIS
11	BP	108	HIS
11	BP	135	ASN
11	BP	188	GLN

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Mol	Chain	Res	Type
11	BP	207	ASN
11	BP	423	GLN
11	BQ	47	HIS
11	BQ	108	HIS
11	BQ	135	ASN
11	BQ	188	GLN
11	BQ	207	ASN
11	BQ	423	GLN
1	CA	35	GLN
1	CA	107	GLN
1	CA	114	GLN
1	CA	131	ASN
1	CA	206	GLN
1	CA	260	GLN
1	CA	394	ASN
1	CA	488	ASN
1	CA	490	ASN
1	CA	499	HIS
1	CA	556	GLN
1	CA	801	GLN
1	CA	808	GLN
1	CA	809	ASN
1	CB	35	GLN
1	CB	114	GLN
1	CB	131	ASN
1	CB	218	GLN
1	CB	276	ASN
1	CB	324	GLN
1	CB	397	GLN
1	CB	404	ASN
1	CB	809	ASN
1	CB	905	GLN
1	CC	114	GLN
1	CC	136	ASN
1	CC	154	GLN
1	CC	289	ASN
1	CC	332	GLN
1	CC	388	ASN
1	CC	488	ASN
1	CC	490	ASN
1	CC	494	ASN
1	CC	499	HIS

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Mol	Chain	Res	Type
1	CC	517	ASN
1	CC	779	ASN
1	CC	808	GLN
1	CC	815	HIS
2	CD	98	ASN
2	CD	165	GLN
2	CD	298	HIS
2	CD	342	GLN
2	CD	378	GLN
2	CD	456	GLN
2	CD	563	HIS
2	CD	620	HIS
2	CD	682	HIS
2	CD	717	GLN
2	CD	733	ASN
2	CD	787	GLN
2	CD	803	GLN
2	CD	825	HIS
2	CD	826	HIS
2	CD	848	GLN
2	CD	1311	HIS
2	CD	1320	ASN
3	CE	2	ASN
3	CE	33	ASN
3	CF	33	ASN
3	CG	33	ASN
4	CH	226	GLN
4	CH	243	GLN
4	CH	287	GLN
4	CH	381	GLN
4	CH	511	GLN
4	CH	591	GLN
4	CH	731	GLN
4	CH	763	ASN
4	CH	1137	ASN
5	CJ	185	GLN
5	CJ	272	HIS
5	CJ	385	GLN
5	CJ	439	ASN
5	CJ	452	ASN
5	CJ	527	ASN
5	CJ	556	ASN

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Mol	Chain	Res	Type
5	CJ	560	ASN
5	CJ	562	GLN
6	CL	47	GLN
7	CI	112	ASN
7	CI	121	GLN
8	CK	108	HIS
8	CK	164	ASN
9	CM	102	HIS
10	CN	44	GLN
11	CO	47	HIS
11	CO	183	GLN
11	CO	423	GLN
11	CO	479	HIS
11	CP	47	HIS
11	CP	188	GLN
11	CP	207	ASN
11	CP	423	GLN
11	CQ	47	HIS
11	CQ	108	HIS
11	CQ	135	ASN
11	CQ	188	GLN
11	CQ	207	ASN
11	CQ	423	GLN
1	DA	18	GLN
1	DA	35	GLN
1	DA	107	GLN
1	DA	114	GLN
1	DA	131	ASN
1	DA	206	GLN
1	DA	260	GLN
1	DA	394	ASN
1	DA	488	ASN
1	DA	490	ASN
1	DA	499	HIS
1	DA	556	GLN
1	DA	561	ASN
1	DA	801	GLN
1	DA	808	GLN
1	DB	35	GLN
1	DB	114	GLN
1	DB	131	ASN
1	DB	218	GLN

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Mol	Chain	Res	Type
1	DB	276	ASN
1	DB	324	GLN
1	DB	397	GLN
1	DB	404	ASN
1	DB	809	ASN
1	DB	905	GLN
1	DC	114	GLN
1	DC	136	ASN
1	DC	154	GLN
1	DC	289	ASN
1	DC	332	GLN
1	DC	388	ASN
1	DC	488	ASN
1	DC	490	ASN
1	DC	494	ASN
1	DC	499	HIS
1	DC	517	ASN
1	DC	779	ASN
1	DC	808	GLN
1	DC	815	HIS
2	DD	165	GLN
2	DD	298	HIS
2	DD	322	ASN
2	DD	342	GLN
2	DD	378	GLN
2	DD	456	GLN
2	DD	563	HIS
2	DD	682	HIS
2	DD	717	GLN
2	DD	787	GLN
2	DD	825	HIS
2	DD	826	HIS
2	DD	848	GLN
2	DD	1311	HIS
2	DD	1320	ASN
3	DE	33	ASN
3	DF	33	ASN
4	DH	226	GLN
4	DH	243	GLN
4	DH	287	GLN
4	DH	381	GLN
4	DH	511	GLN

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Mol	Chain	Res	Type
4	DH	549	GLN
4	DH	591	GLN
4	DH	731	GLN
4	DH	780	GLN
4	DH	1137	ASN
7	DI	59	ASN
7	DI	112	ASN
7	DI	121	GLN
8	DK	46	GLN
9	DM	102	HIS
10	DN	44	GLN
10	DN	46	HIS
11	DO	47	HIS
11	DO	115	GLN
11	DO	183	GLN
11	DO	423	GLN
11	DO	479	HIS
11	DP	47	HIS
11	DP	108	HIS
11	DP	135	ASN
11	DP	188	GLN
11	DP	207	ASN
11	DP	423	GLN
11	DQ	47	HIS
11	DQ	108	HIS
11	DQ	135	ASN
11	DQ	188	GLN
11	DQ	207	ASN
11	DQ	423	GLN
1	EA	35	GLN
1	EA	107	GLN
1	EA	114	GLN
1	EA	131	ASN
1	EA	206	GLN
1	EA	260	GLN
1	EA	394	ASN
1	EA	488	ASN
1	EA	490	ASN
1	EA	499	HIS
1	EA	556	GLN
1	EA	801	GLN
1	EA	808	GLN

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Mol	Chain	Res	Type
1	EA	809	ASN
1	EB	35	GLN
1	EB	114	GLN
1	EB	131	ASN
1	EB	276	ASN
1	EB	324	GLN
1	EB	397	GLN
1	EB	404	ASN
1	EB	809	ASN
1	EB	905	GLN
1	EC	114	GLN
1	EC	136	ASN
1	EC	276	ASN
1	EC	289	ASN
1	EC	332	GLN
1	EC	388	ASN
1	EC	488	ASN
1	EC	490	ASN
1	EC	494	ASN
1	EC	499	HIS
1	EC	517	ASN
1	EC	779	ASN
1	EC	808	GLN
1	EC	815	HIS
2	ED	165	GLN
2	ED	298	HIS
2	ED	322	ASN
2	ED	342	GLN
2	ED	378	GLN
2	ED	456	GLN
2	ED	563	HIS
2	ED	682	HIS
2	ED	717	GLN
2	ED	733	ASN
2	ED	787	GLN
2	ED	803	GLN
2	ED	825	HIS
2	ED	826	HIS
2	ED	848	GLN
2	ED	1311	HIS
2	ED	1320	ASN
3	EE	2	ASN

