



Full wwPDB EM Validation Report ⓘ

Mar 20, 2026 – 05:08 AM UTC

PDB ID : 7S78 / pdb_00007s78
EMDB ID : EMD-24881
Title : Structure of a cell-entry defective human adenovirus provides insights into precursor proteins and capsid maturation
Authors : Reddy, V.S.; Yu, X.
Deposited on : 2021-09-15
Resolution : 3.72 Å(reported)
Based on initial model : 3IYN

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

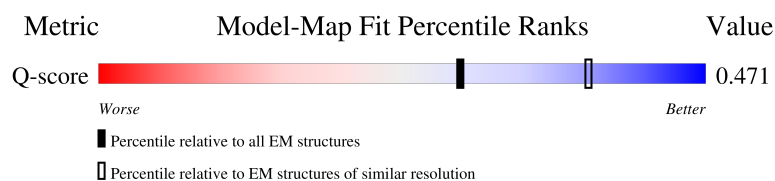
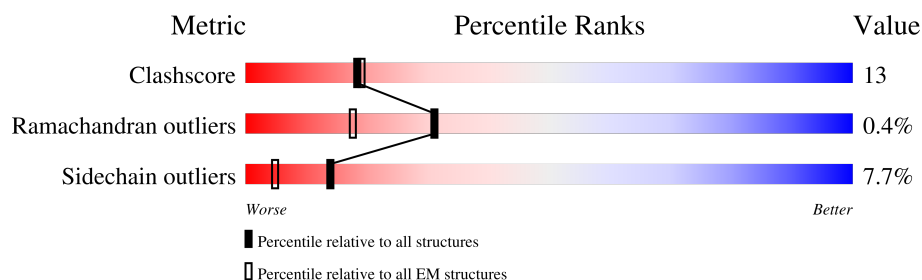
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.72 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.



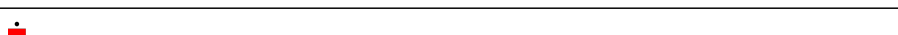
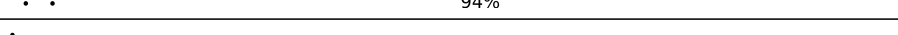
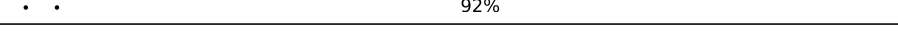
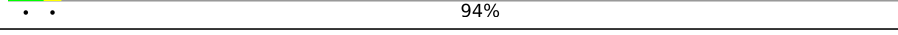
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	10474 (3.22 - 4.22)

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

Mol	Chain	Length	Quality of chain
1	A	952	
1	B	952	
1	C	952	
1	D	952	

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Mol	Chain	Length	Quality of chain
1	E	952	 62%30% . . .
1	F	952	 63%29%6% . .
1	G	952	 66%27% . .
1	H	952	 65%29% . .
1	I	952	 65%27%5% .
1	J	952	 63%30%5% . .
1	K	952	 65%28% . . .
1	L	952	 62%31% . .
2	N	571	 45%27%8% . 18%
3	M	585	 44%15% . 39%
4	P	140	 11%64%25% . . .
4	Q	140	 12%70%17%6%6%
4	R	140	 6%58%12% . 28%
4	S	140	 53%16% . 31%
5	U	227	 44%23%6%27%
5	V	227	 7%46%26%8%19%
6	0	250	 94% . .
6	1	250	 9%11% . 77%
6	2	250	 92% . .
6	3	250	 14%8% . 76%
6	4	250	 94% . .
6	W	250	 5%5% . . 86%
6	X	250	 19%9% . 69%
6	Y	250	 6%11%6% . 76%
6	Z	250	 5% . . . 90%

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Mol	Chain	Length	Quality of chain
7	5	16	50% 100%
8	6	10	20% 100%

2 Entry composition

There are 8 unique types of molecules in this entry. The entry contains 104715 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 Hexon protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	929	Total	C	N	O	S	0	0
			7427	4718	1258	1415	36		
1	B	929	Total	C	N	O	S	0	0
			7429	4719	1258	1416	36		
1	C	933	Total	C	N	O	S	0	0
			7456	4736	1262	1422	36		
1	D	929	Total	C	N	O	S	0	0
			7427	4718	1258	1415	36		
1	E	926	Total	C	N	O	S	0	0
			7408	4708	1255	1409	36		
1	F	929	Total	C	N	O	S	0	0
			7430	4721	1258	1415	36		
1	G	931	Total	C	N	O	S	0	0
			7441	4726	1260	1419	36		
1	H	933	Total	C	N	O	S	0	0
			7455	4736	1262	1420	37		
1	I	927	Total	C	N	O	S	0	0
			7417	4713	1256	1412	36		
1	J	928	Total	C	N	O	S	0	0
			7419	4713	1256	1414	36		
1	K	931	Total	C	N	O	S	0	0
			7442	4728	1260	1418	36		
1	L	929	Total	C	N	O	S	0	0
			7427	4718	1258	1415	36		

- Molecule 2 is a protein called Penton protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	N	466	Total	C	N	O	S	0	0
			3734	2365	646	711	12		

- Molecule 3 is a protein called Pre-hexon-linking protein IIIa.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	M	359	Total	C	N	O	S	0	0
			2813	1752	517	535	9		

- Molecule 4 is a protein called Hexon-interlacing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	P	134	Total	C	N	O	S	0	0
			972	600	171	199	2		
4	Q	131	Total	C	N	O	S	0	0
			952	587	168	195	2		
4	R	101	Total	C	N	O	S	0	0
			751	470	128	151	2		
4	S	97	Total	C	N	O	S	0	0
			727	448	128	149	2		

- Molecule 5 is a protein called Pre-hexon-linking protein VIII.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	U	165	Total	C	N	O	S	0	0
			1268	797	223	243	5		
5	V	184	Total	C	N	O	S	0	0
			1414	890	248	272	4		

- Molecule 6 is a protein called Pre-protein VI.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	W	35	Total	C	N	O	S	0	0
			262	165	48	47	2		
6	X	78	Total	C	N	O	S	0	0
			577	361	107	106	3		
6	Y	61	Total	C	N	O	S	0	0
			485	305	90	87	3		
6	Z	25	Total	C	N	O	S	0	0
			179	109	35	34	1		
6	0	16	Total	C	N	O	S	0	0
			114	68	23	22	1		
6	1	57	Total	C	N	O	S	0	0
			449	279	84	83	3		
6	2	19	Total	C	N	O	S	0	0
			133	81	26	25	1		
6	3	60	Total	C	N	O	S	0	0
			471	293	87	88	3		

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Mol	Chain	Residues	Atoms					AltConf	Trace
6	4	15	Total	C	N	O	S	0	0
			106	64	21	20	1		

- Molecule 7 is a protein called Unknown-1.

Mol	Chain	Residues	Atoms				AltConf	Trace
7	5	16	Total	C	N	O	0	0
			80	48	16	16		

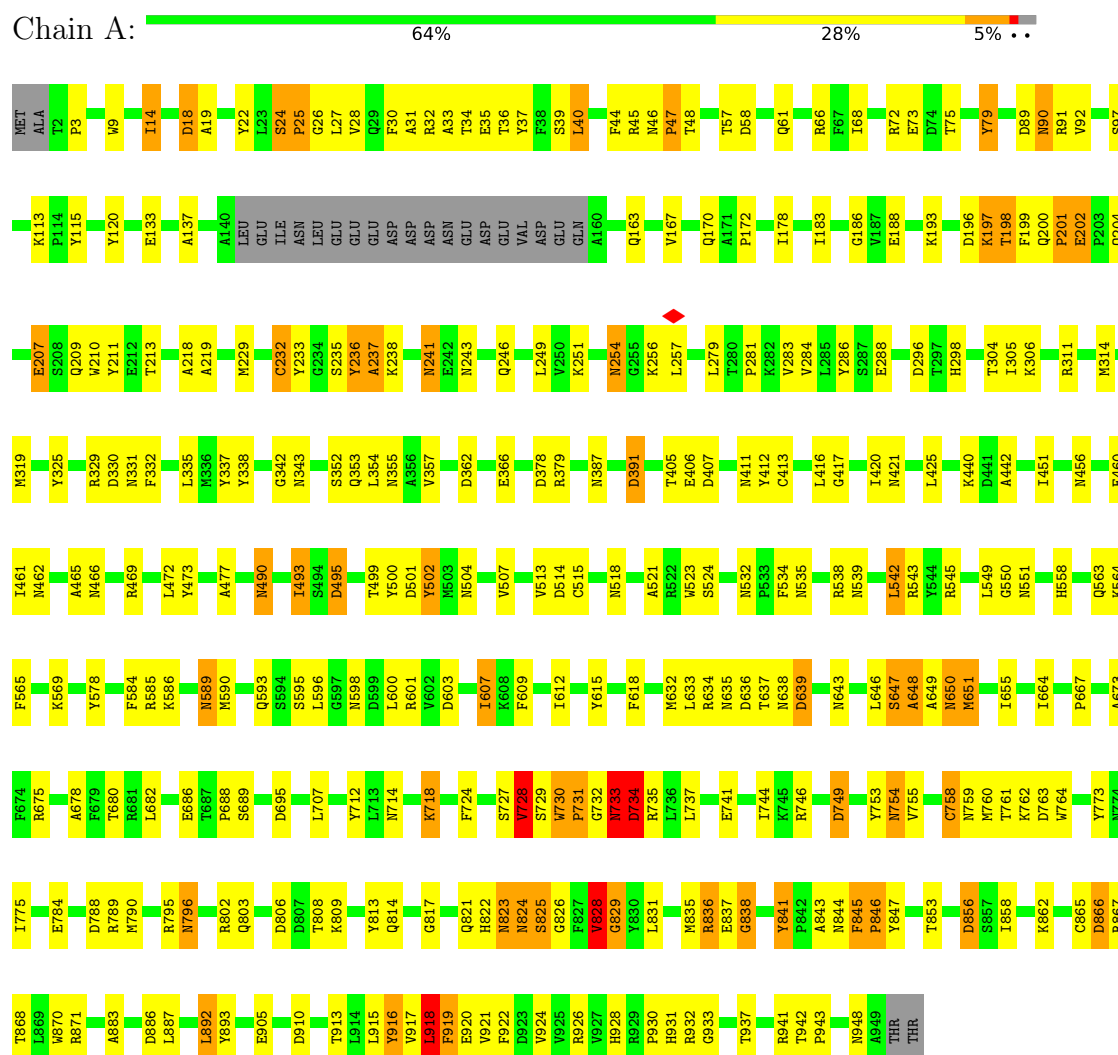
- Molecule 8 is a protein called Unknown-2.

Mol	Chain	Residues	Atoms				AltConf	Trace
8	6	10	Total	C	N	O	0	0
			50	30	10	10		

3 Residue-property plots

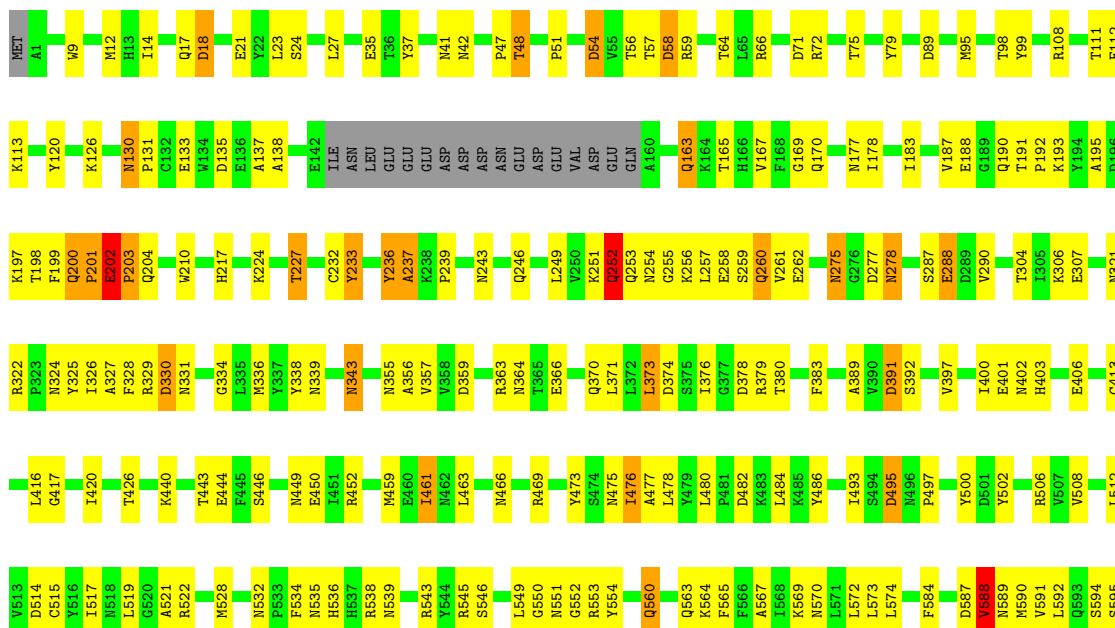
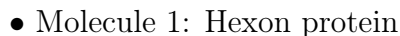
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