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Mol	Chain	Res	Type
3	EE	33	ASN
3	EF	33	ASN
3	EG	33	ASN
4	EH	226	GLN
4	EH	243	GLN
4	EH	287	GLN
4	EH	381	GLN
4	EH	511	GLN
4	EH	731	GLN
4	EH	763	ASN
4	EH	1137	ASN
5	EJ	185	GLN
5	EJ	272	HIS
5	EJ	385	GLN
5	EJ	389	ASN
5	EJ	439	ASN
5	EJ	452	ASN
5	EJ	527	ASN
5	EJ	560	ASN
5	EJ	562	GLN
6	EL	47	GLN
7	EI	59	ASN
7	EI	61	GLN
7	EI	112	ASN
7	EI	121	GLN
8	EK	108	HIS
8	EK	164	ASN
9	EM	102	HIS
10	EN	44	GLN
11	EO	47	HIS
11	EO	183	GLN
11	EO	207	ASN
11	EO	423	GLN
11	EO	479	HIS
11	EP	47	HIS
11	EP	108	HIS
11	EP	135	ASN
11	EP	188	GLN
11	EP	207	ASN
11	EP	423	GLN
11	EQ	47	HIS
11	EQ	108	HIS

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Mol	Chain	Res	Type
11	EQ	135	ASN
11	EQ	188	GLN
11	EQ	207	ASN
11	EQ	423	GLN
1	FA	35	GLN
1	FA	107	GLN
1	FA	114	GLN
1	FA	131	ASN
1	FA	206	GLN
1	FA	260	GLN
1	FA	488	ASN
1	FA	490	ASN
1	FA	499	HIS
1	FA	556	GLN
1	FA	561	ASN
1	FA	801	GLN
1	FA	808	GLN
1	FA	809	ASN
1	FB	35	GLN
1	FB	114	GLN
1	FB	131	ASN
1	FB	218	GLN
1	FB	276	ASN
1	FB	324	GLN
1	FB	404	ASN
1	FB	809	ASN
1	FB	905	GLN
1	FC	114	GLN
1	FC	136	ASN
1	FC	154	GLN
1	FC	276	ASN
1	FC	289	ASN
1	FC	332	GLN
1	FC	388	ASN
1	FC	488	ASN
1	FC	490	ASN
1	FC	494	ASN
1	FC	499	HIS
1	FC	517	ASN
1	FC	779	ASN
1	FC	808	GLN
1	FC	815	HIS

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Mol	Chain	Res	Type
2	FD	298	HIS
2	FD	322	ASN
2	FD	342	GLN
2	FD	378	GLN
2	FD	456	GLN
2	FD	563	HIS
2	FD	620	HIS
2	FD	682	HIS
2	FD	717	GLN
2	FD	733	ASN
2	FD	787	GLN
2	FD	803	GLN
2	FD	825	HIS
2	FD	826	HIS
2	FD	848	GLN
2	FD	1311	HIS
2	FD	1320	ASN
3	FE	33	ASN
3	FF	33	ASN
3	FG	33	ASN
4	FH	226	GLN
4	FH	243	GLN
4	FH	287	GLN
4	FH	381	GLN
4	FH	511	GLN
4	FH	731	GLN
4	FH	1137	ASN
7	FI	59	ASN
7	FI	112	ASN
7	FI	121	GLN
8	FK	46	GLN
8	FK	108	HIS
8	FK	136	GLN
8	FK	138	ASN
9	FM	102	HIS
10	FN	44	GLN
11	FO	47	HIS
11	FO	183	GLN
11	FO	207	ASN
11	FO	423	GLN
11	FO	479	HIS
11	FP	47	HIS

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Mol	Chain	Res	Type
11	FP	108	HIS
11	FP	135	ASN
11	FP	188	GLN
11	FP	207	ASN
11	FP	423	GLN
11	FQ	47	HIS
11	FQ	108	HIS
11	FQ	135	ASN
11	FQ	188	GLN
11	FQ	207	ASN
11	FQ	423	GLN

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.

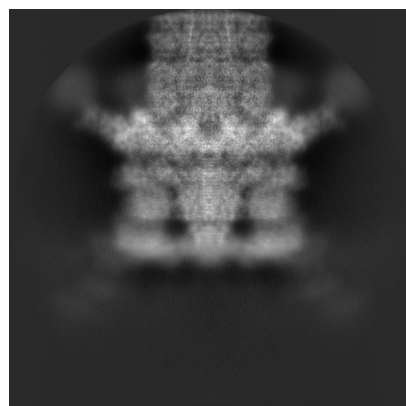
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-12029. These allow visual inspection of the internal detail of the map and identification of artifacts.

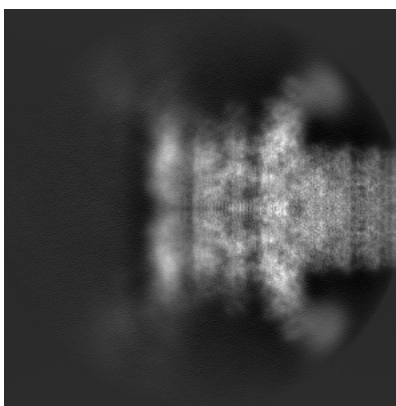
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