• Molecule 1: Hexon protein

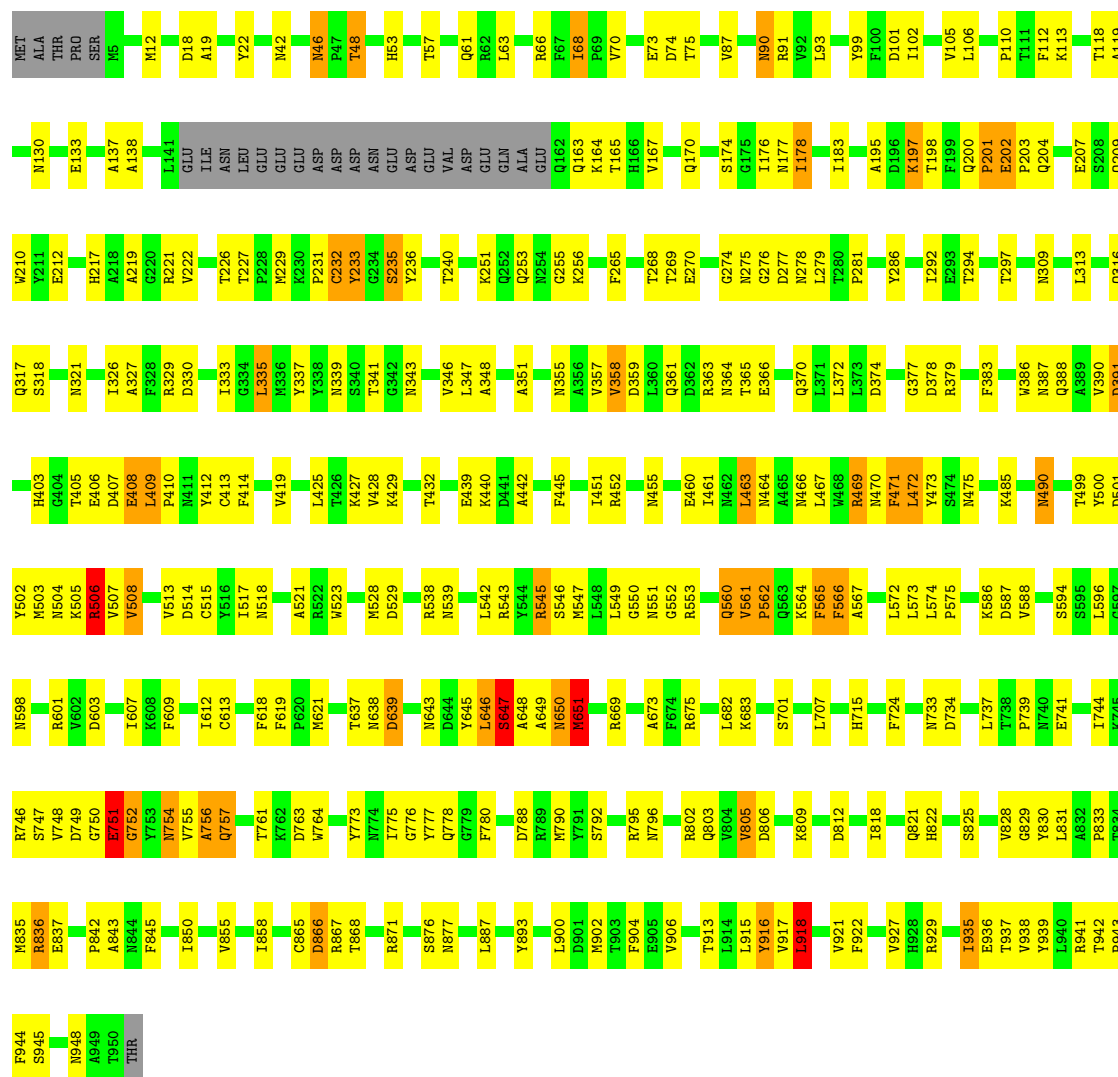


• Molecule 1: Hexon protein

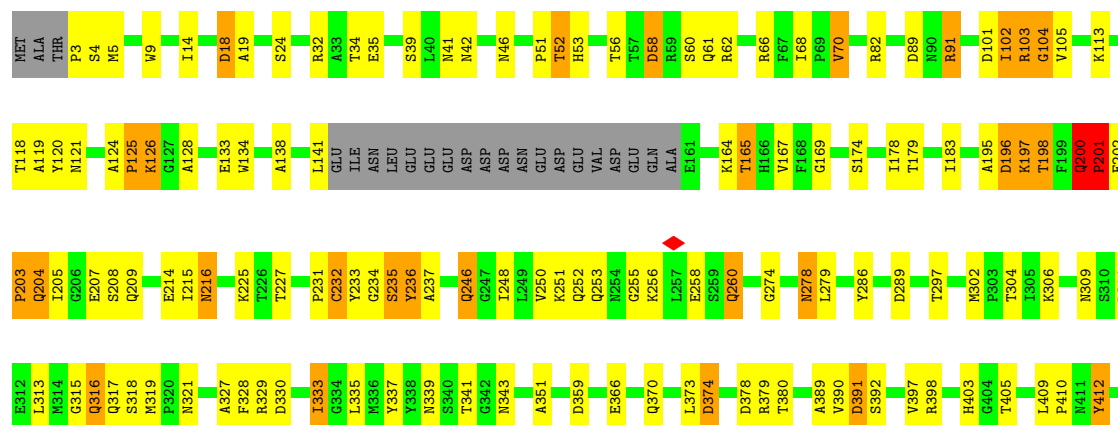


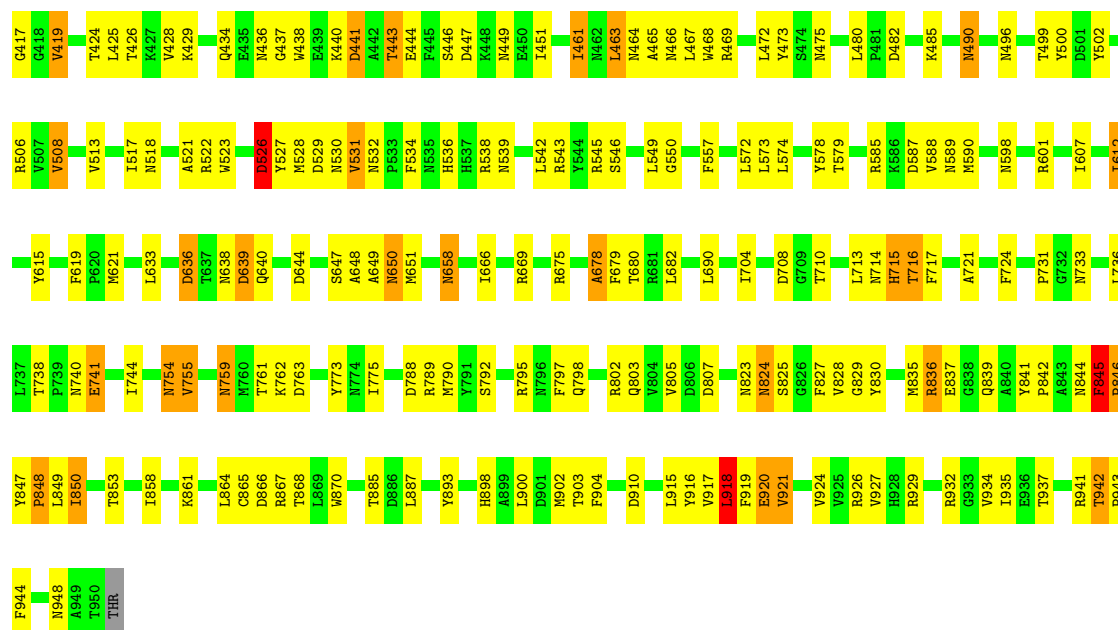






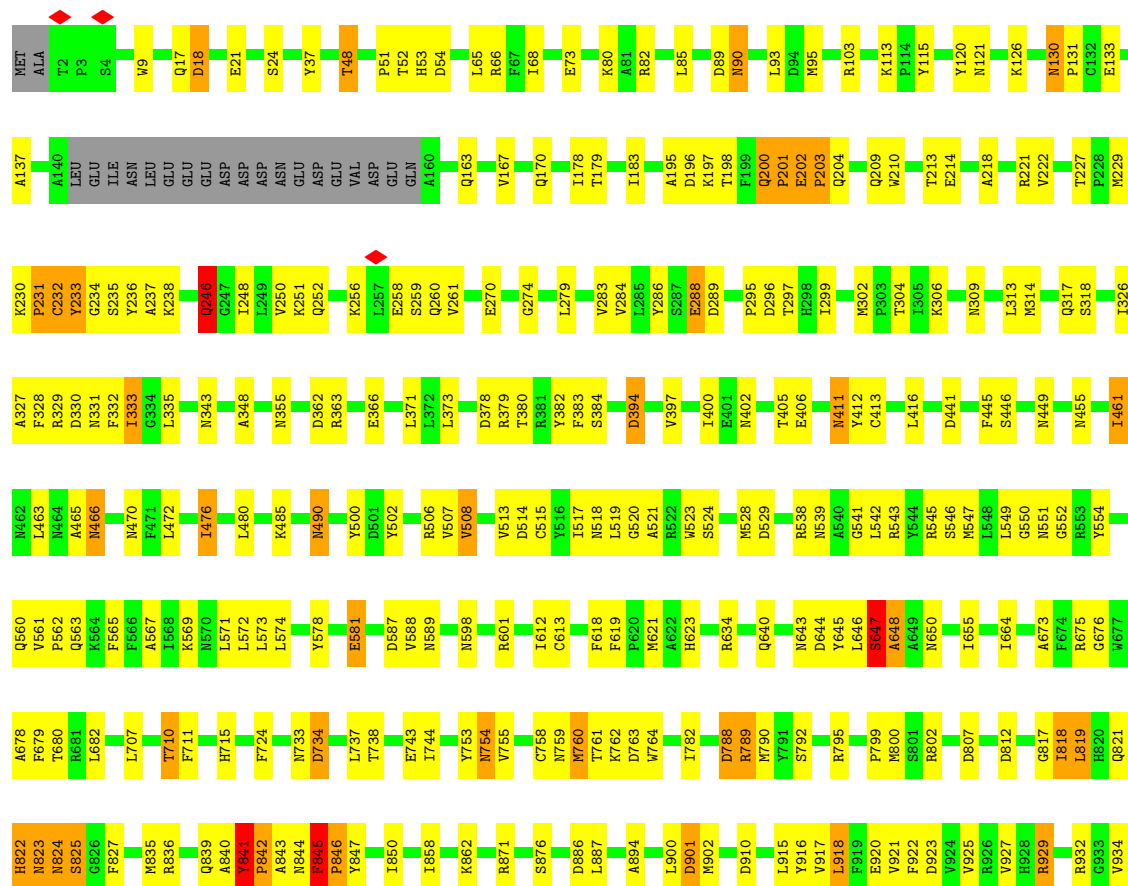
Chain F: 63% 29% 6% ..

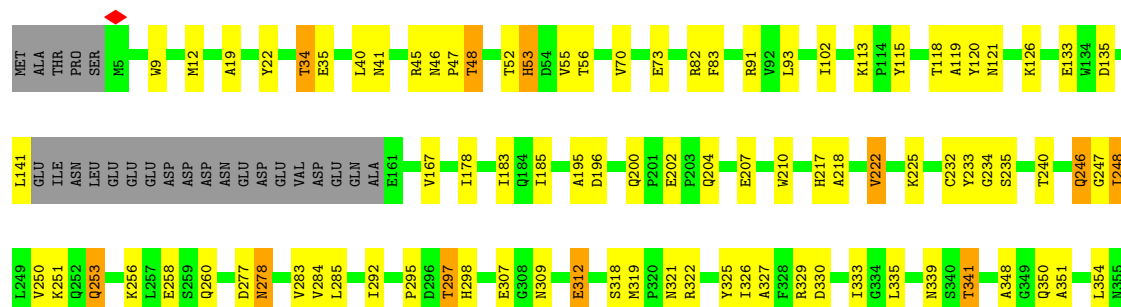


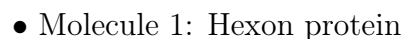


• Molecule 1: Hexon protein

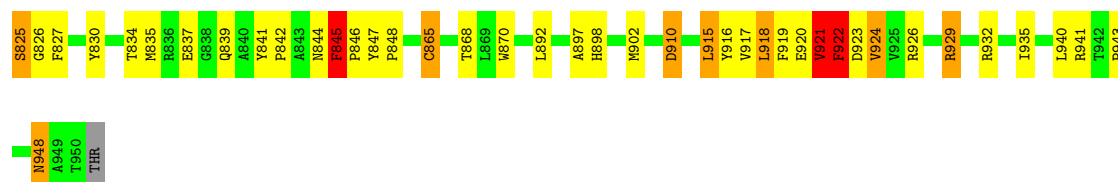
Chain G: 66% 27%





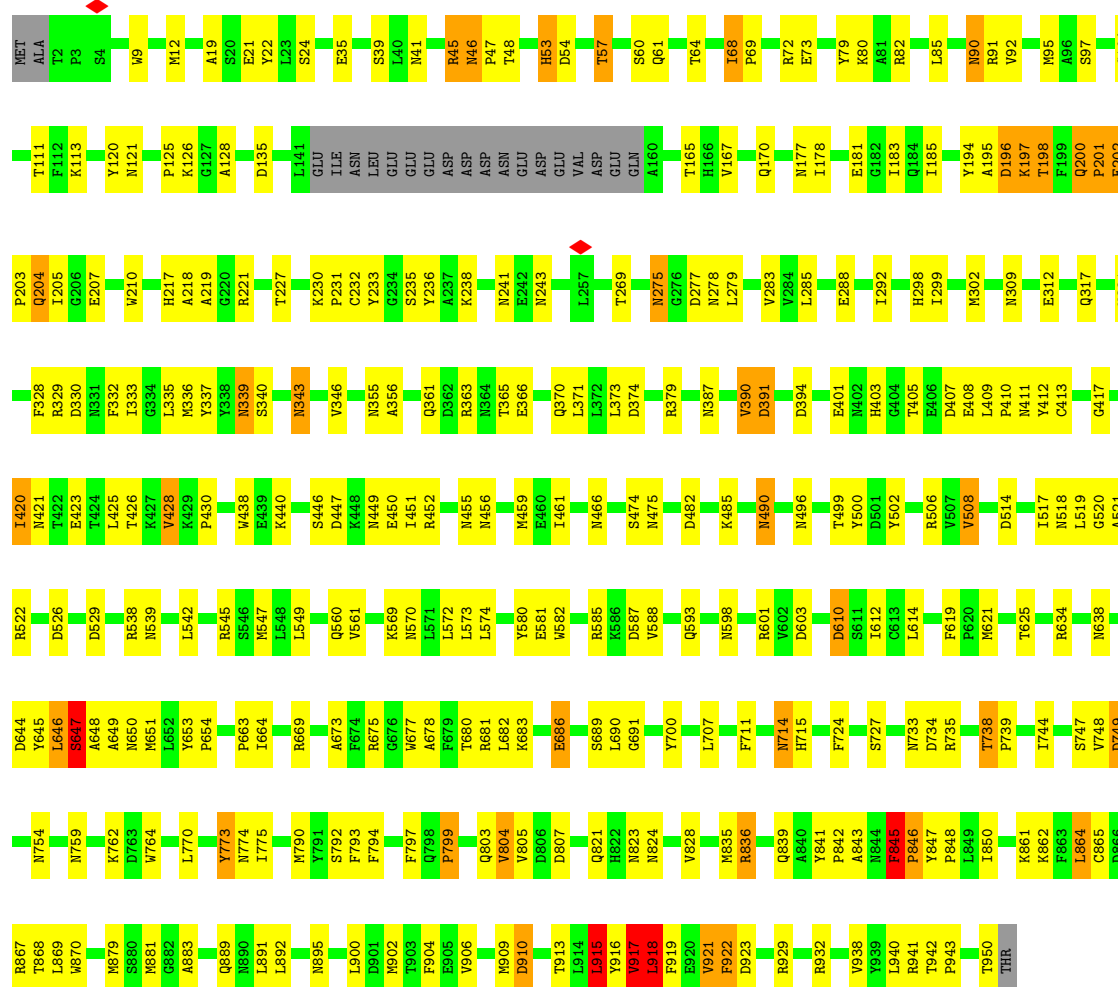


Y700	S595	N496	K306	Q209	Y120	MET
S701	N598	P497	I400	W210	N121	ALA
Y706	N599	T499	H403	E212	K126	THR
L600	L600	Y500	Q317	T213	N130	PRO
D708	R601	R506	D407	E214	C132	S4
G709	I612	V507	E408	I215	P131	Q17
T710	I612	V508	N411	H217	C132	D18
M714	F618	N518	Y325	A218	A137	E21
H715	F620	L519	L416	A219	A140	S24
N733	M621	G520	F328	K225	LEU	S24
D734	A622	A521	R329	T226	GLU	E35
H623	H623	R522	D330	T227	ILE	T36
L737	L629	W523	N331	P228	ASN	Y37
I744	M632	D529	N339	W229	LEU	L40
Y753	L633	F534	K344	K230	GLU	N41
N754	R634	R638	G345	C232	GLU	N42
W755	N635	N638	V346	G234	ASP	K43
L760	D636	N539	L347	S235	ASP	F44
T637	T637	A540	A348	T236	ASN	R45
N638	N638	G541	G349	A237	GLU	P51
D639	D639	S446	Q350	N241	ASP	P51
T761	Q640	D447	A351	E242	GLU	D58
H762	S641	S546	F448	N243	VAL	L65
W764	F642	M547	N449	K246	GLU	R66
M643	M643	N551	E450	Q246	GLN	F67
D644	D644	N551	I451	K251	A160	I68
Y645	Y645	Q560	D362	K251	GLN	I68
L646	L646	V561	R363	Q252	Q163	R72
S647	S647	A648	E366	Q253	E73	E73
A649	A649	Q563	I461	N254	Q170	D74
M650	M650	K564	T369	G255	M177	T75
M651	M651	F565	L462	K256	I178	A76
I664	I664	A567	L463	L257	Y77	Y77
F797	F797	L568	N464	E258	S76	S76
Q798	Q798	K569	A465	T179	K190	Y79
P799	P799	L572	L466	A271	E181	R82
A673	A673	L572	L467	I183	G182	R82
R674	R674	T579	G377	L279	Q184	N90
N675	N675	T579	D378	V283	Y194	R91
G676	G676	R379	R379	V284	A195	V92
A677	A677	E581	T380	Y286	D94	L93
M678	M678	W582	F383	L285	K197	M95
F7810	F7810	R585	S384	D289	T198	R103
H811	H811	K586	N475	F199	Q200	G104
D812	D812	D587	I476	T297	P201	V105
L813	L813	V588	K485	H298	E202	L106
Q814	Q814	M589	Y486	T299	P202	L106
I818	I818	N590	S487	K302	Q204	K113
L819	L819	V591	S392	P303	E207	T118
N823	N823	L592	Y393	T304	E207	T118
H824	H824	Q593	D394	P304	E207	T118
W824	W824	S594	V491	T304	E207	T118



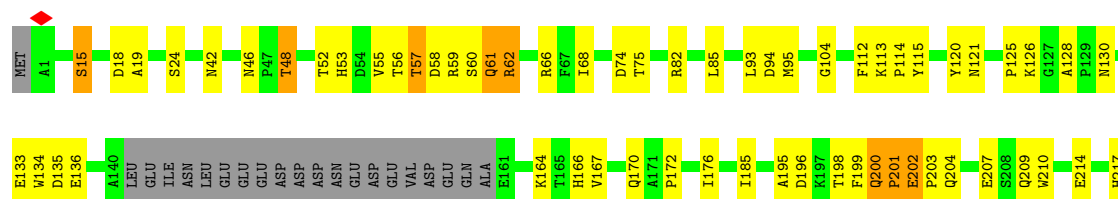
• Molecule 1: Hexon protein

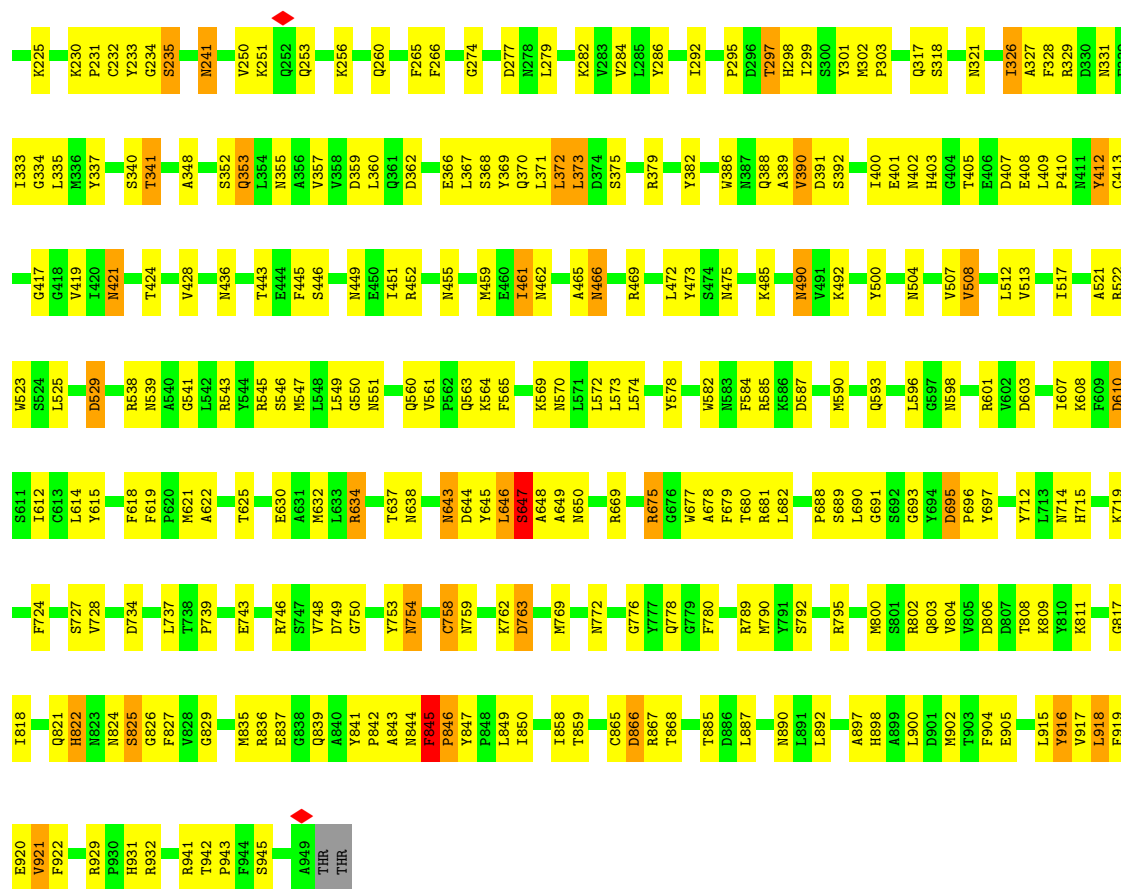
Chain K: 65% 28%



• Molecule 1: Hexon protein

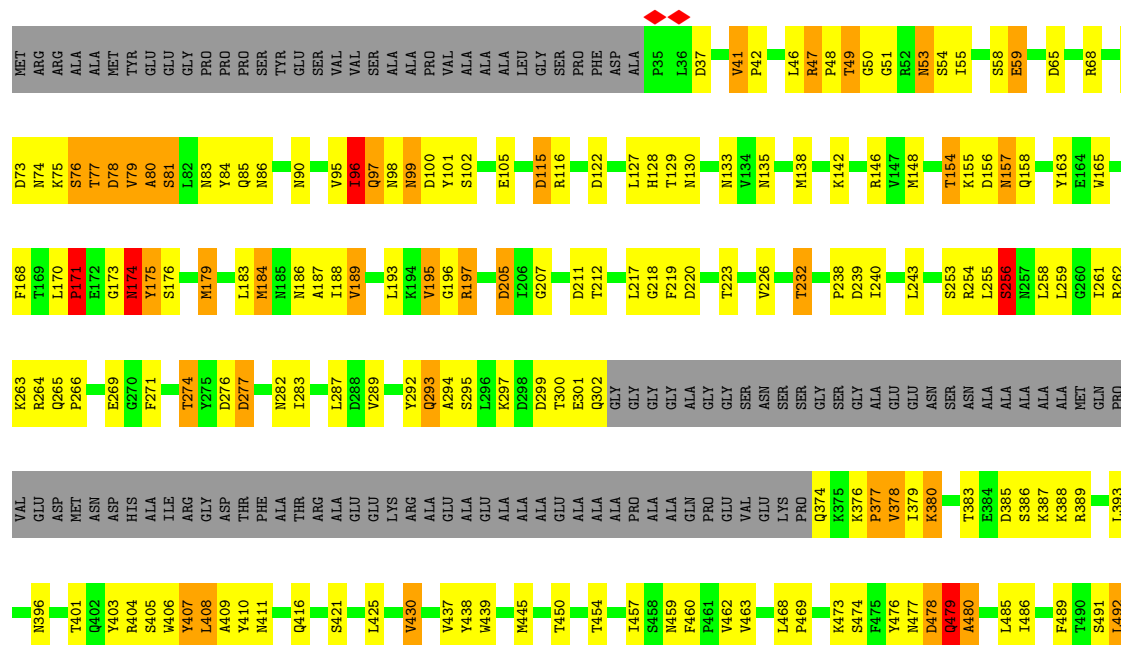
Chain L: 62% 31%



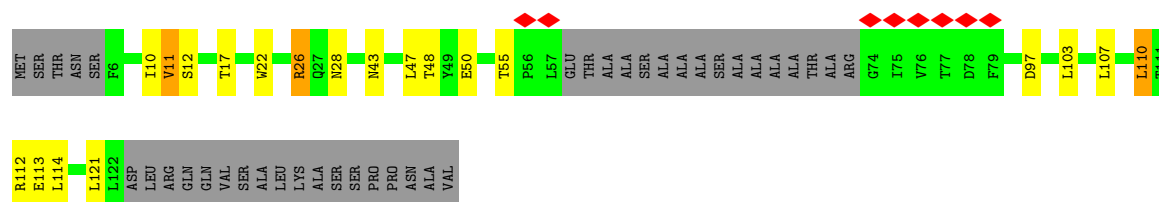


• Molecule 2: Penton protein

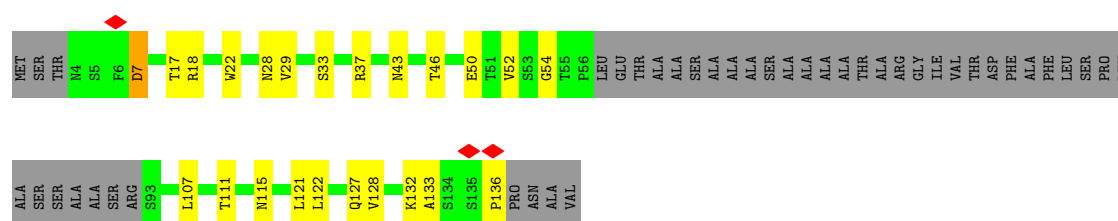
Chain N:



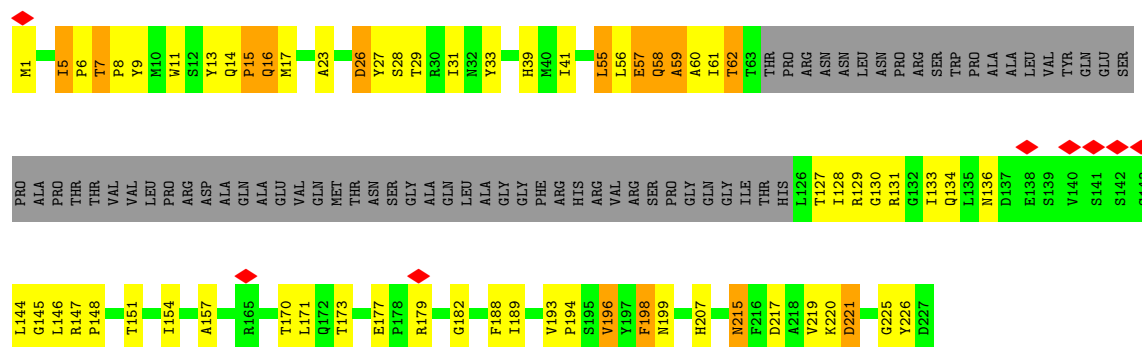
Chain R:



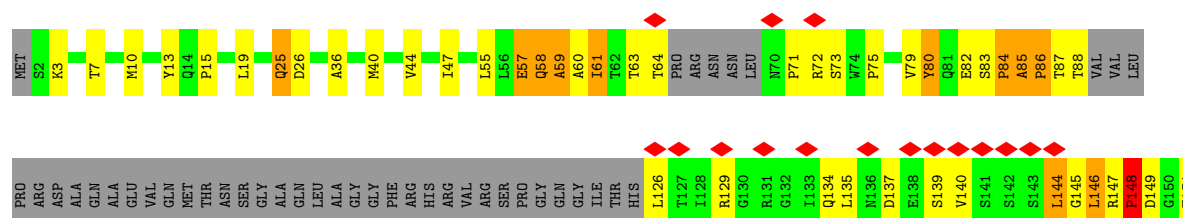
Chain S: 53% 16% 31%



Chain U:

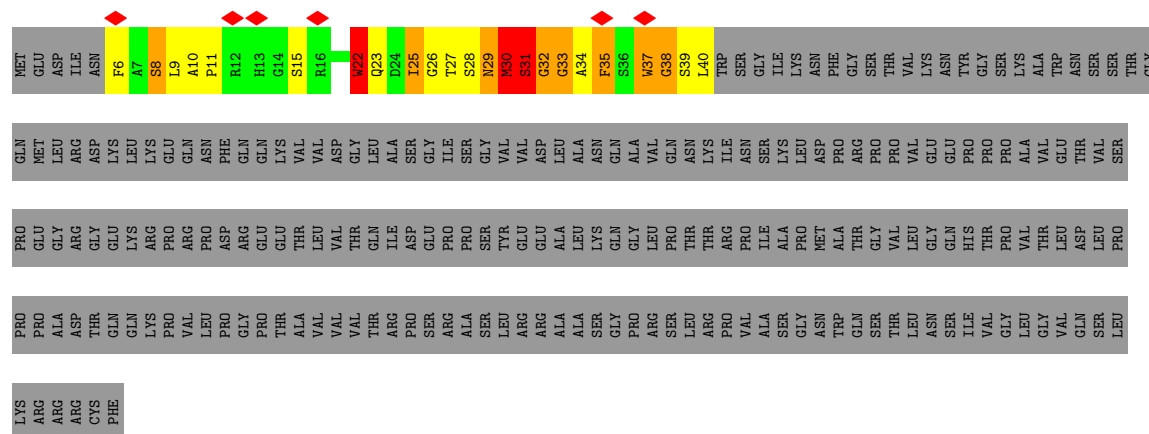


Chain V:

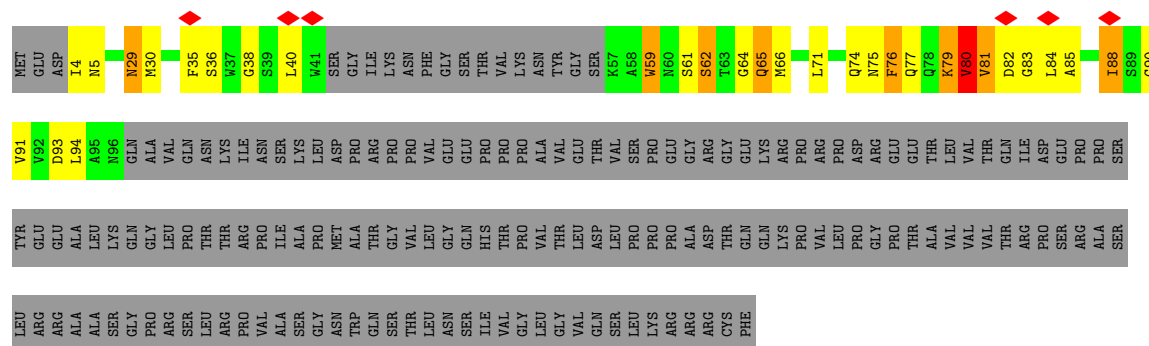




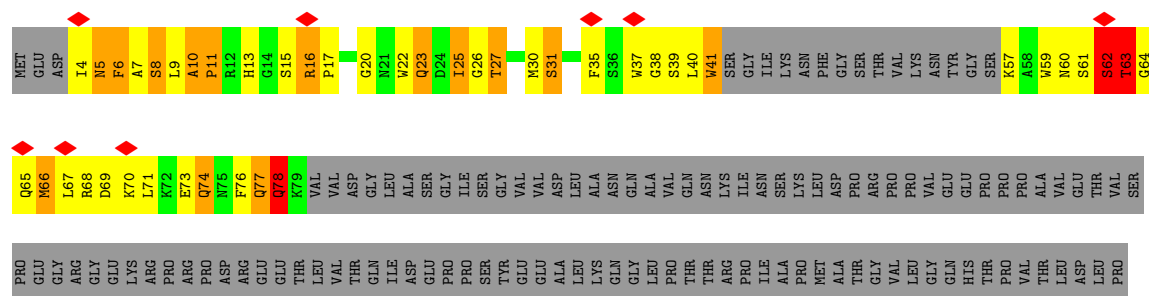
● Molecule 6: Pre-protein VI



● Molecule 6: Pre-protein VI



● Molecule 6: Pre-protein VI

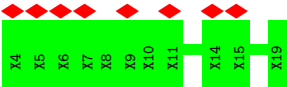


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CYS
PHE

● Molecule 7: Unknown-1



● Molecule 8: Unknown-2



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, I	Depositor
Number of particles used	11277	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 ($e^-/\text{\AA}^2$)	12	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	3000	Depositor
Magnification	22500	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	36.862	Depositor
Minimum map value	-27.573	Depositor
Average map value	-0.024	Depositor
Map value standard deviation	3.164	Depositor
Recommended contour level	3.15	Depositor
Map size (Å)	1089.9199, 1089.9199, 1089.9199	wwPDB
Map dimensions	832, 832, 832	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.31, 1.31, 1.31	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.90	48/7626 (0.6%)	0.81	43/10371 (0.4%)
1	B	0.85	43/7628 (0.6%)	0.78	50/10374 (0.5%)
1	C	0.81	37/7655 (0.5%)	0.75	35/10411 (0.3%)
1	D	0.92	43/7626 (0.6%)	0.83	47/10371 (0.5%)
1	E	0.87	47/7606 (0.6%)	0.72	22/10343 (0.2%)
1	F	0.89	55/7629 (0.7%)	0.78	36/10374 (0.3%)
1	G	0.75	33/7640 (0.4%)	0.70	27/10391 (0.3%)
1	H	0.74	29/7654 (0.4%)	0.70	30/10409 (0.3%)
1	I	0.71	28/7615 (0.4%)	0.63	17/10355 (0.2%)
1	J	0.88	50/7617 (0.7%)	0.73	31/10357 (0.3%)
1	K	0.76	34/7641 (0.4%)	0.71	33/10392 (0.3%)
1	L	0.82	42/7626 (0.6%)	0.73	35/10371 (0.3%)
2	N	1.29	43/3827 (1.1%)	1.23	59/5215 (1.1%)
3	M	0.61	4/2869 (0.1%)	0.63	3/3908 (0.1%)
4	P	0.85	6/986 (0.6%)	0.98	13/1347 (1.0%)
4	Q	0.49	0/964	0.63	3/1315 (0.2%)
4	R	0.77	2/762 (0.3%)	0.65	4/1039 (0.4%)
4	S	0.23	0/736	0.43	0/1002
5	U	1.14	15/1300 (1.2%)	0.86	5/1764 (0.3%)
5	V	1.13	15/1452 (1.0%)	1.15	17/1977 (0.9%)
6	0	1.05	0/115	1.15	2/152 (1.3%)
6	1	1.67	5/460 (1.1%)	2.16	20/615 (3.3%)
6	2	1.17	1/135 (0.7%)	1.35	3/178 (1.7%)
6	3	0.81	0/482	1.28	7/646 (1.1%)
6	4	1.26	1/107 (0.9%)	1.34	2/141 (1.4%)
6	W	1.72	3/271 (1.1%)	2.32	16/365 (4.4%)
6	X	1.08	1/590 (0.2%)	1.46	14/794 (1.8%)
6	Y	1.62	8/498 (1.6%)	2.07	20/667 (3.0%)
6	Z	1.69	4/182 (2.2%)	1.98	11/242 (4.5%)
All	All	0.87	597/107299 (0.6%)	0.81	605/145886 (0.4%)