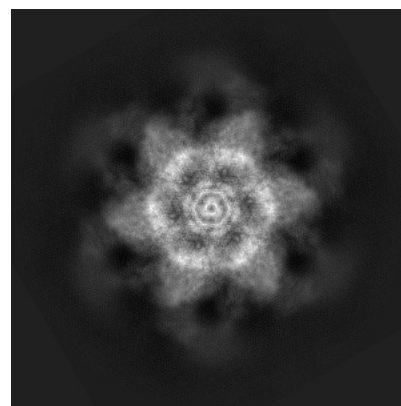
6.1.1 Primary map



X

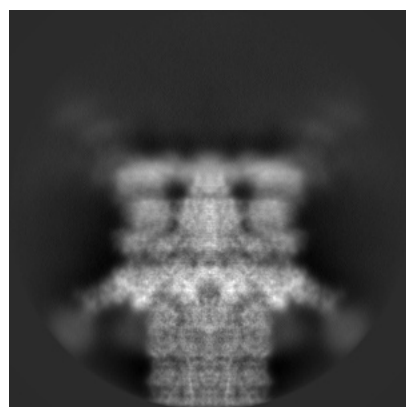


Y

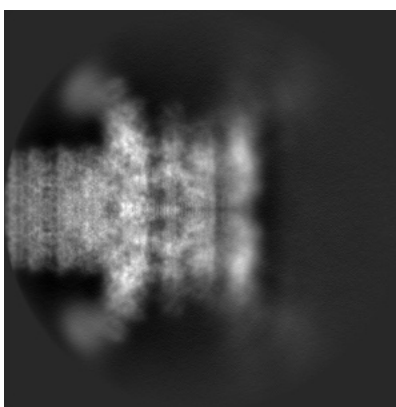


Z

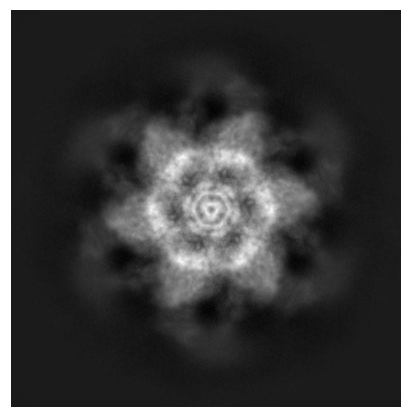
6.1.2 Raw map



X



Y

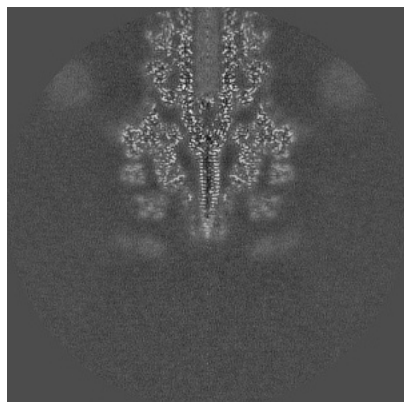


Z

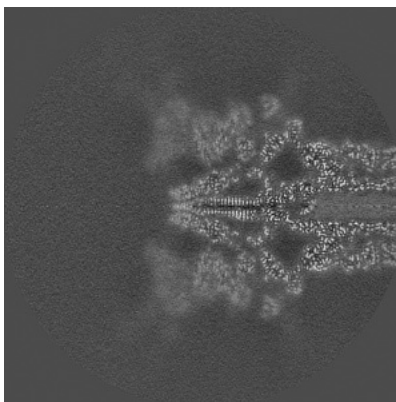
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

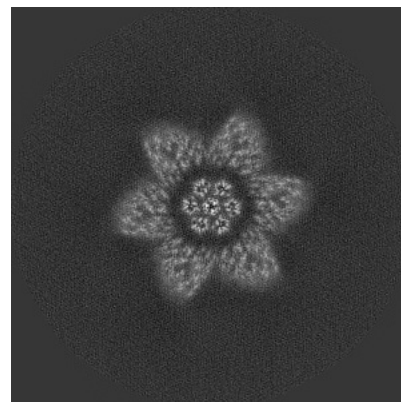
6.2.1 Primary map



X Index: 256

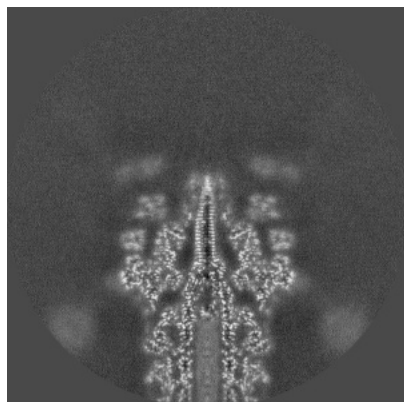


Y Index: 256

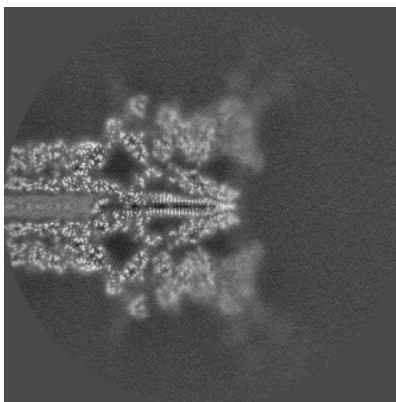


Z Index: 256

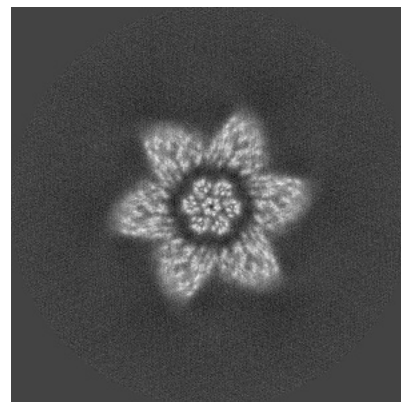
6.2.2 Raw map



X Index: 256



Y Index: 256

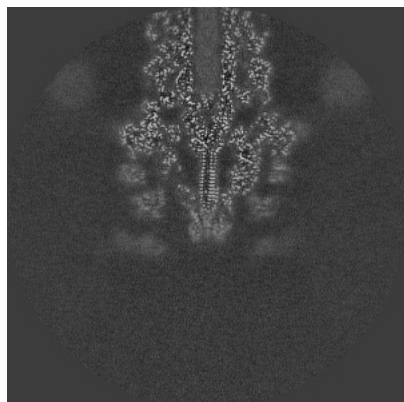


Z Index: 256

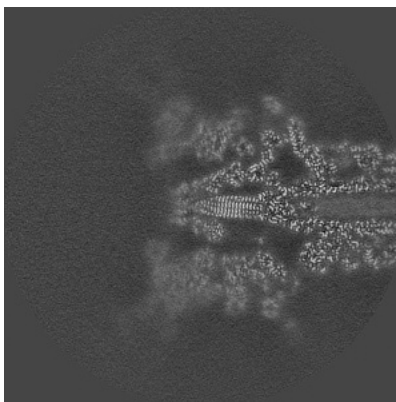
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