All (597) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	39	SER	CA-C	-11.57	1.37	1.52
6	W	30	MET	CA-C	-11.17	1.39	1.52
1	H	594	SER	CA-C	-10.50	1.39	1.52
1	J	915	LEU	CA-C	-9.54	1.41	1.52
1	F	649	ALA	CA-CB	-9.46	1.44	1.53
5	V	199	ASN	CA-C	-9.38	1.42	1.52
1	D	667	PRO	CA-C	-9.35	1.42	1.52
1	E	649	ALA	CA-C	-9.30	1.41	1.52
1	L	915	LEU	CA-C	-9.01	1.41	1.52
1	E	916	TYR	CA-C	-8.98	1.41	1.52
1	E	646	LEU	CA-C	-8.92	1.42	1.53
1	D	471	PHE	CA-C	-8.85	1.41	1.52
1	H	825	SER	CA-C	-8.77	1.41	1.52
1	J	348	ALA	CA-C	-8.67	1.42	1.52
1	G	841	TYR	CA-C	-8.63	1.42	1.52
1	C	845	PHE	C-N	-8.62	1.26	1.33
1	G	647	SER	CA-C	-8.55	1.42	1.53
1	A	196	ASP	CA-C	-8.55	1.42	1.52
1	H	595	SER	CA-C	-8.50	1.43	1.52
1	E	915	LEU	CA-C	-8.47	1.42	1.52
1	F	531	VAL	CA-C	-8.44	1.43	1.53
1	K	646	LEU	CA-C	-8.38	1.43	1.53
1	B	649	ALA	CA-C	-8.32	1.42	1.52
1	J	917	VAL	CA-C	-8.32	1.42	1.52
1	J	496	ASN	CA-C	-8.30	1.44	1.53
1	A	915	LEU	CA-C	-8.30	1.42	1.52
1	E	203	PRO	CA-C	-8.30	1.43	1.52
1	J	344	MET	CA-C	-8.28	1.42	1.52
1	B	368	SER	CA-C	-8.25	1.42	1.52
1	K	915	LEU	CA-C	-8.22	1.42	1.52
1	I	695	ASP	CA-C	-8.20	1.42	1.52
1	C	946	ALA	CA-C	-8.16	1.43	1.52
2	N	256	SER	CA-C	-8.15	1.42	1.52
1	B	646	LEU	CA-C	-8.15	1.44	1.53
1	L	15	SER	CA-C	-8.09	1.42	1.52
1	C	868	THR	CA-C	-8.08	1.42	1.52
1	A	650	ASN	CA-C	-8.07	1.42	1.52
1	D	474	SER	CA-C	-8.06	1.42	1.52
1	C	846	PRO	CA-CB	-8.05	1.44	1.53
6	2	31	SER	CA-C	-8.05	1.48	1.52
1	F	825	SER	CA-C	-8.02	1.42	1.52
1	K	649	ALA	CA-C	-8.01	1.42	1.52
1	J	201	PRO	CA-C	-7.99	1.43	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	J	350	GLN	CA-C	-7.99	1.43	1.53
1	D	237	ALA	CA-C	-7.97	1.43	1.52
1	E	756	ALA	CA-C	-7.95	1.43	1.53
1	C	588	VAL	CA-C	-7.93	1.43	1.52
1	F	201	PRO	CA-C	-7.92	1.41	1.52
1	J	347	LEU	CA-C	-7.92	1.43	1.52
1	B	917	VAL	CA-C	-7.91	1.43	1.52
2	N	271	PHE	CA-C	-7.91	1.46	1.53
1	I	915	LEU	CA-C	-7.88	1.43	1.52
1	H	842	PRO	CA-C	-7.87	1.43	1.52
1	K	647	SER	CA-C	-7.87	1.42	1.52
1	H	471	PHE	CA-C	-7.86	1.42	1.52
1	F	844	ASN	CA-C	-7.83	1.42	1.53
1	B	201	PRO	CA-C	-7.81	1.44	1.53
1	D	473	TYR	CA-C	-7.80	1.42	1.52
1	L	649	ALA	CA-C	-7.76	1.43	1.52
1	B	920	GLU	CA-C	-7.70	1.42	1.52
5	U	26	ASP	CA-C	-7.68	1.42	1.52
1	B	469	ARG	CA-C	-7.67	1.43	1.52
1	I	916	TYR	CA-C	-7.66	1.43	1.52
1	E	232	CYS	CA-C	-7.65	1.42	1.52
4	R	11	VAL	CA-C	-7.65	1.43	1.52
1	F	915	LEU	CA-C	-7.63	1.43	1.53
1	E	504	ASN	CA-C	-7.62	1.43	1.52
1	A	733	ASN	CA-C	-7.62	1.42	1.52
1	E	647	SER	CA-C	-7.61	1.42	1.52
1	A	918	LEU	CA-C	-7.58	1.43	1.52
5	U	17	MET	CA-C	-7.58	1.42	1.52
1	F	649	ALA	CA-C	-7.58	1.44	1.53
1	L	825	SER	C-O	-7.58	1.15	1.23
1	J	921	VAL	CA-CB	-7.55	1.44	1.54
1	A	40	LEU	N-CA	-7.54	1.38	1.46
1	K	648	ALA	CA-C	-7.54	1.43	1.52
1	B	918	LEU	CA-C	-7.53	1.44	1.53
1	L	916	TYR	CA-C	-7.53	1.43	1.52
1	H	703	SER	CA-C	-7.53	1.43	1.52
1	C	846	PRO	CA-C	-7.49	1.45	1.52
1	L	649	ALA	CA-CB	-7.46	1.43	1.53
3	M	51	ALA	CA-C	-7.44	1.43	1.52
1	A	501	ASP	CA-C	-7.43	1.43	1.52
1	D	647	SER	CA-C	-7.43	1.42	1.52
1	H	845	PHE	CA-C	-7.42	1.43	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	664	ILE	CA-C	-7.42	1.44	1.52
5	V	193	VAL	CA-C	-7.42	1.45	1.52
1	I	46	ASN	CA-C	-7.41	1.45	1.52
1	B	915	LEU	CA-C	-7.38	1.43	1.52
1	J	497	PRO	CA-C	-7.38	1.44	1.52
1	B	471	PHE	CA-C	-7.37	1.43	1.52
5	U	58	GLN	CA-C	-7.37	1.43	1.52
1	E	755	VAL	CA-C	-7.36	1.43	1.52
1	F	918	LEU	CA-C	-7.36	1.44	1.53
1	J	647	SER	CA-C	-7.35	1.43	1.52
1	B	643	ASN	CA-C	-7.34	1.44	1.53
1	K	864	LEU	CA-C	-7.34	1.43	1.52
1	L	845	PHE	CA-C	-7.34	1.43	1.52
5	U	59	ALA	CA-C	-7.33	1.43	1.52
1	D	662	VAL	CA-C	-7.31	1.45	1.52
1	F	105	VAL	CA-C	-7.29	1.43	1.52
5	V	57	GLU	CA-C	-7.29	1.43	1.52
1	D	666	ILE	CA-C	-7.28	1.45	1.52
2	N	41	VAL	CA-C	-7.26	1.47	1.52
1	B	350	GLN	CA-C	-7.25	1.43	1.52
1	I	687	THR	CA-C	-7.25	1.45	1.53
1	A	917	VAL	CA-C	-7.24	1.43	1.52
1	G	232	CYS	CA-C	-7.23	1.43	1.52
5	V	59	ALA	CA-C	-7.21	1.43	1.52
1	D	730	TRP	CA-C	-7.20	1.43	1.52
1	E	203	PRO	N-CA	-7.19	1.42	1.47
1	L	695	ASP	CA-C	-7.19	1.43	1.52
1	D	731	PRO	CA-C	-7.18	1.42	1.52
1	B	647	SER	CA-C	-7.17	1.42	1.52
1	B	730	TRP	CA-C	-7.16	1.44	1.52
1	A	649	ALA	CA-C	-7.12	1.44	1.52
1	C	237	ALA	CA-C	-7.11	1.44	1.52
1	G	202	GLU	CA-C	-7.11	1.47	1.52
1	E	201	PRO	CA-C	-7.09	1.44	1.52
2	N	49	THR	CA-C	-7.08	1.43	1.52
2	N	378	VAL	CA-C	-7.08	1.44	1.52
1	I	917	VAL	CA-C	-7.07	1.44	1.52
6	1	6	PHE	CA-C	-7.07	1.45	1.53
4	P	56	PRO	CA-C	-7.06	1.42	1.52
2	N	98	ASN	CA-C	-7.05	1.44	1.52
1	I	696	PRO	CA-C	-7.04	1.41	1.52
1	E	236	TYR	CA-C	-7.03	1.44	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	921	VAL	CA-CB	-7.03	1.45	1.54
1	C	201	PRO	CA-C	-7.02	1.44	1.52
1	H	469	ARG	CA-C	-7.01	1.43	1.52
1	E	500	TYR	CA-C	-7.00	1.43	1.52
1	J	845	PHE	CA-C	-7.00	1.44	1.52
5	U	8	PRO	CA-C	-7.00	1.44	1.52
1	D	842	PRO	CA-C	-6.95	1.43	1.52
2	N	256	SER	C-O	-6.95	1.16	1.24
6	Y	13	HIS	CA-C	-6.95	1.43	1.53
1	A	236	TYR	CA-C	-6.94	1.44	1.52
1	B	469	ARG	C-O	-6.93	1.16	1.24
1	K	46	ASN	CA-C	-6.90	1.43	1.52
1	C	715	HIS	CA-C	-6.89	1.43	1.52
1	L	680	THR	CA-C	-6.89	1.44	1.52
1	J	844	ASN	CA-C	-6.89	1.44	1.52
1	C	919	PHE	CA-C	-6.88	1.44	1.52
1	K	202	GLU	CA-C	-6.87	1.45	1.52
1	H	197	LYS	CA-C	-6.87	1.44	1.52
1	I	842	PRO	CA-C	-6.86	1.44	1.52
2	N	545	ASP	CA-C	-6.86	1.45	1.53
1	K	201	PRO	CA-C	-6.86	1.44	1.52
2	N	171	PRO	CA-C	-6.85	1.44	1.52
1	D	300	SER	CA-C	-6.85	1.43	1.52
1	L	368	SER	CA-C	-6.85	1.44	1.52
5	U	27	TYR	CA-C	-6.83	1.44	1.52
1	E	202	GLU	CA-C	-6.83	1.44	1.52
2	N	377	PRO	CA-C	-6.83	1.46	1.52
4	P	55	THR	CA-C	-6.83	1.44	1.52
1	D	30	PHE	CA-C	-6.80	1.44	1.52
1	I	648	ALA	CA-C	-6.80	1.43	1.53
1	G	561	VAL	CA-C	-6.79	1.45	1.52
1	A	232	CYS	CA-C	-6.79	1.44	1.52
1	G	643	ASN	CA-C	-6.79	1.44	1.52
2	N	80	ALA	CA-C	-6.78	1.44	1.52
1	I	845	PHE	CA-C	-6.77	1.44	1.52
1	J	346	VAL	CA-C	-6.77	1.44	1.52
6	Y	74	GLN	CA-C	-6.77	1.44	1.52
1	A	647	SER	CA-C	-6.76	1.43	1.52
1	G	846	PRO	CA-CB	-6.76	1.44	1.53
1	A	730	TRP	CA-C	-6.75	1.44	1.52
1	A	30	PHE	CA-C	-6.74	1.44	1.52
2	N	47	ARG	CA-C	-6.74	1.45	1.53

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	917	VAL	CA-C	-6.73	1.44	1.52
1	K	916	TYR	CA-C	-6.73	1.44	1.52
1	F	715	HIS	CA-C	-6.72	1.44	1.52
1	F	678	ALA	CA-CB	-6.71	1.42	1.53
1	H	846	PRO	CA-CB	-6.69	1.45	1.53
1	B	650	ASN	CA-C	-6.69	1.44	1.52
1	G	825	SER	C-O	-6.68	1.14	1.23
1	J	921	VAL	CA-C	-6.66	1.44	1.52
5	V	86	PRO	CA-C	-6.66	1.45	1.52
1	L	649	ALA	N-CA	-6.65	1.38	1.46
1	I	844	ASN	CA-C	-6.65	1.44	1.52
1	A	825	SER	CA-C	-6.65	1.44	1.52
1	J	470	ASN	CA-C	-6.64	1.44	1.52
1	F	648	ALA	CA-CB	-6.63	1.45	1.53
1	E	502	TYR	CA-C	-6.62	1.44	1.52
1	L	920	GLU	CA-C	-6.61	1.44	1.52
5	V	58	GLN	CA-C	-6.61	1.44	1.52
1	F	824	ASN	CA-C	-6.61	1.44	1.53
1	K	846	PRO	CA-CB	-6.59	1.45	1.53
1	H	701	SER	CA-C	-6.58	1.43	1.52
1	D	659	ALA	CA-C	-6.58	1.44	1.52
1	I	649	ALA	CA-C	-6.58	1.44	1.52
1	G	819	LEU	CA-C	-6.57	1.43	1.52
1	A	733	ASN	N-CA	-6.56	1.37	1.46
1	D	201	PRO	CA-C	-6.56	1.45	1.52
1	L	372	LEU	CA-C	-6.55	1.44	1.52
1	E	565	PHE	CA-C	-6.55	1.44	1.52
1	I	648	ALA	CA-CB	-6.54	1.45	1.53
1	G	201	PRO	CA-C	-6.54	1.44	1.52
5	V	197	TYR	CA-C	-6.52	1.44	1.52
5	V	199	ASN	C-O	-6.51	1.18	1.24
1	E	648	ALA	CA-C	-6.51	1.44	1.52
1	J	677	TRP	CA-C	-6.50	1.44	1.52
1	H	198	THR	CA-C	-6.50	1.43	1.52
1	I	689	SER	CA-C	-6.48	1.44	1.52
1	J	473	TYR	CA-C	-6.47	1.44	1.52
1	F	916	TYR	CA-C	-6.45	1.44	1.52
1	C	227	THR	CA-C	-6.44	1.46	1.53
1	D	233	TYR	CA-C	-6.43	1.44	1.52
1	L	201	PRO	CA-C	-6.43	1.45	1.52
1	E	197	LYS	CA-C	-6.43	1.44	1.52
1	K	919	PHE	CA-C	-6.43	1.45	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	U	8	PRO	CA-CB	-6.42	1.44	1.53
1	E	650	ASN	CA-C	-6.42	1.44	1.52
1	K	648	ALA	N-CA	-6.42	1.38	1.46
1	K	918	LEU	CA-C	-6.40	1.44	1.52
1	C	588	VAL	CA-CB	-6.39	1.47	1.54
1	L	678	ALA	CA-CB	-6.39	1.43	1.53
1	F	847	TYR	CA-C	-6.38	1.45	1.52
1	H	595	SER	N-CA	-6.38	1.38	1.46
1	K	842	PRO	CA-C	-6.38	1.44	1.52
1	L	370	GLN	CA-C	-6.37	1.44	1.52
3	M	347	THR	CA-C	-6.37	1.44	1.52
1	D	232	CYS	CA-C	-6.36	1.44	1.52
5	U	5	ILE	CA-C	-6.36	1.46	1.52
1	E	825	SER	CA-C	-6.34	1.44	1.53
1	A	731	PRO	CA-C	-6.33	1.43	1.52
1	A	28	VAL	CA-C	-6.32	1.45	1.52
1	I	692	SER	CA-C	-6.32	1.44	1.52
5	U	9	TYR	CA-C	-6.31	1.45	1.52
5	V	148	PRO	CA-C	-6.31	1.43	1.52
1	F	527	TYR	CA-C	-6.30	1.43	1.52
1	L	648	ALA	CA-C	-6.30	1.44	1.52
1	L	846	PRO	CA-CB	-6.30	1.45	1.53
1	A	30	PHE	N-CA	-6.29	1.38	1.46
1	J	917	VAL	N-CA	-6.29	1.38	1.46
1	C	823	ASN	CA-C	-6.28	1.45	1.52
1	D	669	ARG	CA-C	-6.27	1.45	1.52
1	K	845	PHE	CA-C	-6.26	1.45	1.52
1	F	463	LEU	CA-C	-6.26	1.44	1.53
1	H	927	VAL	CA-CB	-6.26	1.46	1.54
1	J	842	PRO	CA-C	-6.24	1.44	1.52
1	K	394	ASP	CA-C	-6.24	1.46	1.52
1	G	844	ASN	CA-C	-6.23	1.45	1.53
1	C	845	PHE	CA-C	-6.23	1.45	1.52
1	A	202	GLU	CA-C	-6.22	1.46	1.53
1	B	648	ALA	CA-C	-6.21	1.44	1.52
1	J	499	THR	CA-C	-6.21	1.45	1.52
1	H	844	ASN	CA-C	-6.20	1.44	1.53
1	J	464	ASN	CA-C	-6.20	1.44	1.52
1	F	680	THR	C-O	-6.20	1.17	1.24
1	F	845	PHE	CA-C	-6.20	1.45	1.52
1	C	943	PRO	CA-CB	-6.19	1.45	1.53
1	F	844	ASN	N-CA	-6.19	1.40	1.46

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	G	847	TYR	CA-C	-6.18	1.44	1.52
1	E	917	VAL	CA-CB	-6.17	1.46	1.54
5	U	14	GLN	CA-C	-6.17	1.46	1.52
6	Y	10	ALA	CA-C	-6.16	1.45	1.52
1	A	734	ASP	CA-C	-6.16	1.44	1.52
1	C	236	TYR	CA-C	-6.15	1.45	1.52
2	N	174	ASN	CA-C	-6.15	1.44	1.52
1	H	201	PRO	CA-C	-6.14	1.44	1.52
1	D	409	LEU	CA-C	-6.13	1.45	1.52
1	E	203	PRO	CA-CB	-6.13	1.46	1.53
1	C	825	SER	CA-C	-6.13	1.44	1.53
1	F	126	LYS	CA-C	-6.13	1.44	1.52
1	L	917	VAL	CA-C	-6.13	1.45	1.52
1	B	731	PRO	CA-C	-6.12	1.42	1.52
1	G	845	PHE	CA-C	-6.12	1.45	1.52
1	B	917	VAL	CA-CB	-6.11	1.47	1.54
1	L	917	VAL	CA-CB	-6.11	1.47	1.54
6	W	8	SER	CA-C	-6.11	1.44	1.52
1	L	845	PHE	C-N	-6.11	1.26	1.33
1	F	527	TYR	N-CA	-6.10	1.38	1.46
1	F	716	THR	CA-C	-6.09	1.45	1.53
1	C	259	SER	CA-C	-6.09	1.45	1.52
1	L	847	TYR	CA-C	-6.09	1.44	1.52
1	A	24	SER	CA-C	-6.08	1.46	1.53
6	4	30	MET	CA-C	-6.08	1.46	1.52
2	N	477	ASN	CA-C	-6.07	1.45	1.52
1	A	824	ASN	CA-C	-6.07	1.45	1.53
1	F	921	VAL	CA-CB	-6.07	1.44	1.55
1	E	471	PHE	CA-C	-6.07	1.44	1.52
1	F	917	VAL	CA-C	-6.07	1.45	1.52
1	K	799	PRO	CA-C	-6.06	1.44	1.52
1	I	699	THR	N-CA	-6.06	1.39	1.46
1	B	470	ASN	CA-C	-6.04	1.44	1.52
2	N	41	VAL	N-CA	-6.04	1.40	1.46
1	H	824	ASN	CA-C	-6.04	1.45	1.53
1	I	918	LEU	CA-C	-6.04	1.44	1.53
2	N	53	ASN	CA-C	-6.03	1.45	1.52
1	K	921	VAL	CA-CB	-6.03	1.46	1.54
1	L	367	LEU	CA-C	-6.02	1.44	1.52
5	U	7	THR	CA-C	-6.02	1.47	1.53
1	K	196	ASP	CA-C	-6.01	1.45	1.52
1	I	846	PRO	CA-CB	-6.01	1.45	1.53

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	F	233	TYR	CA-C	-6.00	1.45	1.52
1	K	197	LYS	CA-C	-6.00	1.44	1.52
1	L	917	VAL	C-O	-6.00	1.17	1.24
1	J	921	VAL	N-CA	-6.00	1.38	1.46
1	A	648	ALA	CA-C	-5.99	1.45	1.52
1	A	201	PRO	CA-C	-5.99	1.47	1.52
2	N	219	PHE	CA-C	-5.99	1.45	1.52
1	G	261	VAL	CA-C	-5.98	1.45	1.52
2	N	265	GLN	CA-C	-5.98	1.45	1.52
1	F	125	PRO	CA-C	-5.97	1.44	1.52
1	J	565	PHE	CA-C	-5.97	1.44	1.52
1	I	689	SER	CA-CB	-5.97	1.45	1.52
6	Y	11	PRO	CA-C	-5.96	1.45	1.52
1	C	288	GLU	CA-C	-5.96	1.45	1.52
1	D	561	VAL	CA-C	-5.96	1.46	1.52
1	C	649	ALA	CA-C	-5.96	1.44	1.52
2	N	75	LYS	C-O	5.96	1.31	1.24
1	I	824	ASN	CA-C	-5.95	1.45	1.53
1	L	646	LEU	CA-C	-5.95	1.44	1.52
6	1	13	HIS	CA-C	-5.95	1.46	1.53
1	A	650	ASN	N-CA	-5.94	1.38	1.46
1	G	823	ASN	CA-C	-5.94	1.45	1.52
1	A	846	PRO	CA-CB	-5.93	1.45	1.53
1	J	917	VAL	CA-CB	-5.93	1.46	1.55
1	L	61	GLN	CA-C	-5.93	1.45	1.52
1	B	735	ARG	N-CA	-5.93	1.39	1.46
1	H	233	TYR	CA-C	-5.92	1.45	1.52
1	A	504	ASN	CA-C	-5.92	1.44	1.52
1	D	565	PHE	CA-C	-5.91	1.44	1.52
1	E	917	VAL	CA-C	-5.91	1.44	1.52
1	D	659	ALA	CA-CB	-5.91	1.43	1.54
1	F	680	THR	CA-C	-5.90	1.45	1.52
1	H	844	ASN	N-CA	-5.90	1.40	1.46
5	U	15	PRO	CA-C	-5.89	1.43	1.52
1	D	670	ASN	CA-C	-5.89	1.45	1.52
1	E	647	SER	N-CA	-5.89	1.39	1.46
1	G	562	PRO	CA-CB	-5.89	1.45	1.53
1	D	295	PRO	CA-C	-5.89	1.46	1.52
5	V	196	VAL	CA-CB	-5.88	1.47	1.54
1	B	372	LEU	CA-C	-5.88	1.45	1.52
2	N	100	ASP	CA-C	-5.88	1.45	1.52
6	Z	10	ALA	CA-C	-5.88	1.46	1.53

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	K	650	ASN	CA-C	-5.87	1.45	1.52
1	A	502	TYR	CA-C	-5.86	1.45	1.52
1	J	581	GLU	CA-C	-5.86	1.45	1.52
6	W	10	ALA	CA-C	-5.85	1.45	1.52
1	K	203	PRO	CA-C	-5.85	1.43	1.52
1	B	477	ALA	CA-C	-5.84	1.45	1.52
1	G	261	VAL	CA-CB	-5.82	1.47	1.54
2	N	535	ILE	CA-C	-5.82	1.45	1.52
1	D	299	ILE	CA-CB	-5.81	1.47	1.54
1	K	201	PRO	CA-CB	-5.81	1.46	1.53
1	F	918	LEU	N-CA	-5.81	1.39	1.46
1	B	703	SER	CA-C	-5.80	1.45	1.53
1	A	845	PHE	CA-C	-5.80	1.45	1.52
1	B	474	SER	CA-C	-5.80	1.45	1.52
1	D	329	ARG	CA-C	-5.79	1.45	1.53
1	A	823	ASN	CA-C	-5.79	1.45	1.52
1	A	237	ALA	CA-C	-5.79	1.45	1.52
1	B	643	ASN	C-O	-5.79	1.18	1.24
6	Y	8	SER	CA-C	-5.78	1.45	1.52
1	J	918	LEU	CA-C	-5.78	1.45	1.53
1	C	589	ASN	CA-C	-5.78	1.45	1.52
1	I	695	ASP	C-N	-5.78	1.26	1.34
1	E	202	GLU	C-N	-5.78	1.29	1.33
2	N	540	ARG	CA-C	-5.77	1.45	1.52
1	K	867	ARG	CA-C	-5.77	1.45	1.53
1	J	348	ALA	CA-CB	-5.77	1.44	1.53
1	D	197	LYS	CA-C	-5.77	1.45	1.52
1	D	644	ASP	CA-C	-5.76	1.45	1.52
1	H	200	GLN	N-CA	-5.76	1.41	1.46
1	J	471	PHE	CA-C	-5.76	1.45	1.52
1	J	649	ALA	CA-C	-5.76	1.44	1.53
1	A	916	TYR	CA-C	-5.75	1.45	1.52
6	Z	30	MET	CA-C	-5.75	1.45	1.52
1	C	203	PRO	CA-C	-5.75	1.43	1.52
1	H	232	CYS	CA-C	-5.75	1.45	1.52
1	H	205	ILE	CA-C	-5.74	1.45	1.52
1	K	845	PHE	C-N	-5.72	1.27	1.33
1	C	202	GLU	CA-C	-5.72	1.46	1.52
3	M	50	GLN	CA-C	-5.72	1.45	1.52
1	D	660	THR	N-CA	-5.72	1.41	1.46
1	J	923	ASP	CA-C	-5.72	1.45	1.52
2	N	41	VAL	CA-CB	-5.72	1.50	1.54

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	L	650	ASN	CA-C	-5.71	1.45	1.52
1	K	865	CYS	CA-C	-5.71	1.45	1.52
1	G	825	SER	CA-C	-5.70	1.45	1.53
1	H	202	GLU	CA-C	-5.69	1.45	1.52
1	D	846	PRO	CA-CB	-5.69	1.46	1.53
2	N	408	LEU	CA-C	-5.69	1.45	1.52
1	J	561	VAL	CA-C	-5.69	1.47	1.52
1	D	469	ARG	CA-C	-5.68	1.45	1.52
1	C	716	THR	CA-C	-5.68	1.45	1.52
1	D	201	PRO	CA-CB	-5.68	1.46	1.53
1	J	579	THR	CA-C	-5.67	1.46	1.52
2	N	407	TYR	CA-C	-5.67	1.45	1.52
1	E	195	ALA	CA-C	-5.67	1.45	1.53
1	K	917	VAL	CA-C	-5.67	1.45	1.52
1	E	561	VAL	CA-CB	-5.66	1.46	1.54
1	H	591	VAL	CA-CB	-5.65	1.46	1.54
1	E	472	LEU	CA-C	-5.65	1.45	1.52
1	D	731	PRO	CA-CB	-5.64	1.44	1.53
2	N	294	ALA	CA-C	-5.64	1.45	1.52
1	A	26	GLY	CA-C	-5.63	1.45	1.52
1	B	644	ASP	CA-C	-5.63	1.45	1.52
2	N	293	GLN	CA-C	-5.63	1.45	1.52
1	F	531	VAL	CA-CB	-5.62	1.47	1.53
1	B	207	GLU	CA-C	-5.61	1.45	1.52
2	N	264	ARG	CA-C	-5.61	1.45	1.52
1	F	236	TYR	CA-C	-5.61	1.45	1.52
2	N	536	GLY	CA-C	-5.60	1.47	1.52
3	M	55	SER	CA-C	-5.59	1.45	1.52
1	L	918	LEU	CA-C	-5.59	1.45	1.52
1	F	845	PHE	C-N	-5.59	1.28	1.33
5	V	201	PHE	CA-C	-5.58	1.45	1.53
1	F	650	ASN	CA-C	-5.57	1.45	1.52
1	A	500	TYR	CA-C	-5.56	1.45	1.52
1	J	497	PRO	CA-CB	-5.56	1.47	1.53
1	A	501	ASP	C-O	-5.55	1.17	1.24
1	B	649	ALA	N-CA	-5.55	1.39	1.46
1	C	916	TYR	CA-C	-5.55	1.45	1.52
1	J	920	GLU	CA-C	-5.55	1.46	1.52
1	E	406	GLU	CA-C	-5.55	1.45	1.53
1	D	562	PRO	CA-CB	-5.54	1.45	1.53
1	I	844	ASN	N-CA	-5.54	1.40	1.46
1	B	269	THR	CA-C	-5.54	1.45	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	F	680	THR	CA-CB	-5.54	1.45	1.53
1	F	917	VAL	CA-CB	-5.54	1.46	1.53
1	D	845	PHE	CA-C	-5.54	1.46	1.52
1	F	842	PRO	CA-C	-5.53	1.46	1.52
1	K	918	LEU	N-CA	-5.53	1.39	1.46
1	B	367	LEU	CA-C	-5.53	1.45	1.52
1	B	649	ALA	CA-CB	-5.52	1.44	1.53
1	F	825	SER	N-CA	-5.52	1.39	1.46
1	D	205	ILE	CA-C	-5.52	1.45	1.52
1	E	751	GLU	CA-C	-5.52	1.45	1.52
5	U	57	GLU	CA-C	-5.52	1.45	1.52
1	A	35	GLU	CA-C	-5.51	1.45	1.52
1	E	201	PRO	CA-CB	-5.51	1.46	1.53
1	F	648	ALA	CA-C	-5.51	1.46	1.52
1	J	650	ASN	CA-C	-5.51	1.45	1.52
1	A	836	ARG	CA-C	-5.51	1.45	1.52
1	B	916	TYR	CA-C	-5.50	1.46	1.52
1	C	650	ASN	CA-C	-5.50	1.45	1.52
1	G	561	VAL	C-O	-5.50	1.17	1.24
1	D	661	ASN	CA-C	-5.50	1.45	1.52
1	G	561	VAL	CA-CB	-5.50	1.47	1.54
6	Z	12	ARG	CA-C	-5.49	1.46	1.52
1	I	917	VAL	CA-CB	-5.49	1.47	1.54
1	L	677	TRP	CA-C	-5.49	1.46	1.52
1	F	920	GLU	CA-C	-5.48	1.46	1.52
1	H	845	PHE	C-N	-5.48	1.27	1.33
1	L	919	PHE	CA-C	-5.48	1.45	1.52
5	U	56	LEU	CA-C	-5.48	1.45	1.52
1	C	197	LYS	CA-C	-5.47	1.45	1.52
1	K	921	VAL	CA-C	-5.47	1.45	1.52
1	G	563	GLN	CA-C	-5.46	1.46	1.52
1	I	698	TYR	CA-C	-5.45	1.45	1.53
1	F	846	PRO	CA-C	-5.45	1.47	1.52
1	H	848	PRO	CA-CB	-5.44	1.47	1.53
1	K	45	ARG	CA-C	-5.44	1.46	1.52
1	F	915	LEU	C-O	-5.43	1.17	1.23
1	E	227	THR	CA-C	-5.43	1.46	1.53
1	B	351	ALA	CA-C	-5.43	1.45	1.52
1	F	846	PRO	CA-CB	-5.43	1.46	1.53
1	F	105	VAL	CA-CB	-5.43	1.47	1.54
1	E	226	THR	CA-C	-5.42	1.45	1.52
1	J	680	THR	CA-CB	-5.42	1.44	1.53

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	J	825	SER	CA-C	-5.42	1.45	1.53
2	N	77	THR	CA-C	-5.42	1.45	1.52
4	R	11	VAL	CA-CB	-5.42	1.47	1.54
1	B	203	PRO	CA-C	-5.42	1.46	1.52
5	V	199	ASN	C-N	-5.41	1.26	1.33
1	A	31	ALA	CA-C	-5.41	1.45	1.52
1	L	824	ASN	CA-C	-5.40	1.46	1.53
5	V	61	ILE	CA-C	-5.39	1.46	1.52
1	J	582	TRP	CA-C	-5.39	1.46	1.52
1	J	847	TYR	CA-C	-5.39	1.47	1.53
1	E	463	LEU	CA-C	-5.39	1.46	1.52
2	N	81	SER	N-CA	-5.39	1.39	1.46
1	L	368	SER	C-O	-5.38	1.17	1.24
6	1	15	SER	CA-C	-5.38	1.45	1.53
1	G	647	SER	CA-CB	-5.38	1.45	1.53
1	K	653	TYR	C-O	-5.38	1.18	1.24
1	J	648	ALA	CA-C	-5.37	1.46	1.52
1	L	844	ASN	CA-C	-5.37	1.46	1.53
1	A	501	ASP	N-CA	-5.36	1.39	1.46
1	C	842	PRO	CA-C	-5.36	1.46	1.52
1	J	201	PRO	CA-CB	-5.35	1.46	1.53
1	G	259	SER	CA-C	-5.34	1.46	1.52
1	F	198	THR	CA-C	-5.34	1.45	1.52
1	G	246	GLN	N-CA	-5.34	1.40	1.47
1	G	824	ASN	CA-C	-5.34	1.46	1.53
1	F	848	PRO	CA-CB	-5.34	1.46	1.53
1	C	843	ALA	CA-C	-5.33	1.46	1.52
1	J	346	VAL	N-CA	-5.33	1.40	1.46
1	B	233	TYR	CA-C	-5.33	1.46	1.52
1	I	825	SER	CA-CB	-5.33	1.45	1.53
1	C	915	LEU	CA-C	-5.33	1.44	1.53
6	Z	27	THR	N-CA	5.33	1.53	1.46
1	L	410	PRO	CA-C	-5.32	1.45	1.52
1	F	124	ALA	CA-C	-5.32	1.46	1.53
1	J	561	VAL	CA-CB	-5.32	1.47	1.54
6	Y	15	SER	CA-C	-5.32	1.45	1.52
1	C	588	VAL	N-CA	-5.31	1.40	1.46
1	E	233	TYR	CA-C	-5.31	1.46	1.52
1	F	232	CYS	CA-C	-5.31	1.45	1.52
5	V	84	PRO	CA-C	-5.31	1.47	1.53
1	K	804	VAL	CA-CB	-5.30	1.47	1.55
1	F	101	ASP	CA-C	-5.30	1.48	1.53

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	H	593	GLN	CA-C	-5.30	1.46	1.52
1	C	260	GLN	N-CA	-5.29	1.39	1.46
1	J	823	ASN	CA-C	-5.29	1.46	1.52
1	L	921	VAL	N-CA	-5.28	1.39	1.46
1	J	824	ASN	CA-C	-5.28	1.46	1.53
1	E	469	ARG	CA-C	-5.27	1.46	1.52
1	J	648	ALA	CA-CB	-5.27	1.45	1.53
2	N	76	SER	C-O	-5.26	1.17	1.24
1	C	917	VAL	CA-CB	-5.25	1.47	1.54
1	K	799	PRO	CA-CB	-5.25	1.46	1.53
2	N	379	ILE	N-CA	-5.25	1.39	1.46
1	G	648	ALA	CA-CB	-5.24	1.45	1.53
1	E	561	VAL	CA-C	-5.24	1.47	1.52
4	P	35	ASP	CA-C	-5.24	1.46	1.52
6	Y	10	ALA	CA-CB	-5.24	1.46	1.53
1	C	943	PRO	CA-C	-5.23	1.45	1.52
1	F	202	GLU	CA-C	-5.23	1.46	1.52
1	G	850	ILE	CA-C	-5.23	1.48	1.52
1	L	368	SER	N-CA	-5.23	1.40	1.46
1	L	59	ARG	CA-C	-5.23	1.46	1.53
4	P	55	THR	N-CA	-5.23	1.41	1.46
1	F	713	LEU	N-CA	-5.22	1.40	1.46
1	E	915	LEU	C-O	-5.22	1.17	1.24
1	B	701	SER	CA-C	-5.22	1.45	1.52
1	H	201	PRO	CA-CB	-5.21	1.46	1.53
1	J	346	VAL	C-O	-5.21	1.19	1.24
2	N	95	VAL	N-CA	-5.21	1.40	1.46
6	1	10	ALA	CA-C	-5.20	1.46	1.53
1	E	562	PRO	CA-CB	-5.20	1.46	1.53
1	A	199	PHE	CA-C	-5.20	1.45	1.52
1	G	201	PRO	CA-CB	-5.19	1.47	1.53
2	N	499	PHE	CA-C	-5.17	1.46	1.52
6	1	21	ASN	CA-C	-5.17	1.46	1.52
2	N	558	LEU	CA-C	-5.17	1.46	1.52
2	N	179	MET	C-O	-5.17	1.18	1.24
1	E	651	MET	N-CA	-5.16	1.39	1.45
1	A	844	ASN	CA-C	-5.16	1.45	1.52
2	N	258	LEU	CA-C	-5.16	1.46	1.52
1	D	658	ASN	CA-C	-5.16	1.45	1.52
1	E	407	ASP	CA-C	-5.16	1.44	1.52
1	G	197	LYS	CA-C	-5.16	1.46	1.52
1	G	844	ASN	C-O	-5.15	1.18	1.24

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	N	42	PRO	CA-C	-5.15	1.47	1.52
2	N	408	LEU	C-O	-5.15	1.18	1.24
1	D	30	PHE	N-CA	-5.15	1.40	1.46
1	C	290	VAL	CA-C	-5.14	1.46	1.52
1	F	125	PRO	CA-CB	-5.14	1.46	1.53
1	B	267	SER	CA-CB	-5.14	1.47	1.53
1	D	33	ALA	CA-C	-5.14	1.46	1.52
1	E	917	VAL	C-O	-5.13	1.18	1.24
1	L	647	SER	CA-C	-5.13	1.45	1.52
1	A	197	LYS	CA-C	-5.13	1.45	1.52
1	E	409	LEU	CA-CB	-5.12	1.46	1.53
1	F	102	ILE	CA-CB	-5.12	1.49	1.54
1	A	825	SER	N-CA	-5.12	1.39	1.46
6	Y	78	GLN	CA-C	-5.11	1.46	1.53
2	N	567	SER	CA-C	-5.11	1.46	1.52
4	P	62	SER	CA-C	-5.11	1.46	1.52
1	A	917	VAL	N-CA	-5.10	1.40	1.46
1	F	103	ARG	CA-C	-5.10	1.46	1.52
1	L	62	ARG	CA-C	-5.10	1.46	1.52
1	F	716	THR	N-CA	-5.09	1.40	1.46
1	I	649	ALA	N-CA	-5.09	1.39	1.46
1	L	825	SER	CA-CB	-5.09	1.46	1.53
1	B	201	PRO	CA-CB	-5.09	1.48	1.53
1	G	195	ALA	CA-CB	-5.09	1.45	1.53
5	U	27	TYR	N-CA	-5.08	1.40	1.46
1	H	927	VAL	C-O	-5.08	1.18	1.24
1	J	469	ARG	CA-C	-5.08	1.46	1.52
1	A	919	PHE	CA-C	-5.08	1.46	1.52
1	L	15	SER	CA-CB	-5.07	1.45	1.53
1	A	917	VAL	CA-CB	-5.07	1.47	1.54
1	D	474	SER	N-CA	-5.06	1.40	1.46
1	B	365	THR	CA-C	-5.06	1.45	1.52
1	G	231	PRO	CA-CB	-5.06	1.47	1.54
1	L	680	THR	C-O	-5.06	1.17	1.23
6	X	61	SER	CA-C	-5.06	1.46	1.53
1	J	582	TRP	C-O	-5.05	1.17	1.23
1	D	299	ILE	C-O	-5.05	1.19	1.24
1	E	918	LEU	CA-C	-5.05	1.46	1.52
5	V	193	VAL	CA-CB	-5.04	1.47	1.54
1	E	503	MET	C-O	-5.03	1.18	1.24
1	G	644	ASP	CA-C	-5.03	1.46	1.52
2	N	408	LEU	N-CA	-5.03	1.40	1.46

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	371	LEU	CA-C	-5.03	1.46	1.52
4	P	33	SER	CA-C	-5.02	1.46	1.52
1	F	124	ALA	CA-CB	-5.02	1.45	1.53
1	B	267	SER	CA-C	-5.01	1.46	1.53
1	I	248	ILE	CA-CB	-5.01	1.48	1.54
1	I	846	PRO	CA-C	-5.01	1.46	1.52
2	N	380	LYS	CA-C	-5.01	1.46	1.52
1	B	919	PHE	CA-C	-5.00	1.46	1.52

All (605) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	1	26	GLY	N-CA-C	24.37	144.68	111.54
6	3	26	GLY	N-CA-C	20.30	150.30	113.76
6	Y	26	GLY	N-CA-C	19.80	144.65	110.80
6	W	26	GLY	N-CA-C	18.11	137.94	110.96
1	A	45	ARG	N-CA-C	16.76	135.50	113.72
6	W	32	GLY	N-CA-C	-15.77	92.14	115.63
1	C	845	PHE	N-CA-C	15.53	133.16	112.35
6	1	77	GLN	N-CA-C	14.83	127.44	111.28
5	V	146	LEU	N-CA-C	14.78	131.23	111.28
1	K	649	ALA	N-CA-C	-14.71	86.73	109.52
6	Y	40	LEU	N-CA-C	-14.31	95.77	111.36
1	D	201	PRO	N-CA-C	-14.02	89.64	110.80
1	D	845	PHE	N-CA-C	13.75	130.77	112.35
1	K	201	PRO	N-CA-C	-13.69	90.13	110.80
1	C	942	THR	N-CA-C	13.60	130.57	112.35
5	V	198	PHE	N-CA-C	13.59	126.18	111.36
1	L	845	PHE	CA-C-N	-13.22	106.02	119.90
1	L	845	PHE	C-N-CA	-13.22	106.02	119.90
1	B	270	GLU	N-CA-C	-13.07	97.04	111.28
1	E	201	PRO	N-CA-C	-12.78	91.50	110.80
1	H	845	PHE	CA-C-N	-12.62	106.65	119.90
1	H	845	PHE	C-N-CA	-12.62	106.65	119.90
1	J	201	PRO	N-CA-C	-12.62	91.75	110.80
1	K	845	PHE	CA-C-N	-12.20	107.09	119.90
1	K	845	PHE	C-N-CA	-12.20	107.09	119.90
1	H	200	GLN	CA-C-N	-11.96	107.80	119.76
1	H	200	GLN	C-N-CA	-11.96	107.80	119.76
4	P	59	THR	N-CA-C	-11.96	98.32	111.36
1	I	691	GLY	N-CA-C	11.95	127.06	112.73
2	N	378	VAL	N-CA-C	-11.65	99.24	110.42