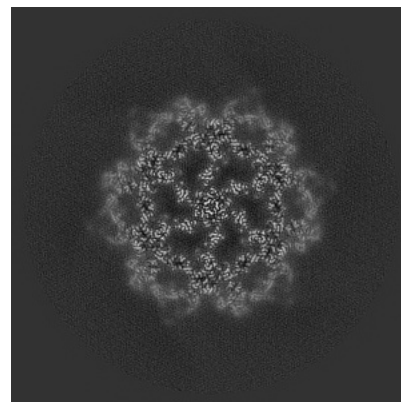
6.3.1 Primary map



X Index: 252

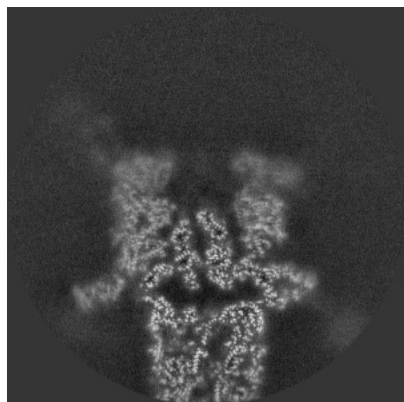


Y Index: 249

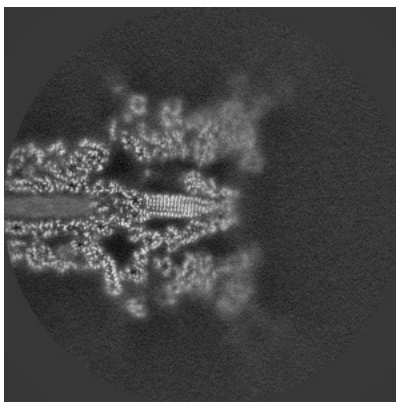


Z Index: 349

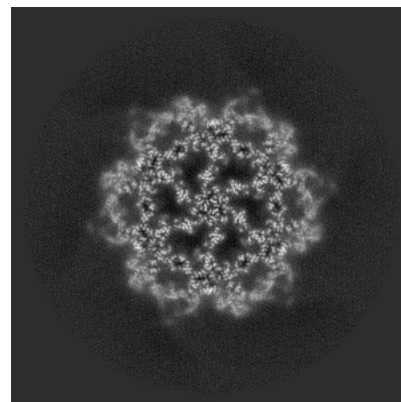
6.3.2 Raw map



X Index: 216



Y Index: 262

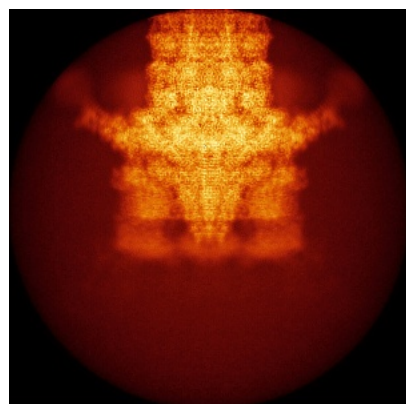


Z Index: 162

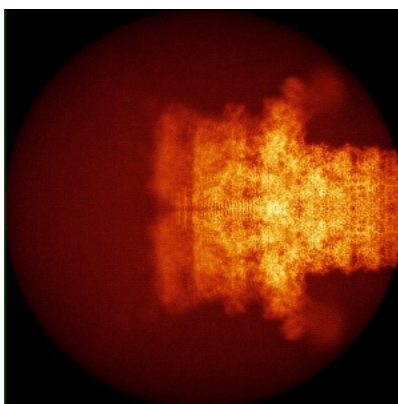
The images above show the largest variance slices of the map in three orthogonal directions.

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

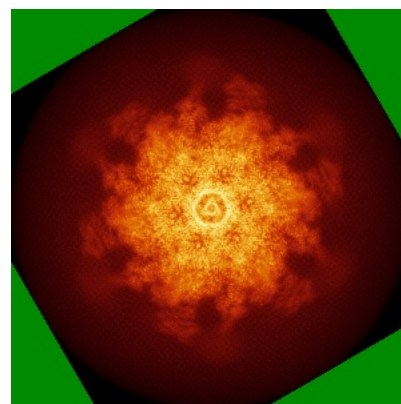
6.4.1 Primary map



X

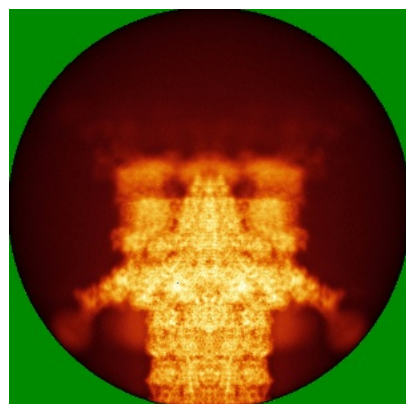


Y

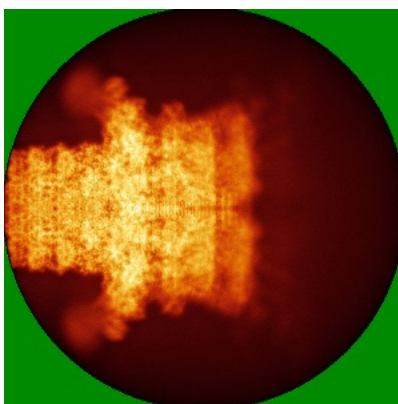


Z

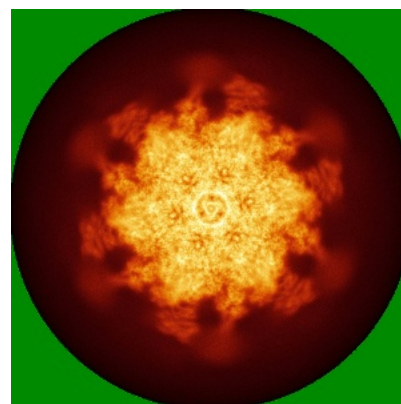
6.4.2 Raw map



X



Y

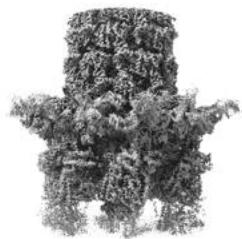


Z

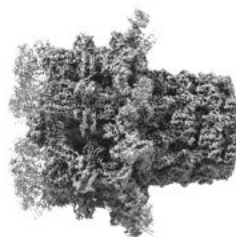
The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



X



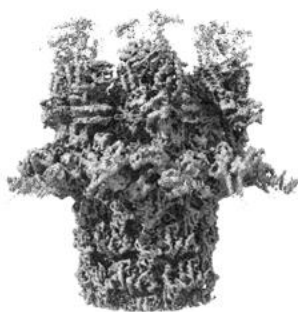
Y



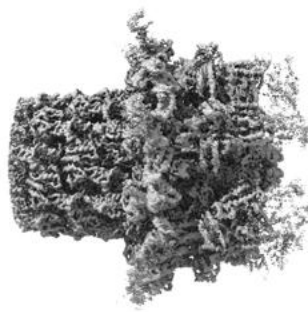
Z

The images above show the 3D surface view of the map at the recommended contour level 0.0275. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

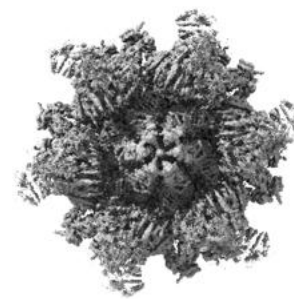
6.5.2 Raw map



X



Y



Z

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.