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	H	201	PRO	N-CA-C	-11.62	92.95	111.19
1	E	751	GLU	N-CA-C	-11.59	99.14	113.97
1	A	732	GLY	N-CA-C	11.51	127.32	110.97
1	C	201	PRO	N-CA-C	-11.51	93.42	110.80
1	G	841	TYR	CA-C-N	-11.47	108.26	119.85
1	G	841	TYR	C-N-CA	-11.47	108.26	119.85
6	Y	63	THR	N-CA-C	11.45	123.76	111.28
1	G	845	PHE	CA-C-N	-11.41	107.51	119.83
1	G	845	PHE	C-N-CA	-11.41	107.51	119.83
6	W	38	GLY	N-CA-C	11.35	127.07	112.54
1	A	845	PHE	CA-C-N	-11.31	108.45	119.76
1	A	845	PHE	C-N-CA	-11.31	108.45	119.76
6	Y	38	GLY	N-CA-C	11.22	127.53	111.14
1	H	204	GLN	N-CA-C	11.20	123.56	111.36
6	W	37	TRP	N-CA-C	11.17	127.21	109.79
1	J	347	LEU	N-CA-C	-11.16	90.71	108.90
1	A	841	TYR	CA-C-N	-11.12	109.53	120.21
1	A	841	TYR	C-N-CA	-11.12	109.53	120.21
6	X	90	GLY	N-CA-C	11.05	127.24	111.10
2	N	299	ASP	N-CA-C	-10.89	99.49	111.36
1	D	200	GLN	CA-C-N	-10.84	108.52	119.90
1	D	200	GLN	C-N-CA	-10.84	108.52	119.90
1	D	730	TRP	N-CA-C	10.65	128.29	113.16
2	N	98	ASN	N-CA-C	-10.64	92.74	109.23
1	F	200	GLN	N-CA-C	10.61	127.18	112.75
1	B	200	GLN	N-CA-C	10.61	128.22	113.16
5	V	200	PRO	N-CA-C	10.60	127.68	111.14
1	B	738	THR	N-CA-C	-10.60	94.26	109.62
1	F	845	PHE	CA-C-N	-10.59	107.20	120.23
1	F	845	PHE	C-N-CA	-10.59	107.20	120.23
6	Z	9	LEU	N-CA-C	-10.57	99.92	112.92
2	N	501	GLU	N-CA-C	10.54	122.77	111.28
1	E	202	GLU	CA-C-N	-10.52	108.95	120.94
1	E	202	GLU	C-N-CA	-10.52	108.95	120.94
1	D	845	PHE	CA-C-N	-10.50	108.87	119.90
1	D	845	PHE	C-N-CA	-10.50	108.87	119.90
1	I	845	PHE	CA-C-N	-10.39	108.61	119.83
1	I	845	PHE	C-N-CA	-10.39	108.61	119.83
1	G	200	GLN	CA-C-N	-10.30	108.87	119.99
1	G	200	GLN	C-N-CA	-10.30	108.87	119.99
5	V	84	PRO	N-CA-C	10.21	126.84	110.40
1	L	201	PRO	N-CA-C	-10.16	95.45	110.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	V	149	ASP	N-CA-C	-10.16	94.61	110.36
6	Z	26	GLY	CA-C-O	-10.15	114.96	122.37
1	C	252	GLN	N-CA-C	10.09	122.00	108.07
6	X	76	PHE	N-CA-C	10.05	124.34	109.07
1	F	531	VAL	CB-CA-C	-10.02	100.42	111.35
6	1	10	ALA	N-CA-C	9.98	124.57	110.20
2	N	78	ASP	N-CA-C	9.96	121.90	111.14
1	D	294	THR	CA-C-N	-9.96	110.68	120.83
1	D	294	THR	C-N-CA	-9.96	110.68	120.83
1	J	845	PHE	CA-C-N	-9.95	109.09	119.83
1	J	845	PHE	C-N-CA	-9.95	109.09	119.83
1	J	679	PHE	N-CA-C	9.78	122.65	108.86
2	N	479	GLN	N-CA-C	-9.77	101.37	113.20
1	G	200	GLN	N-CA-C	9.75	126.00	112.75
6	X	80	VAL	N-CA-C	-9.74	103.24	111.91
1	B	272	THR	N-CA-C	-9.74	100.27	114.39
1	D	247	GLY	N-CA-C	9.72	122.73	111.36
1	D	28	VAL	N-CA-C	-9.63	101.00	110.72
1	B	268	THR	N-CA-C	9.59	121.73	111.28
2	N	197	ARG	N-CA-C	-9.58	100.84	111.28
1	C	845	PHE	CA-C-N	-9.56	106.40	120.46
1	C	845	PHE	C-N-CA	-9.56	106.40	120.46
1	B	730	TRP	N-CA-C	9.53	125.13	112.35
6	2	29	ASN	N-CA-C	-9.50	95.56	108.38
1	H	592	LEU	N-CA-C	-9.49	95.00	109.14
6	X	59	TRP	N-CA-C	-9.46	100.83	111.71
1	G	201	PRO	N-CA-C	-9.46	95.14	111.32
1	H	200	GLN	N-CA-C	9.43	125.58	112.75
6	Y	31	SER	N-CA-C	9.43	124.44	110.48
1	E	463	LEU	N-CA-C	9.38	121.11	111.07
1	D	471	PHE	N-CA-C	-9.29	99.96	111.11
1	E	649	ALA	N-CA-C	-9.28	93.28	109.06
1	A	838	GLY	N-CA-C	9.28	124.37	112.68
6	1	78	GLN	N-CA-C	9.25	120.11	108.45
1	C	255	GLY	N-CA-C	-9.16	91.48	113.18
6	W	27	THR	N-CA-C	9.12	123.37	109.23
6	Z	15	SER	N-CA-C	-9.04	101.43	111.28
2	N	380	LYS	CA-C-N	-8.96	110.53	119.76
2	N	380	LYS	C-N-CA	-8.96	110.53	119.76
1	D	200	GLN	N-CA-C	8.96	129.62	109.81
6	2	30	MET	N-CA-C	8.96	121.04	111.28
2	N	77	THR	N-CA-C	-8.94	101.43	111.71

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	K	845	PHE	N-CA-C	8.93	129.54	109.81
6	1	16	ARG	CA-C-N	-8.92	110.84	119.85
6	1	16	ARG	C-N-CA	-8.92	110.84	119.85
1	J	200	GLN	CA-C-N	-8.87	110.59	119.90
1	J	200	GLN	C-N-CA	-8.87	110.59	119.90
1	J	845	PHE	N-CA-C	8.85	129.37	109.81
2	N	173	GLY	N-CA-C	8.84	125.21	114.69
4	P	56	PRO	N-CA-C	-8.83	94.28	112.47
1	L	841	TYR	CA-C-N	-8.82	111.29	120.03
1	L	841	TYR	C-N-CA	-8.82	111.29	120.03
2	N	555	TYR	N-CA-C	8.78	120.93	111.36
1	K	204	GLN	N-CA-C	8.76	120.83	111.28
1	D	412	TYR	N-CA-C	8.72	123.28	109.50
6	X	83	GLY	N-CA-C	-8.69	101.20	111.36
2	N	378	VAL	CB-CA-C	-8.67	100.87	111.97
1	A	829	GLY	N-CA-C	8.66	126.57	112.89
1	L	200	GLN	CA-C-N	-8.66	110.81	119.90
1	L	200	GLN	C-N-CA	-8.66	110.81	119.90
1	A	730	TRP	CA-C-N	-8.65	109.45	119.05
1	A	730	TRP	C-N-CA	-8.65	109.45	119.05
1	D	731	PRO	N-CA-C	-8.64	101.12	113.47
1	B	472	LEU	N-CA-C	8.63	120.31	111.07
6	Y	64	GLY	N-CA-C	-8.63	102.38	112.73
1	D	204	GLN	N-CA-C	8.62	120.68	111.28
6	Y	5	ASN	N-CA-C	-8.61	102.49	113.16
1	E	200	GLN	CA-C-N	-8.55	110.92	119.90
1	E	200	GLN	C-N-CA	-8.55	110.92	119.90
1	B	471	PHE	N-CA-C	-8.52	101.95	111.07
1	F	841	TYR	CA-C-N	-8.50	112.05	120.21
1	F	841	TYR	C-N-CA	-8.50	112.05	120.21
1	D	841	TYR	CA-C-N	-8.47	111.64	120.03
1	D	841	TYR	C-N-CA	-8.47	111.64	120.03
1	D	730	TRP	CA-C-N	-8.45	110.19	118.97
1	D	730	TRP	C-N-CA	-8.45	110.19	118.97
1	H	843	ALA	N-CA-C	8.43	122.08	109.95
1	F	847	TYR	CA-C-N	-8.42	111.34	119.76
1	F	847	TYR	C-N-CA	-8.42	111.34	119.76
1	I	918	LEU	CB-CA-C	-8.40	99.50	111.85
2	N	41	VAL	CA-C-N	-8.37	111.76	120.38
2	N	41	VAL	C-N-CA	-8.37	111.76	120.38
1	G	847	TYR	N-CA-C	-8.35	99.28	109.72
2	N	50	GLY	N-CA-C	-8.35	99.70	112.89

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	X	62	SER	N-CA-C	-8.34	103.69	114.04
1	B	202	GLU	N-CA-C	8.34	119.19	109.60
4	Q	129	SER	N-CA-C	-8.24	102.30	111.28
1	F	845	PHE	N-CA-C	8.23	128.00	109.81
1	C	200	GLN	N-CA-C	8.19	127.91	109.81
1	A	841	TYR	N-CA-C	-8.18	100.77	108.13
1	B	350	GLN	N-CA-C	-8.14	102.40	111.28
1	K	45	ARG	N-CA-C	8.13	121.67	108.41
1	K	841	TYR	CA-C-N	-8.13	111.98	120.03
1	K	841	TYR	C-N-CA	-8.13	111.98	120.03
2	N	96	ILE	N-CA-C	8.11	119.88	108.93
1	L	412	TYR	N-CA-C	8.10	122.08	109.52
1	A	731	PRO	N-CA-C	-8.09	102.28	113.53
1	A	200	GLN	N-CA-C	8.02	127.54	109.81
1	G	845	PHE	N-CA-C	8.02	127.53	109.81
1	B	730	TRP	CA-C-N	-7.98	110.50	119.28
1	B	730	TRP	C-N-CA	-7.98	110.50	119.28
1	D	670	ASN	N-CA-C	-7.96	97.29	109.95
1	F	526	ASP	N-CA-C	7.95	119.58	111.07
1	G	648	ALA	N-CA-C	7.94	120.06	108.86
1	L	200	GLN	N-CA-C	7.92	123.53	112.75
1	I	841	TYR	CA-C-N	-7.89	112.22	120.03
1	I	841	TYR	C-N-CA	-7.89	112.22	120.03
3	M	313	SER	N-CA-C	7.89	126.35	113.89
1	K	200	GLN	CA-C-N	-7.88	111.62	119.90
1	K	200	GLN	C-N-CA	-7.88	111.62	119.90
6	4	28	SER	N-CA-C	-7.86	95.60	108.41
1	B	474	SER	N-CA-C	7.84	119.90	111.36
1	A	845	PHE	N-CA-C	7.83	127.12	109.81
6	0	29	ASN	N-CA-C	-7.82	98.36	110.17
1	A	843	ALA	N-CA-C	7.81	120.60	110.53
1	C	841	TYR	CA-C-N	-7.81	112.71	120.21
1	C	841	TYR	C-N-CA	-7.81	112.71	120.21
6	1	27	THR	CB-CA-C	-7.80	97.65	110.14
1	F	124	ALA	CA-C-N	-7.78	111.98	119.76
1	F	124	ALA	C-N-CA	-7.78	111.98	119.76
1	C	943	PRO	N-CA-C	-7.78	96.45	112.47
2	N	411	ASN	N-CA-C	7.76	119.82	111.36
1	L	677	TRP	N-CA-C	-7.75	97.61	109.85
6	Y	35	PHE	N-CA-C	7.74	121.81	110.59
1	K	200	GLN	N-CA-C	7.74	124.14	113.16
1	B	649	ALA	N-CA-C	-7.73	96.97	108.79

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	I	845	PHE	N-CA-C	7.69	126.81	109.81
1	F	105	VAL	CB-CA-C	-7.68	100.16	110.98
1	E	408	GLU	N-CA-C	7.64	119.61	111.28
6	1	30	MET	N-CA-C	7.63	119.68	111.36
2	N	478	ASP	N-CA-C	-7.61	104.14	113.50
1	A	37	TYR	N-CA-C	7.59	122.78	112.68
6	W	15	SER	N-CA-C	-7.59	103.00	111.28
1	H	847	TYR	N-CA-C	-7.57	100.25	109.72
2	N	175	TYR	N-CA-C	7.55	122.59	111.34
1	F	200	GLN	CA-C-N	-7.54	110.41	119.84
1	F	200	GLN	C-N-CA	-7.54	110.41	119.84
6	1	37	TRP	N-CA-C	7.54	121.65	111.24
6	Y	27	THR	N-CA-C	7.53	121.49	108.76
4	P	60	ALA	N-CA-C	-7.51	103.18	111.36
1	F	650	ASN	N-CA-C	7.48	121.24	110.10
5	U	16	GLN	N-CA-C	7.47	119.42	111.28
6	W	35	PHE	N-CA-C	-7.43	101.11	111.52
1	L	680	THR	CB-CA-C	-7.42	96.64	111.17
1	B	473	TYR	N-CA-C	-7.41	103.21	111.28
1	F	917	VAL	CB-CA-C	-7.41	102.87	111.09
6	X	65	GLN	N-CA-C	-7.38	103.38	112.38
5	V	61	ILE	CB-CA-C	-7.37	102.53	111.97
1	C	917	VAL	N-CA-C	-7.37	97.48	108.46
6	X	85	ALA	N-CA-C	7.33	121.35	109.40
1	F	202	GLU	CA-C-N	-7.32	110.69	119.84
1	F	202	GLU	C-N-CA	-7.32	110.69	119.84
5	V	199	ASN	CA-C-N	-7.30	112.24	119.76
5	V	199	ASN	C-N-CA	-7.30	112.24	119.76
6	Y	13	HIS	CB-CA-C	-7.30	101.12	111.85
2	N	383	THR	N-CA-C	7.29	120.66	111.69
1	A	30	PHE	N-CA-C	-7.26	103.37	111.28
6	W	30	MET	CB-CA-C	-7.25	99.79	110.96
6	1	10	ALA	CA-C-N	-7.25	112.53	119.85
6	1	10	ALA	C-N-CA	-7.25	112.53	119.85
1	K	647	SER	N-CA-C	-7.22	99.35	110.10
1	J	677	TRP	N-CA-C	-7.20	98.47	109.85
1	D	564	LYS	N-CA-C	7.20	124.13	114.12
6	1	65	GLN	N-CA-C	-7.20	103.60	112.38
1	K	648	ALA	N-CA-C	7.20	119.11	108.60
1	H	595	SER	N-CA-C	-7.18	103.13	112.68
6	Y	10	ALA	CA-C-N	-7.17	112.38	119.76
6	Y	10	ALA	C-N-CA	-7.17	112.38	119.76

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	733	ASN	N-CA-C	-7.16	98.37	109.76
1	B	475	ASN	CA-C-N	-7.16	115.57	123.16
1	B	475	ASN	C-N-CA	-7.16	115.57	123.16
1	F	104	GLY	N-CA-C	7.16	122.28	110.55
1	J	918	LEU	CB-CA-C	-7.15	101.11	111.70
1	L	61	GLN	N-CA-C	-7.13	98.23	109.07
6	W	31	SER	N-CA-C	7.13	125.99	110.80
1	J	823	ASN	N-CA-C	-7.11	98.34	109.72
1	B	740	ASN	N-CA-C	7.10	120.42	111.69
6	Z	27	THR	N-CA-C	7.09	125.91	110.80
6	3	27	THR	N-CA-C	7.09	120.08	108.52
1	C	227	THR	CA-C-N	-7.08	112.70	119.85
1	C	227	THR	C-N-CA	-7.08	112.70	119.85
2	N	474	SER	N-CA-C	7.07	121.20	109.46
1	C	588	VAL	CB-CA-C	-7.07	102.92	111.97
1	J	921	VAL	CB-CA-C	-7.06	99.71	111.29
1	C	254	ASN	N-CA-C	-7.05	98.59	109.52
1	D	847	TYR	CA-C-N	-7.03	112.52	119.90
1	D	847	TYR	C-N-CA	-7.03	112.52	119.90
1	I	648	ALA	N-CA-C	7.02	117.54	108.34
6	W	10	ALA	CA-C-N	-7.00	112.55	119.76
6	W	10	ALA	C-N-CA	-7.00	112.55	119.76
4	R	11	VAL	CA-C-N	-6.99	112.48	123.24
4	R	11	VAL	C-N-CA	-6.99	112.48	123.24
2	N	265	GLN	N-CA-C	-6.98	98.43	109.04
1	A	847	TYR	N-CA-C	-6.97	99.51	109.62
1	B	731	PRO	N-CA-C	-6.95	104.27	113.65
2	N	265	GLN	CA-C-N	-6.94	111.16	119.84
2	N	265	GLN	C-N-CA	-6.94	111.16	119.84
4	P	63	ALA	CA-C-N	-6.94	112.54	123.23
4	P	63	ALA	C-N-CA	-6.94	112.54	123.23
1	K	46	ASN	CA-C-N	-6.94	111.17	119.84
1	K	46	ASN	C-N-CA	-6.94	111.17	119.84
1	D	33	ALA	N-CA-C	6.92	118.91	111.36
1	L	917	VAL	CB-CA-C	-6.92	100.39	110.63
2	N	195	VAL	N-CA-C	6.92	119.88	112.96
1	J	564	LYS	N-CA-C	6.91	123.98	113.61
1	H	469	ARG	N-CA-C	-6.91	103.75	111.28
1	L	681	ARG	N-CA-C	6.90	120.15	108.90
1	A	501	ASP	N-CA-C	-6.89	103.84	111.36
1	D	562	PRO	CB-CA-C	-6.89	100.19	111.56
2	N	269	GLU	N-CA-C	6.88	119.40	110.53

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	1	36	SER	N-CA-C	6.88	119.40	110.53
1	A	823	ASN	N-CA-C	-6.87	98.87	109.24
1	B	369	TYR	N-CA-C	-6.87	103.80	111.28
1	C	915	LEU	CB-CA-C	-6.86	102.28	112.09
1	D	30	PHE	N-CA-C	-6.84	103.82	111.28
1	I	246	GLN	N-CA-C	-6.84	98.91	109.52
6	X	94	LEU	N-CA-C	6.83	125.34	110.80
4	P	55	THR	CA-C-N	-6.79	111.36	119.84
4	P	55	THR	C-N-CA	-6.79	111.36	119.84
2	N	95	VAL	N-CA-C	-6.78	104.24	110.82
2	N	189	VAL	N-CA-C	-6.76	102.60	111.05
1	J	922	PHE	CB-CA-C	-6.74	101.95	111.85
1	E	200	GLN	N-CA-C	6.73	122.72	113.16
4	R	12	SER	N-CA-C	6.73	121.73	107.67
1	G	230	LYS	CA-C-N	-6.70	113.36	120.66
1	G	230	LYS	C-N-CA	-6.70	113.36	120.66
1	H	841	TYR	CA-C-N	-6.68	113.80	120.21
1	H	841	TYR	C-N-CA	-6.68	113.80	120.21
6	1	70	LYS	N-CA-C	-6.68	104.00	111.28
1	H	206	GLY	N-CA-C	6.63	120.30	110.42
1	C	200	GLN	CA-C-N	-6.61	112.96	119.90
1	C	200	GLN	C-N-CA	-6.61	112.96	119.90
1	A	728	VAL	CB-CA-C	-6.61	104.05	111.45
1	D	668	SER	N-CA-C	6.61	119.82	110.23
2	N	75	LYS	N-CA-C	-6.61	105.08	113.01
1	D	666	ILE	N-CA-C	-6.60	94.62	108.88
1	L	372	LEU	N-CA-C	-6.58	104.03	111.07
1	J	204	GLN	N-CA-C	6.57	119.42	111.40
1	F	679	PHE	N-CA-C	6.56	118.73	108.96
1	F	196	ASP	N-CA-C	6.55	120.86	107.69
1	B	230	LYS	CA-C-N	-6.54	113.24	119.85
1	B	230	LYS	C-N-CA	-6.54	113.24	119.85
2	N	495	VAL	N-CA-C	6.54	122.95	109.34
1	L	843	ALA	N-CA-C	6.51	120.00	110.17
1	K	799	PRO	CB-CA-C	-6.50	102.46	110.98
1	F	648	ALA	N-CA-C	6.49	116.63	108.45
1	A	649	ALA	N-CA-C	-6.49	97.20	108.69
1	J	344	MET	N-CA-C	-6.48	99.45	109.24
3	M	55	SER	CA-C-N	-6.48	112.02	120.44
3	M	55	SER	C-N-CA	-6.48	112.02	120.44
1	B	191	THR	CA-C-N	-6.47	113.62	120.03
1	B	191	THR	C-N-CA	-6.47	113.62	120.03

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	N	570	THR	N-CA-C	6.47	121.18	108.18
1	E	822	HIS	N-CA-C	6.46	120.34	107.62
1	L	844	ASN	N-CA-C	6.44	123.36	112.99
1	J	499	THR	CB-CA-C	-6.43	98.64	109.50
6	3	24	ASP	N-CA-C	6.41	118.61	108.67
1	E	648	ALA	N-CA-C	6.40	117.95	108.60
2	N	74	ASN	N-CA-C	-6.38	105.46	113.18
1	J	680	THR	CB-CA-C	-6.37	97.74	110.42
2	N	408	LEU	N-CA-C	-6.37	104.25	111.07
5	U	133	ILE	N-CA-C	-6.36	98.36	107.77
1	L	410	PRO	CB-CA-C	-6.34	102.77	111.21
1	E	564	LYS	N-CA-C	6.34	121.96	113.72
1	D	473	TYR	N-CA-C	-6.34	104.37	111.28
1	J	917	VAL	N-CA-C	-6.33	99.10	108.85
2	N	49	THR	CB-CA-C	-6.33	100.09	110.85
5	V	63	THR	N-CA-C	-6.32	104.40	111.28
1	L	921	VAL	CB-CA-C	-6.30	100.95	111.29
6	Z	10	ALA	N-CA-C	6.30	118.78	110.08
1	L	202	GLU	N-CA-C	6.29	119.47	109.40
1	H	822	HIS	N-CA-C	6.29	120.01	107.62
1	F	201	PRO	N-CA-C	-6.29	99.52	112.47
1	A	44	PHE	N-CA-C	-6.28	99.43	108.60
6	1	39	SER	N-CA-C	6.28	118.89	110.35
6	W	22	TRP	N-CA-C	-6.28	104.13	110.97
4	P	62	SER	CA-C-N	-6.28	112.92	122.21
4	P	62	SER	C-N-CA	-6.28	112.92	122.21
2	N	47	ARG	CA-C-N	-6.25	112.73	119.98
2	N	47	ARG	C-N-CA	-6.25	112.73	119.98
1	K	916	TYR	N-CA-C	-6.25	99.01	109.07
1	K	919	PHE	N-CA-C	-6.25	98.72	108.90
2	N	499	PHE	CA-C-N	-6.24	112.03	119.84
2	N	499	PHE	C-N-CA	-6.24	112.03	119.84
1	F	101	ASP	N-CA-C	6.24	117.97	109.11
1	F	412	TYR	N-CA-C	6.23	119.34	109.50
1	I	650	ASN	N-CA-C	6.23	119.26	110.23
6	Y	62	SER	N-CA-C	6.22	124.05	110.80
6	W	29	ASN	N-CA-C	-6.22	99.77	109.72
1	K	915	LEU	N-CA-C	-6.22	99.06	109.07
6	X	88	ILE	N-CA-C	6.22	122.28	109.34
1	J	195	ALA	N-CA-C	6.22	118.06	110.41
6	3	29	ASN	N-CA-C	-6.20	97.60	110.80
1	K	654	PRO	N-CA-C	6.20	121.23	111.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	K	922	PHE	N-CA-C	-6.19	100.11	109.95
1	D	472	LEU	N-CA-C	6.17	117.67	111.07
6	X	91	VAL	N-CA-C	-6.14	99.64	108.42
1	D	203	PRO	CB-CA-C	-6.13	102.51	112.62
1	H	844	ASN	N-CA-C	6.13	121.80	112.54
1	I	686	GLU	N-CA-C	6.13	121.15	113.43
1	D	731	PRO	CB-CA-C	-6.13	103.32	113.06
2	N	477	ASN	N-CA-C	-6.12	98.43	108.41
1	C	946	ALA	N-CA-C	-6.12	103.40	113.50
1	F	101	ASP	CB-CA-C	-6.09	102.39	111.72
1	L	643	ASN	CB-CA-C	-6.09	102.32	110.79
6	X	76	PHE	N-CA-CB	-6.09	101.48	111.66
6	Z	10	ALA	CA-C-N	-6.09	113.67	119.76
6	Z	10	ALA	C-N-CA	-6.09	113.67	119.76
1	B	207	GLU	N-CA-C	-6.08	101.41	110.23
1	J	562	PRO	CA-C-O	-6.06	114.15	122.15
4	P	55	THR	CB-CA-C	-6.04	101.71	111.14
1	H	701	SER	CB-CA-C	-6.04	100.01	110.09
1	H	233	TYR	N-CA-C	-6.03	101.12	110.10
1	B	728	VAL	CB-CA-C	-6.02	103.32	111.63
1	C	845	PHE	CB-CA-C	-6.01	103.24	113.04
6	Z	30	MET	CB-CA-C	-6.01	101.45	110.88
1	J	847	TYR	CA-C-N	-6.01	113.57	119.76
1	J	847	TYR	C-N-CA	-6.01	113.57	119.76
1	G	195	ALA	N-CA-C	6.00	117.78	110.41
1	K	646	LEU	N-CA-C	-5.99	98.13	108.56
1	G	819	LEU	CA-C-N	-5.99	113.09	122.49
1	G	819	LEU	C-N-CA	-5.99	113.09	122.49
1	K	921	VAL	CB-CA-C	-5.98	101.48	111.29
4	P	57	LEU	CB-CA-C	-5.98	109.66	116.54
1	J	200	GLN	N-CA-C	5.97	121.64	113.16
5	V	145	GLY	N-CA-C	5.97	118.80	111.93
1	L	645	TYR	N-CA-C	5.97	117.79	111.28
1	L	822	HIS	N-CA-C	5.97	120.14	107.67
2	N	536	GLY	N-CA-C	5.96	120.36	111.18
6	Y	74	GLN	N-CA-C	-5.96	101.45	110.28
1	C	715	HIS	N-CA-C	-5.96	104.78	111.28
1	B	351	ALA	N-CA-C	5.95	117.85	111.36
1	C	921	VAL	N-CA-CB	-5.95	105.47	112.32
1	E	647	SER	N-CA-C	-5.95	101.03	109.96
1	H	471	PHE	CB-CA-C	-5.95	100.92	110.79
1	E	754	ASN	N-CA-C	-5.92	98.20	110.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	H	824	ASN	N-CA-C	-5.92	103.75	111.74
6	Z	11	PRO	N-CA-C	-5.91	101.91	111.19
1	A	27	LEU	N-CA-C	-5.91	104.96	111.82
1	G	261	VAL	CB-CA-C	-5.90	102.04	110.83
1	A	33	ALA	N-CA-C	5.89	117.37	111.07
2	N	95	VAL	CB-CA-C	-5.89	104.33	112.04
1	E	505	LYS	CA-C-N	-5.87	112.51	121.66
1	E	505	LYS	C-N-CA	-5.87	112.51	121.66
1	C	921	VAL	CB-CA-C	-5.86	102.35	110.91
1	L	410	PRO	CA-C-O	-5.86	114.28	121.31
1	F	530	ASN	N-CA-C	-5.85	106.68	113.88
1	D	474	SER	N-CA-C	5.83	117.71	111.36
6	Z	25	ILE	N-CA-C	5.82	121.44	109.34
1	D	32	ARG	N-CA-C	-5.81	104.95	111.28
1	D	233	TYR	N-CA-C	-5.80	101.81	110.23
1	D	662	VAL	CB-CA-C	-5.80	100.80	111.36
1	E	506	ARG	N-CA-C	5.79	117.49	109.15
1	H	847	TYR	CA-C-N	-5.79	114.00	120.14
1	H	847	TYR	C-N-CA	-5.79	114.00	120.14
1	D	300	SER	CB-CA-C	-5.79	100.39	110.17
1	A	917	VAL	N-CA-C	-5.78	99.85	108.46
1	B	477	ALA	N-CA-C	5.78	117.58	111.28
1	K	847	TYR	CA-C-N	-5.78	113.23	120.51
1	K	847	TYR	C-N-CA	-5.78	113.23	120.51
1	L	679	PHE	N-CA-C	5.78	117.63	108.79
1	B	202	GLU	CA-C-N	-5.77	113.91	120.89
1	B	202	GLU	C-N-CA	-5.77	113.91	120.89
1	G	198	THR	N-CA-C	5.76	117.56	111.28
2	N	73	ASP	CA-C-O	5.75	125.47	119.14
1	A	918	LEU	N-CA-C	-5.74	99.05	108.41
1	D	205	ILE	CB-CA-C	-5.74	101.87	111.29
1	G	841	TYR	CB-CA-C	-5.74	103.75	110.76
1	L	367	LEU	N-CA-C	-5.74	105.16	111.82
6	X	77	GLN	N-CA-C	5.74	117.85	108.55
1	A	40	LEU	N-CA-C	-5.74	103.88	112.54
2	N	473	LYS	O-C-N	-5.74	116.27	123.27
1	I	917	VAL	N-CA-C	-5.73	100.22	108.48
1	I	695	ASP	CB-CA-C	-5.73	103.81	110.17
1	D	661	ASN	N-CA-C	-5.70	99.75	108.76
1	C	945	SER	N-CA-C	5.69	117.25	110.19
2	N	554	VAL	N-CA-C	5.69	116.61	107.73
1	J	581	GLU	CB-CA-C	-5.69	97.55	110.07

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	K	203	PRO	CB-CA-C	-5.69	103.24	112.62
1	B	368	SER	CA-C-N	-5.68	112.66	120.28
1	B	368	SER	C-N-CA	-5.68	112.66	120.28
6	4	30	MET	N-CA-C	-5.68	105.44	112.72
1	B	647	SER	N-CA-C	-5.67	101.51	109.96
1	F	233	TYR	N-CA-C	-5.67	102.51	110.50
1	G	204	GLN	N-CA-C	5.67	119.37	112.23
4	P	54	GLY	CA-C-N	-5.66	116.31	123.15
4	P	54	GLY	C-N-CA	-5.66	116.31	123.15
6	X	79	LYS	N-CA-C	5.65	121.20	113.97
1	D	845	PHE	CB-CA-C	-5.65	103.83	113.04
6	Z	26	GLY	N-CA-C	-5.65	106.38	112.08
1	F	409	LEU	CA-C-N	-5.65	112.78	119.84
1	F	409	LEU	C-N-CA	-5.65	112.78	119.84
1	I	695	ASP	N-CA-C	-5.64	98.33	109.10
1	D	646	LEU	N-CA-C	-5.63	105.29	111.82
1	C	202	GLU	N-CA-C	5.63	118.41	109.40
1	B	732	GLY	N-CA-C	5.63	124.32	112.17
1	G	843	ALA	N-CA-C	5.63	118.11	110.35
4	Q	129	SER	CA-C-N	-5.62	111.61	120.60
4	Q	129	SER	C-N-CA	-5.62	111.61	120.60
1	A	34	THR	CB-CA-C	-5.62	99.24	110.42
1	F	915	LEU	CB-CA-C	-5.61	101.57	111.22
1	B	233	TYR	N-CA-C	-5.61	102.73	110.35
1	L	841	TYR	N-CA-C	5.60	113.26	108.22
1	C	233	TYR	N-CA-C	-5.60	101.61	109.96
1	E	750	GLY	N-CA-C	-5.60	103.19	111.03
1	B	733	ASN	N-CA-C	5.59	122.70	110.80
1	B	918	LEU	CB-CA-C	-5.58	103.08	111.73
1	A	46	ASN	N-CA-C	5.58	122.14	109.81
2	N	485	LEU	N-CA-C	-5.58	105.35	111.82
1	C	823	ASN	N-CA-C	-5.57	100.80	109.72
2	N	184	MET	N-CA-C	-5.57	105.21	111.28
6	0	30	MET	N-CA-C	5.56	117.34	111.28
1	L	644	ASP	N-CA-C	5.56	118.29	110.23
1	A	729	SER	N-CA-C	5.54	117.45	108.41
1	L	847	TYR	N-CA-C	-5.54	101.58	109.62
1	L	693	GLY	N-CA-C	-5.54	100.05	113.18
1	B	645	TYR	N-CA-C	5.54	117.31	111.28
1	B	730	TRP	CB-CA-C	-5.53	104.03	113.04
1	G	230	LYS	N-CA-C	-5.52	103.16	108.07
2	N	409	ALA	N-CA-C	5.52	116.98	111.07

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	1	38	GLY	N-CA-C	5.52	126.26	113.18
1	G	822	HIS	N-CA-C	5.51	118.01	107.75
1	A	822	HIS	N-CA-C	5.51	117.50	108.52
1	B	737	LEU	N-CA-C	5.51	116.97	111.07
6	1	24	ASP	N-CA-C	5.49	120.83	112.54
1	D	409	LEU	CA-C-N	-5.48	112.99	119.84
1	D	409	LEU	C-N-CA	-5.48	112.99	119.84
1	E	755	VAL	N-CA-C	-5.46	99.97	108.44
2	N	174	ASN	N-CA-C	-5.46	102.80	110.50
1	A	204	GLN	N-CA-C	5.46	117.66	111.11
1	B	741	GLU	N-CA-C	5.44	117.96	108.76
1	H	217	HIS	N-CA-C	-5.44	99.45	108.75
1	A	202	GLU	N-CA-C	5.44	116.74	109.83
6	1	27	THR	N-CA-C	5.44	117.26	108.34
5	U	130	GLY	N-CA-C	-5.44	100.91	111.02
6	1	8	SER	N-CA-C	-5.43	105.46	111.71
1	K	848	PRO	CA-C-O	-5.43	115.34	122.19
1	F	824	ASN	N-CA-C	-5.43	104.15	111.54
1	A	197	LYS	N-CA-C	5.42	120.31	111.37
1	G	645	TYR	N-CA-C	5.41	117.26	111.36
1	G	233	TYR	N-CA-C	-5.41	102.04	110.10
1	L	845	PHE	N-CA-C	5.40	121.75	109.81
5	V	85	ALA	CA-C-N	-5.40	114.79	120.94
5	V	85	ALA	C-N-CA	-5.40	114.79	120.94
5	V	196	VAL	CB-CA-C	-5.39	103.09	110.96
6	Y	27	THR	CB-CA-C	-5.38	99.96	109.70
6	W	31	SER	N-CA-CB	-5.38	101.40	110.49
1	H	203	PRO	CB-CA-C	-5.37	103.76	112.62
1	B	268	THR	CB-CA-C	-5.37	101.88	110.79
2	N	553	TYR	N-CA-C	5.37	118.84	112.72
1	K	654	PRO	CA-C-O	-5.36	115.14	121.67
5	U	62	THR	N-CA-C	-5.36	102.12	110.10
1	J	675	ARG	N-CA-C	5.35	121.35	114.56
5	V	194	PRO	CA-C-O	-5.34	115.37	121.56
5	V	196	VAL	N-CA-CB	-5.33	104.74	111.46
6	W	33	GLY	N-CA-C	-5.33	100.55	113.18
2	N	171	PRO	CB-CA-C	-5.33	104.88	111.64
1	H	235	SER	N-CA-C	5.33	117.20	108.52
1	C	844	ASN	N-CA-C	5.32	120.25	113.55
1	E	472	LEU	N-CA-C	-5.31	105.18	110.97
1	G	818	ILE	O-C-N	5.30	127.29	121.83
1	B	917	VAL	N-CA-C	-5.30	100.75	108.17