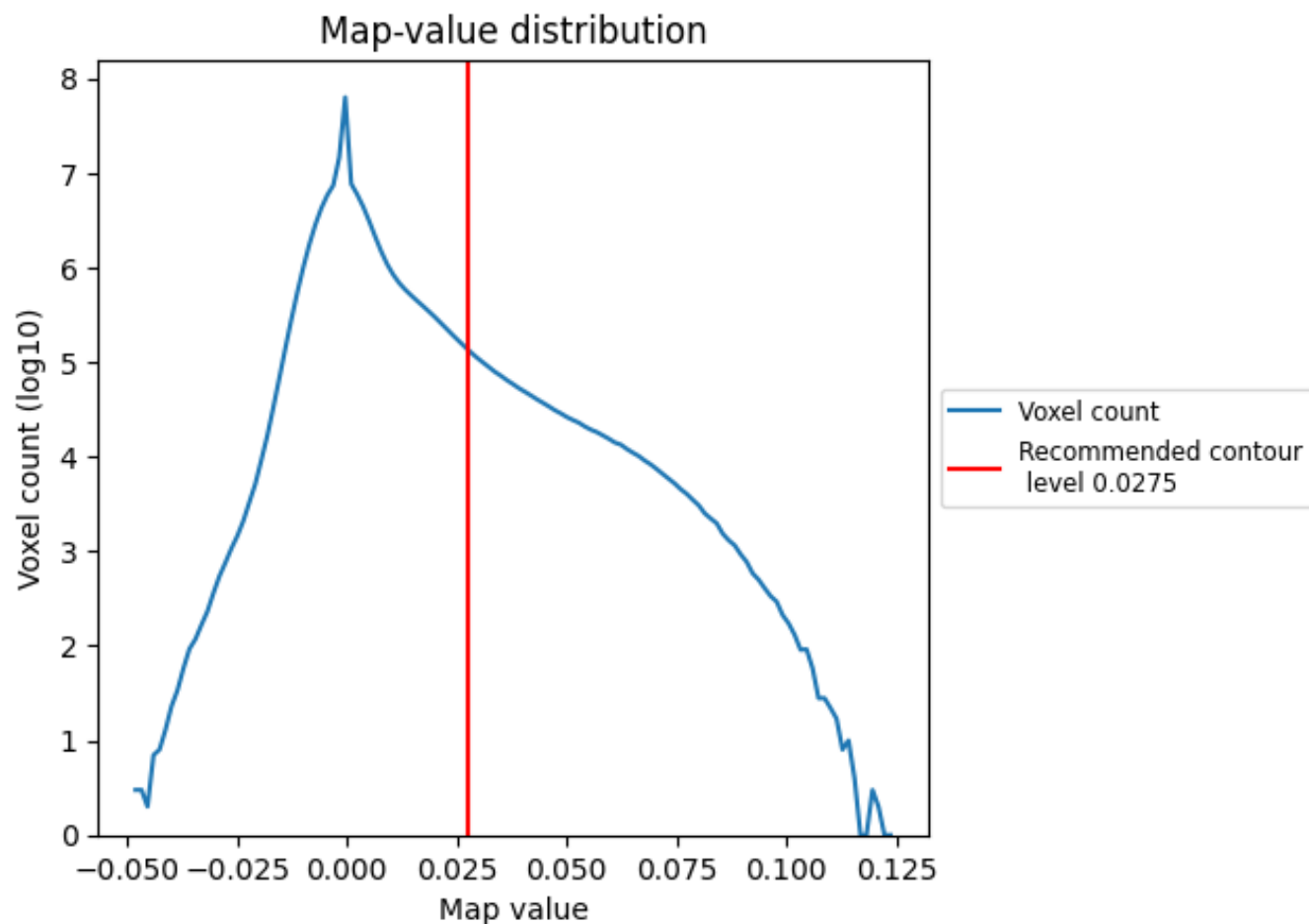
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

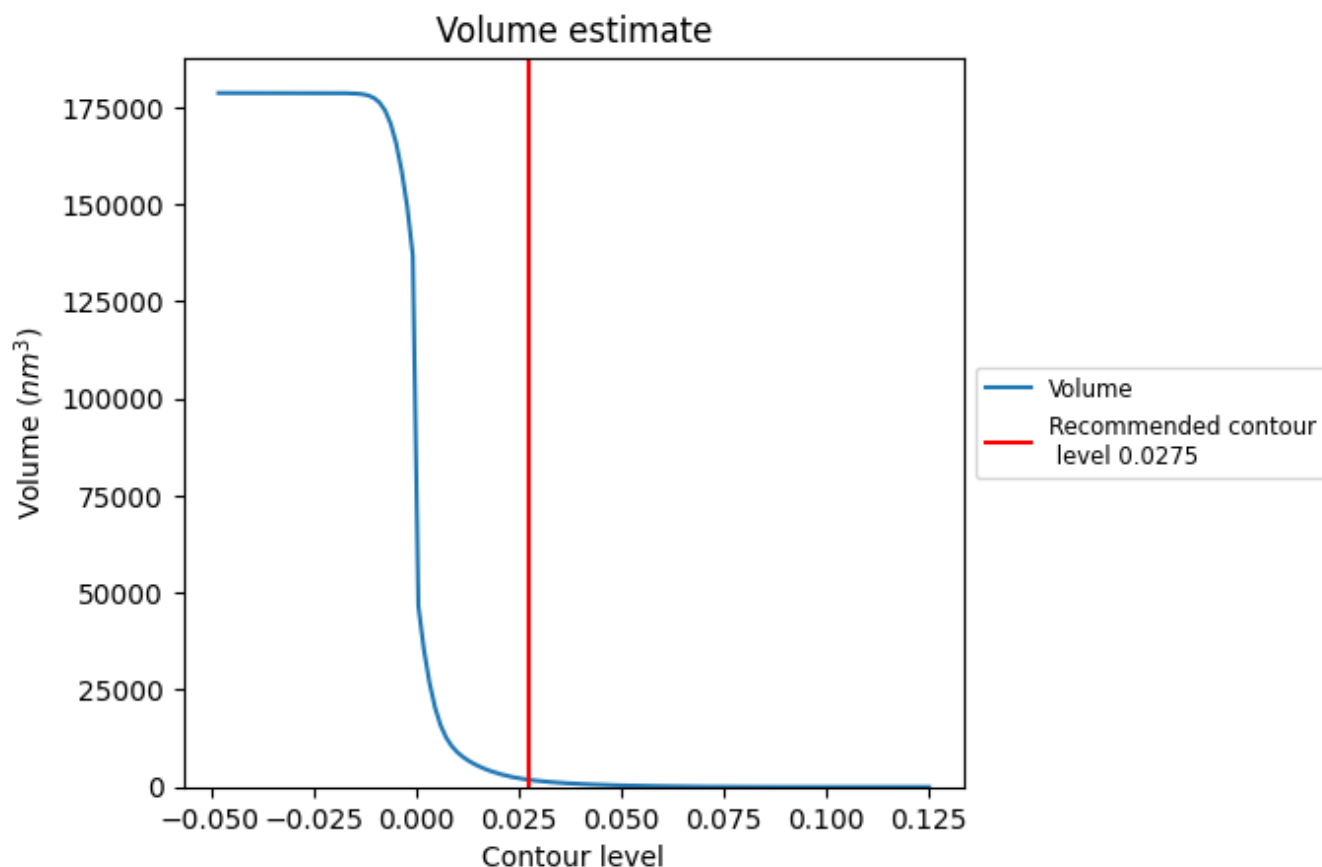
This section contains the results of statistical analysis of the map.

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.

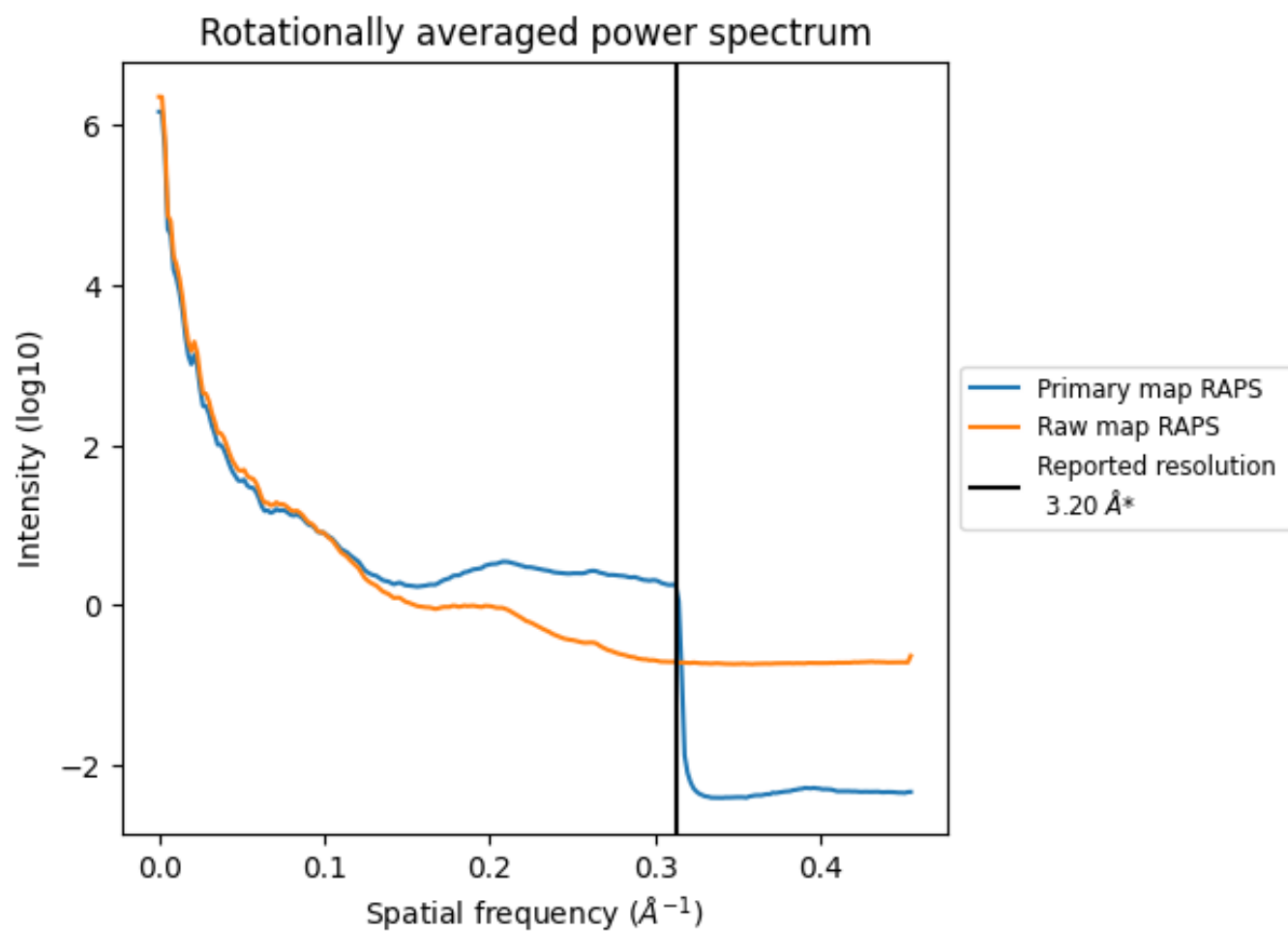
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1849 nm^3 ; this corresponds to an approximate mass of 1670 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 ⓘ

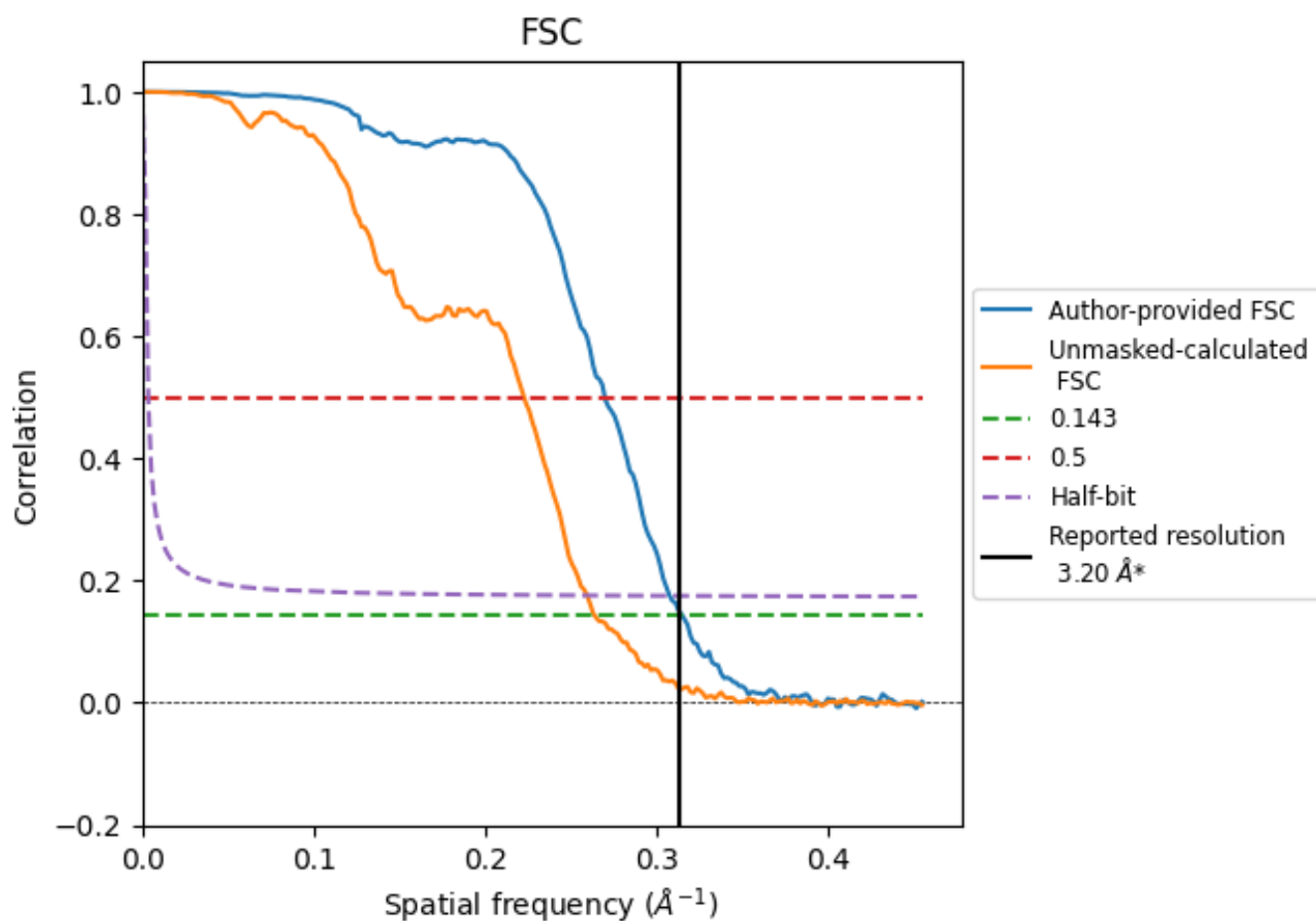


*Reported resolution corresponds to spatial frequency of 0.312 Å⁻¹

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 $0.312 \text{ \AA}^{-1}$

8.2 Resolution estimates [i](#)

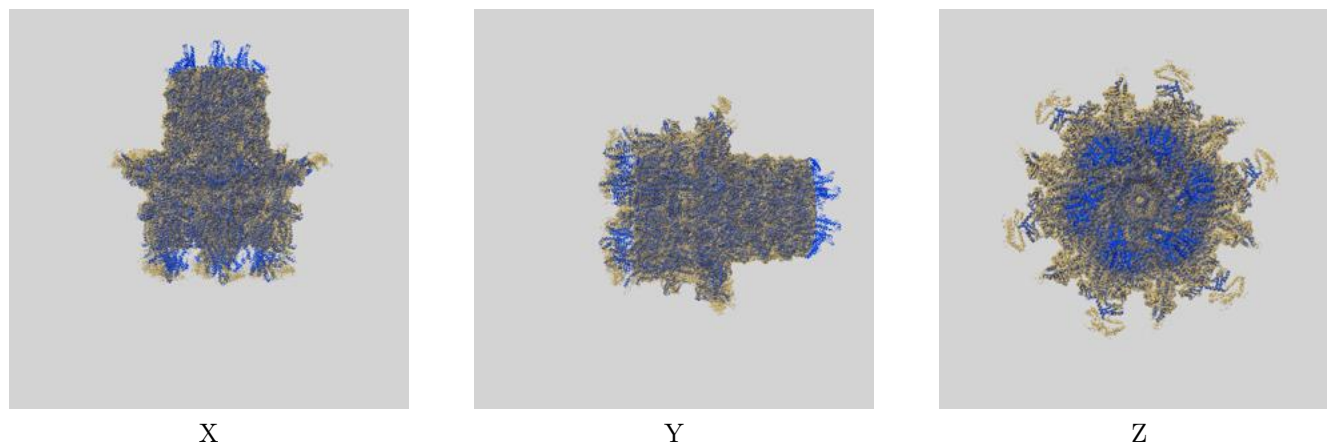
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.20	-	-
Author-provided FSC curve	3.18	3.71	3.25
Unmasked-calculated*	3.79	4.49	3.86

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 3.79 differs from the reported value 3.2 by more than 10 %

9 Map-model fit [i](#)

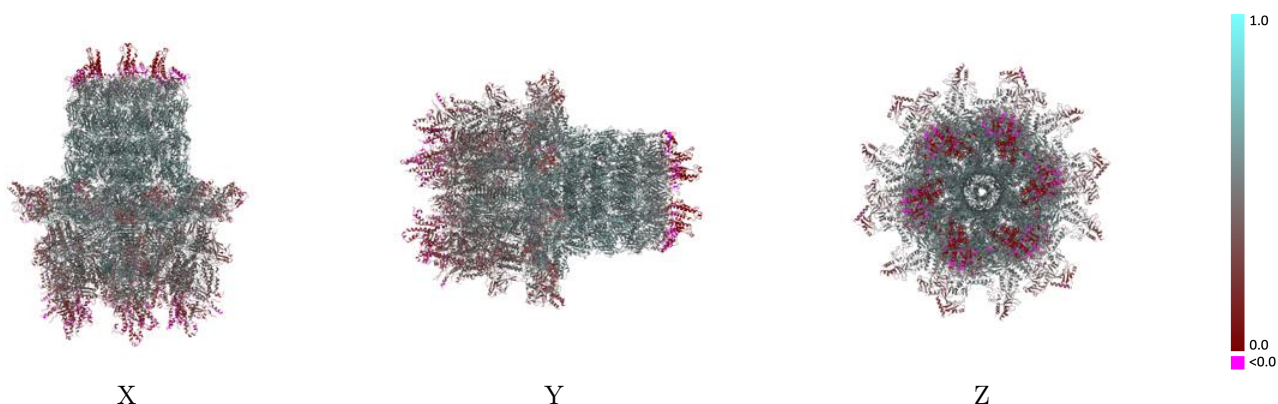
This section contains information regarding the fit between EMDB map EMD-12029 and PDB model 7B5H. Per-residue inclusion information can be found in [section 3](#) on [page 13](#).

9.1 Map-model overlay [i](#)



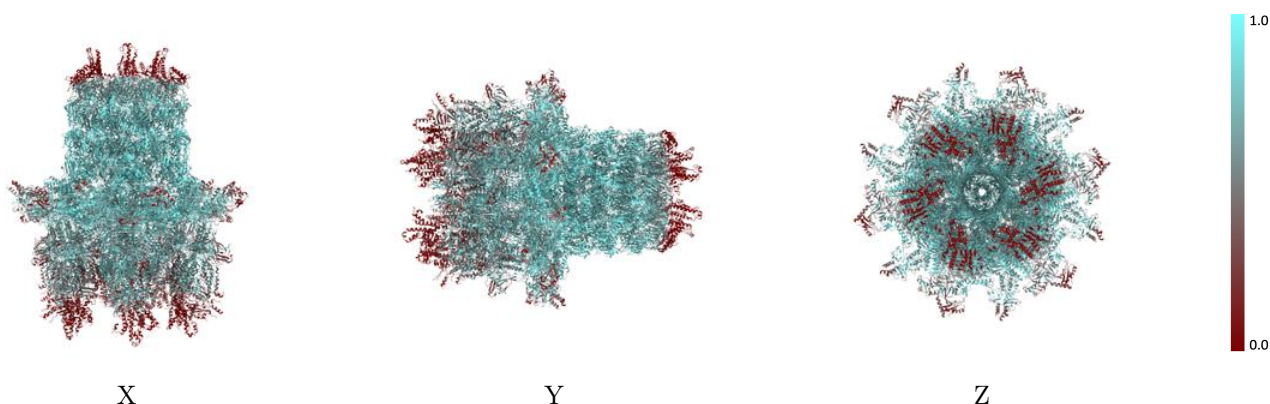
The images above show the 3D surface view of the map at the recommended contour level 0.0275 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



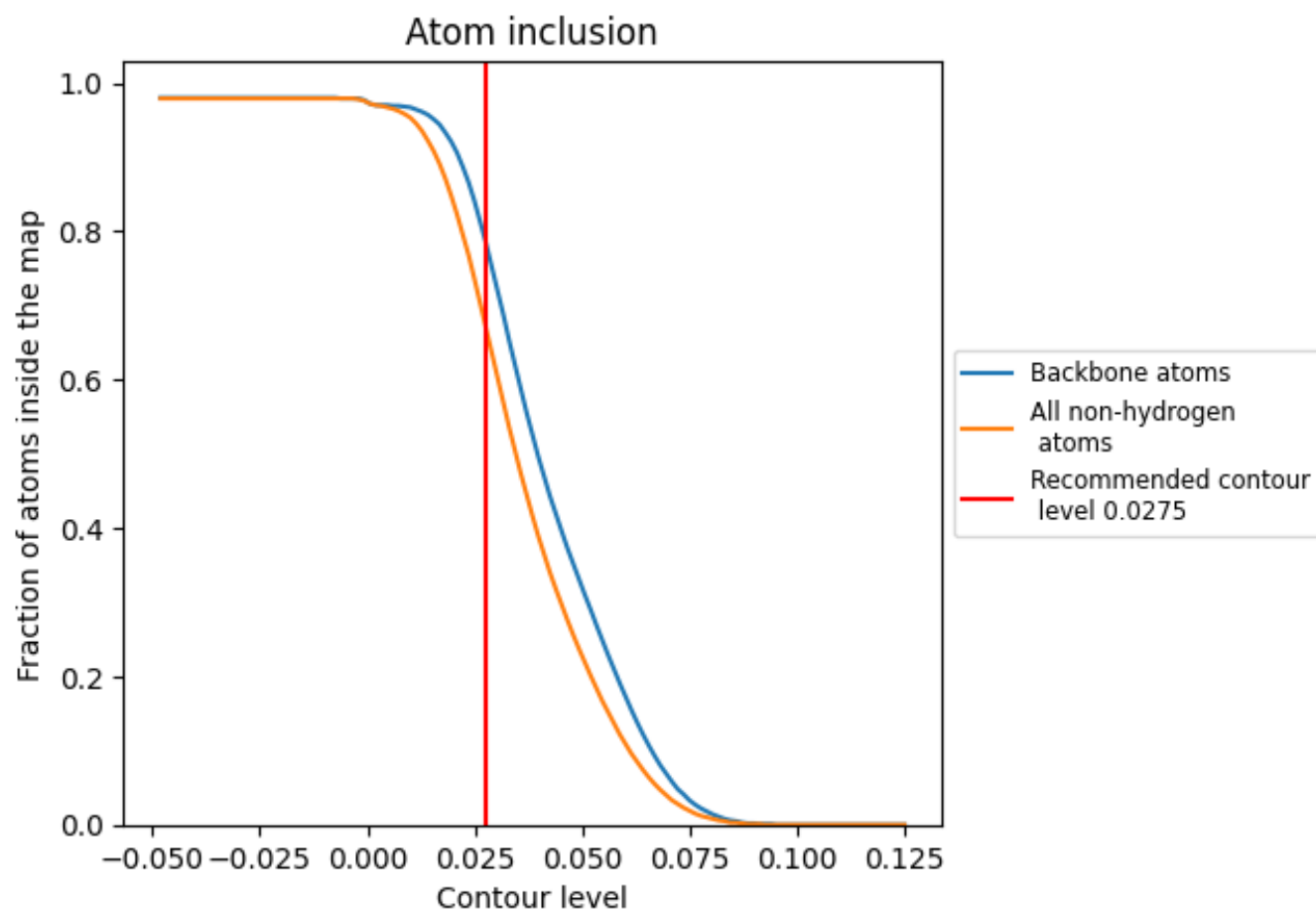
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.0275).

9.4 Atom inclusion [i](#)



At the recommended contour level, 79% of all backbone atoms, 67% 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 (0.0275) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.6730	 0.4590
AA	 0.4530	 0.3810
AB	 0.4450	 0.3390
AC	 0.4950	 0.3720
AD	 0.7380	 0.4730
AE	 0.6960	 0.4270
AF	 0.6710	 0.3870
AG	 0.6320	 0.3600
AH	 0.8620	 0.5540
AI	 0.8570	 0.5680
AJ	 0.9080	 0.5950
AK	 0.8780	 0.5810
AL	 0.6760	 0.5460
AM	 0.8330	 0.5670
AN	 0.6940	 0.4980
AO	 0.8640	 0.5660
AP	 0.7940	 0.5380
AQ	 0.3400	 0.2650
BA	 0.4520	 0.3790
BB	 0.4460	 0.3510
BC	 0.5030	 0.3730
BD	 0.7350	 0.4740
BE	 0.6640	 0.4080
BF	 0.6760	 0.3740
BG	 0.6400	 0.3790
BH	 0.8580	 0.5500
BI	 0.8610	 0.5640
BK	 0.8780	 0.5810
BM	 0.8230	 0.5660
BN	 0.6860	 0.5010
BO	 0.8520	 0.5610
BP	 0.7880	 0.5350
BQ	 0.3450	 0.2620
CA	 0.4560	 0.3780
CB	 0.4430	 0.3390



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Chain	Atom inclusion	Q-score
CC	 0.4940	 0.3720
CD	 0.7400	 0.4730
CE	 0.6920	 0.4310
CF	 0.6840	 0.3920
CG	 0.6390	 0.3620
CH	 0.8610	 0.5510
CI	 0.8560	 0.5660
CJ	 0.9060	 0.5930
CK	 0.8740	 0.5790
CL	 0.6730	 0.5420
CM	 0.8340	 0.5690
CN	 0.6880	 0.5010
CO	 0.8670	 0.5640
CP	 0.7940	 0.5370
CQ	 0.3370	 0.2650
DA	 0.4550	 0.3760
DB	 0.4480	 0.3510
DC	 0.5070	 0.3740
DD	 0.7390	 0.4740
DE	 0.6740	 0.4100
DF	 0.6710	 0.3740
DG	 0.6400	 0.3760
DH	 0.8600	 0.5500
DI	 0.8600	 0.5640
DK	 0.8820	 0.5850
DM	 0.8250	 0.5700
DN	 0.6830	 0.5050
DO	 0.8550	 0.5620
DP	 0.7950	 0.5340
DQ	 0.3460	 0.2640
EA	 0.4530	 0.3810
EB	 0.4410	 0.3380
EC	 0.4930	 0.3710
ED	 0.7410	 0.4710
EE	 0.6990	 0.4290
EF	 0.6790	 0.3890
EG	 0.6350	 0.3600
EH	 0.8610	 0.5510
EI	 0.8500	 0.5670
EJ	 0.9080	 0.5930
EK	 0.8780	 0.5820
EL	 0.6760	 0.5470

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Chain	Atom inclusion	Q-score
EM	 0.8300	 0.5720
EN	 0.6900	 0.5020
EO	 0.8620	 0.5640
EP	 0.7920	 0.5360
EQ	 0.3340	 0.2640
FA	 0.4540	 0.3790
FB	 0.4450	 0.3500
FC	 0.5070	 0.3740
FD	 0.7330	 0.4740
FE	 0.6650	 0.4120
FF	 0.6690	 0.3790
FG	 0.6350	 0.3770
FH	 0.8590	 0.5520
FI	 0.8610	 0.5630
FK	 0.8790	 0.5810
FM	 0.8180	 0.5670
FN	 0.6800	 0.5020
FO	 0.8550	 0.5630
FP	 0.7940	 0.5360
FQ	 0.3430	 0.2630