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	K	917	VAL	CB-CA-C	-5.29	102.61	111.29
6	3	76	PHE	N-CA-C	-5.29	100.77	109.40
1	B	597	GLY	N-CA-C	5.29	122.89	115.43
6	Y	6	PHE	N-CA-C	-5.28	104.99	113.28
1	C	846	PRO	CB-CA-C	-5.28	106.60	111.40
1	A	831	LEU	N-CA-C	5.28	119.01	112.47
1	L	369	TYR	N-CA-C	-5.28	105.61	111.36
2	N	555	TYR	CA-CB-CG	5.27	123.39	113.90
1	A	47	PRO	CB-CA-C	-5.27	104.66	111.46
1	D	33	ALA	CA-C-N	-5.27	114.07	122.66
1	D	33	ALA	C-N-CA	-5.27	114.07	122.66
2	N	79	VAL	N-CA-C	-5.26	98.41	109.34
1	K	394	ASP	CA-C-N	-5.25	113.28	119.84
1	K	394	ASP	C-N-CA	-5.25	113.28	119.84
6	W	8	SER	N-CA-C	-5.25	106.11	112.88
1	K	843	ALA	N-CA-C	5.25	117.30	110.53
1	H	845	PHE	N-CA-C	5.24	121.40	109.81
1	A	39	SER	CB-CA-C	-5.23	100.57	109.51
1	B	915	LEU	N-CA-C	-5.23	100.37	108.90
2	N	486	ILE	N-CA-C	-5.23	105.29	110.62
1	J	471	PHE	CA-C-N	-5.22	113.65	120.44
1	J	471	PHE	C-N-CA	-5.22	113.65	120.44
1	F	128	ALA	N-CA-C	5.22	118.22	110.39
6	1	76	PHE	N-CA-C	5.22	121.92	110.80
1	A	197	LYS	CB-CA-C	-5.21	102.09	110.74
1	I	697	TYR	N-CA-C	5.21	117.44	109.62
6	2	32	GLY	N-CA-C	-5.21	100.92	112.17
1	A	28	VAL	CB-CA-C	-5.21	105.31	111.97
2	N	197	ARG	CA-C-N	-5.20	113.37	120.44
2	N	197	ARG	C-N-CA	-5.20	113.37	120.44
1	F	921	VAL	CB-CA-C	-5.19	101.53	110.30
2	N	569	ARG	CB-CA-C	-5.19	104.22	111.85
1	H	846	PRO	CA-C-O	-5.18	115.12	121.03
1	H	594	SER	CA-C-N	-5.18	112.86	122.60
1	H	594	SER	C-N-CA	-5.18	112.86	122.60
1	F	527	TYR	N-CA-C	-5.18	105.12	111.75
1	B	741	GLU	CB-CA-C	-5.17	100.34	109.70
1	B	739	PRO	N-CA-C	5.16	120.70	113.53
1	A	728	VAL	N-CA-C	5.16	116.04	110.21
1	B	728	VAL	N-CA-C	5.15	116.66	109.55
1	J	466	ASN	N-CA-C	-5.15	105.79	111.71
5	V	86	PRO	N-CA-C	-5.15	108.09	114.68

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	L	370	GLN	N-CA-C	-5.15	105.67	111.28
6	Y	61	SER	N-CA-C	5.14	116.69	111.14
1	E	502	TYR	N-CA-C	-5.13	105.58	111.07
1	C	942	THR	CA-C-N	-5.12	113.44	119.84
1	C	942	THR	C-N-CA	-5.12	113.44	119.84
1	J	848	PRO	CA-C-O	-5.11	115.51	121.34
5	U	14	GLN	N-CA-C	-5.11	99.24	108.85
2	N	410	TYR	N-CA-C	-5.10	105.72	111.28
1	C	843	ALA	N-CA-C	5.10	117.90	109.85
1	D	664	ILE	CB-CA-C	-5.08	102.54	110.52
1	B	599	ASP	N-CA-C	-5.08	102.53	110.10
1	C	253	GLN	N-CA-C	-5.08	100.18	108.67
1	C	748	VAL	N-CA-C	-5.08	108.89	113.71
6	Y	16	ARG	CA-C-N	-5.08	114.53	119.76
6	Y	16	ARG	C-N-CA	-5.08	114.53	119.76
6	3	77	GLN	N-CA-C	-5.07	106.87	113.16
1	G	846	PRO	CA-C-O	-5.07	115.81	121.23
4	R	11	VAL	CB-CA-C	-5.07	105.30	112.14
6	3	28	SER	N-CA-C	-5.06	101.37	109.07
2	N	554	VAL	CB-CA-C	-5.06	104.82	111.25
5	V	193	VAL	CB-CA-C	-5.05	102.17	111.36
1	L	846	PRO	CA-C-O	-5.04	115.29	121.03
1	J	203	PRO	CB-CA-C	-5.03	104.32	112.62
1	I	46	ASN	CA-C-N	-5.02	113.57	119.84
1	I	46	ASN	C-N-CA	-5.02	113.57	119.84
1	L	199	PHE	N-CA-C	5.02	119.40	113.28
1	B	479	TYR	N-CA-C	5.01	119.08	112.92
1	A	201	PRO	N-CA-C	-5.01	102.97	112.33
6	Y	66	MET	N-CA-C	-5.00	105.83	111.28

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	7427	0	7124	218	0
1	B	7429	0	7126	212	0
1	C	7456	0	7156	224	0
1	D	7427	0	7124	213	0
1	E	7408	0	7112	226	0
1	F	7430	0	7131	222	0
1	G	7441	0	7138	205	0
1	H	7455	0	7159	218	0
1	I	7417	0	7118	228	0
1	J	7419	0	7116	216	0
1	K	7442	0	7142	211	0
1	L	7427	0	7127	236	0
2	N	3734	0	3656	107	0
3	M	2813	0	2767	58	0
4	P	972	0	978	31	0
4	Q	952	0	959	27	0
4	R	751	0	757	13	0
4	S	727	0	732	11	0
5	U	1268	0	1227	46	0
5	V	1414	0	1360	45	0
6	0	114	0	104	4	0
6	1	449	0	419	16	0
6	2	133	0	119	4	0
6	3	471	0	441	13	0
6	4	106	0	98	4	0
6	W	262	0	238	22	0
6	X	577	0	526	26	0
6	Y	485	0	458	31	0
6	Z	179	0	166	11	0
7	5	80	0	19	0	0
8	6	50	0	12	0	0
All	All	104715	0	100609	2692	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 13.

All (2692) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:251:LYS:HG2	1:C:258:GLU:HB2	1.48	0.96
4:P:58:GLU:HA	4:P:61:ALA:HB3	1.52	0.92
6:W:32:GLY:C	6:W:34:ALA:H	1.71	0.91

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:N:51:GLY:HA2	2:N:116:ARG:NH2	1.87	0.90
1:B:635:ASN:HD22	3:M:18:PRO:HB3	1.37	0.87
1:H:432:THR:HB	1:H:439:GLU:HB2	1.57	0.86
1:C:921:VAL:HB	1:C:943:PRO:HD2	1.58	0.85
1:E:795:ARG:HH22	6:Y:41:TRP:HA	1.41	0.85
3:M:89:ASP:OD1	3:M:89:ASP:N	2.10	0.84
1:D:574:LEU:H	1:D:929:ARG:HH12	1.25	0.84
1:E:105:VAL:HB	4:P:56:PRO:HG3	1.60	0.81
1:H:574:LEU:H	1:H:929:ARG:HH12	1.28	0.80
1:E:499:THR:HG22	1:E:501:ASP:H	1.46	0.80
1:D:659:ALA:HA	4:R:11:VAL:HG21	1.65	0.79
1:D:485:LYS:HG2	1:D:508:VAL:HB	1.65	0.79
3:M:216:ALA:HA	3:M:252:THR:HA	1.65	0.79
1:E:235:SER:HB3	1:E:292:ILE:HD11	1.65	0.78
1:F:18:ASP:OD1	1:F:18:ASP:N	2.14	0.78
1:C:678:ALA:HB3	1:C:918:LEU:HG	1.66	0.78
1:G:647:SER:HB3	1:G:675:ARG:HH22	1.48	0.78
1:J:58:ASP:HB2	5:V:148:PRO:HG2	1.66	0.78
2:N:51:GLY:HA2	2:N:116:ARG:HH21	1.48	0.77
1:B:686:GLU:HG2	1:B:700:TYR:CZ	2.20	0.77
1:J:921:VAL:HG12	1:J:943:PRO:HG2	1.64	0.77
1:H:573:LEU:HA	1:H:929:ARG:HH22	1.48	0.77
1:L:251:LYS:HB3	1:L:256:LYS:HA	1.66	0.77
1:H:390:VAL:HG21	1:H:790:MET:HE1	1.66	0.77
1:G:573:LEU:HA	1:G:929:ARG:HH12	1.47	0.76
1:B:803:GLN:HE22	1:C:550:GLY:HA3	1.50	0.76
1:C:195:ALA:HB1	1:C:200:GLN:HB3	1.66	0.76
1:J:18:ASP:N	1:J:18:ASP:OD1	2.17	0.76
4:P:79:PHE:HA	4:P:82:LEU:HB2	1.66	0.75
1:B:138:ALA:HB3	1:B:162:GLN:HB3	1.67	0.75
1:L:714:ASN:ND2	1:L:868:THR:O	2.20	0.75
1:C:788:ASP:OD2	1:C:795:ARG:NH1	2.20	0.75
1:G:113:LYS:NZ	1:G:115:TYR:O	2.21	0.74
2:N:292:TYR:HD1	2:N:378:VAL:HA	1.51	0.74
1:L:763:ASP:OD1	1:L:763:ASP:N	2.17	0.74
1:E:821:GLN:HB2	1:E:845:PHE:HB2	1.68	0.74
2:N:493:THR:HB	2:N:495:VAL:HG23	1.68	0.74
1:L:697:TYR:O	4:P:26:ARG:NH2	2.20	0.74
1:L:921:VAL:HB	1:L:943:PRO:HD2	1.69	0.74
1:I:572:LEU:O	1:I:929:ARG:NH1	2.20	0.74
1:L:754:ASN:OD1	1:L:754:ASN:N	2.20	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:714:ASN:ND2	1:J:868:THR:O	2.21	0.74
6:W:31:SER:HB2	6:W:33:GLY:H	1.52	0.73
1:C:72:ARG:NE	1:C:79:TYR:OH	2.22	0.73
1:F:379:ARG:HE	1:F:390:VAL:HB	1.53	0.73
1:J:485:LYS:HG2	1:J:508:VAL:HB	1.70	0.73
1:B:502:TYR:OH	1:B:506:ARG:NH1	2.22	0.73
1:E:795:ARG:HH22	6:Y:41:TRP:CA	2.01	0.72
1:H:178:ILE:HG12	1:H:217:HIS:HD2	1.52	0.72
1:A:18:ASP:HA	1:A:47:PRO:HD2	1.71	0.72
1:F:921:VAL:HB	1:F:943:PRO:HD2	1.70	0.72
1:H:195:ALA:HB1	1:H:200:GLN:HB3	1.70	0.71
1:E:803:GLN:HE22	1:F:550:GLY:HA3	1.53	0.71
1:D:714:ASN:ND2	1:D:868:THR:O	2.22	0.71
1:J:330:ASP:OD1	1:J:331:ASN:ND2	2.24	0.71
1:K:485:LYS:HG2	1:K:508:VAL:HB	1.72	0.71
1:D:754:ASN:ND2	4:P:50:GLU:OE1	2.23	0.71
5:V:129:ARG:HA	5:V:134:GLN:HA	1.72	0.71
1:D:113:LYS:NZ	1:D:115:TYR:O	2.23	0.71
1:I:545:ARG:NH2	1:I:593:GLN:OE1	2.24	0.71
2:N:156:ASP:O	2:N:157:ASN:ND2	2.24	0.71
1:D:550:GLY:HA3	1:F:803:GLN:HE22	1.55	0.70
1:L:573:LEU:HA	1:L:929:ARG:HH12	1.56	0.70
6:W:32:GLY:C	6:W:34:ALA:N	2.36	0.70
1:C:400:ILE:HD11	1:C:476:ILE:HG12	1.73	0.70
1:J:411:ASN:ND2	1:K:466:ASN:OD1	2.25	0.70
1:B:138:ALA:HB2	1:B:164:LYS:HB2	1.74	0.70
1:E:638:ASN:ND2	1:F:24:SER:OG	2.22	0.70
1:J:58:ASP:OD1	1:J:58:ASP:N	2.24	0.70
1:D:456:ASN:O	1:E:836:ARG:NH1	2.25	0.69
1:H:379:ARG:HE	1:H:390:VAL:HB	1.56	0.69
1:K:379:ARG:HE	1:K:390:VAL:HB	1.56	0.69
3:M:72:LYS:NZ	3:M:115:ASP:OD1	2.25	0.69
1:C:502:TYR:OH	1:C:506:ARG:NH1	2.25	0.69
1:L:905:GLU:OE2	4:Q:22:TRP:NE1	2.23	0.69
2:N:171:PRO:HB2	2:N:174:ASN:HD21	1.58	0.69
1:C:754:ASN:N	1:C:754:ASN:OD1	2.25	0.69
1:I:35:GLU:OE2	1:I:41:ASN:ND2	2.26	0.69
4:P:28:ASN:ND2	4:P:43:ASN:OD1	2.25	0.69
5:V:71:PRO:O	5:V:75:PRO:HD2	1.92	0.69
2:N:68:ARG:NH1	2:N:562:SER:OG	2.26	0.69
2:N:254:ARG:C	2:N:256:SER:H	2.01	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:134:TRP:NE1	1:D:136:GLU:OE1	2.25	0.69
1:I:446:SER:O	1:I:449:ASN:ND2	2.24	0.69
1:K:572:LEU:O	1:K:929:ARG:NH1	2.22	0.69
2:N:295:SER:HB3	2:N:377:PRO:HD2	1.74	0.69
1:I:694:TYR:CE2	1:I:696:PRO:HA	2.28	0.69
1:B:252:GLN:HB3	1:B:258:GLU:HG3	1.73	0.69
1:H:407:ASP:OD2	1:H:462:ASN:ND2	2.26	0.69
1:C:921:VAL:HG12	1:C:943:PRO:HB2	1.75	0.68
1:I:235:SER:HB2	1:I:292:ILE:HD11	1.74	0.68
1:D:45:ARG:HH11	6:Z:27:THR:HG22	1.56	0.68
2:N:277:ASP:OD1	2:N:277:ASP:N	2.26	0.68
1:D:46:ASN:O	6:Z:27:THR:HG21	1.93	0.68
1:E:866:ASP:OD1	1:E:866:ASP:N	2.23	0.68
1:K:803:GLN:HE21	1:L:550:GLY:HA3	1.59	0.68
1:L:669:ARG:HH22	1:L:945:SER:H	1.42	0.68
1:A:550:GLY:HA3	1:C:803:GLN:HE22	1.58	0.68
1:I:178:ILE:HG12	1:I:183:ILE:HG22	1.75	0.68
1:K:921:VAL:HG12	1:K:943:PRO:HG2	1.75	0.68
1:G:231:PRO:HG3	1:G:318:SER:HB2	1.74	0.68
1:L:866:ASP:N	1:L:866:ASP:OD1	2.27	0.68
1:D:803:GLN:HE22	1:E:550:GLY:HA3	1.58	0.68
1:H:866:ASP:OD1	1:H:866:ASP:N	2.25	0.68
1:L:795:ARG:NH1	6:3:74:GLN:O	2.27	0.68
1:D:823:ASN:HD22	1:D:846:PRO:HD3	1.59	0.68
1:K:361:GLN:NE2	1:K:690:LEU:O	2.24	0.68
1:F:304:THR:HG22	1:F:306:LYS:H	1.59	0.68
1:L:390:VAL:HG21	1:L:790:MET:HE1	1.75	0.68
1:A:113:LYS:NZ	1:A:115:TYR:O	2.26	0.67
1:A:733:ASN:HB2	1:B:60:SER:HA	1.76	0.67
1:C:188:GLU:HB2	1:C:193:LYS:HE3	1.76	0.67
1:G:550:GLY:HA3	1:I:803:GLN:HE22	1.58	0.67
1:K:574:LEU:HG	1:K:929:ARG:HH11	1.58	0.67
1:F:389:ALA:O	1:F:545:ARG:NH1	2.27	0.67
1:C:391:ASP:HB3	1:C:539:ASN:HD21	1.59	0.67
1:D:251:LYS:HA	1:D:256:LYS:HA	1.76	0.67
1:G:170:GLN:O	1:I:839:GLN:NE2	2.28	0.67
1:G:647:SER:HB3	1:G:675:ARG:NH2	2.08	0.67
1:A:391:ASP:OD1	1:A:391:ASP:N	2.23	0.67
1:G:894:ALA:HB3	1:H:2:THR:HG21	1.76	0.67
1:B:790:MET:SD	1:B:867:ARG:NH2	2.67	0.67
1:D:587:ASP:OD1	1:D:601:ARG:NH2	2.27	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:405:THR:HG21	1:G:465:ALA:HA	1.77	0.67
1:J:759:ASN:OD1	1:J:759:ASN:N	2.28	0.67
1:L:529:ASP:OD2	1:L:715:HIS:NE2	2.25	0.67
1:L:789:ARG:HH11	6:3:75:ASN:HD21	1.40	0.67
1:H:634:ARG:NH1	1:H:931:HIS:O	2.28	0.67
1:J:813:TYR:O	1:J:814:GLN:NE2	2.28	0.67
1:L:407:ASP:OD2	1:L:462:ASN:ND2	2.25	0.66
1:B:737:LEU:HB2	1:B:763:ASP:OD2	1.94	0.66
1:F:317:GLN:HE22	1:F:835:MET:HB2	1.60	0.66
1:G:201:PRO:HG2	1:G:286:TYR:CD1	2.29	0.66
1:H:405:THR:HG21	1:H:465:ALA:HA	1.75	0.66
1:A:311:ARG:NH1	1:B:211:TYR:OH	2.27	0.66
1:E:587:ASP:OD2	1:E:601:ARG:NH2	2.29	0.66
1:E:683:LYS:HA	1:E:913:THR:HG22	1.77	0.66
1:H:485:LYS:HG2	1:H:508:VAL:HB	1.76	0.66
1:B:403:HIS:HD1	1:C:325:TYR:HH	1.41	0.66
1:C:89:ASP:OD1	1:C:932:ARG:NH1	2.28	0.66
1:L:104:GLY:HA2	1:L:610:ASP:HB2	1.77	0.66
1:L:362:ASP:HB2	1:L:941:ARG:HH12	1.60	0.66
6:2:6:PHE:HB3	6:2:9:LEU:HD13	1.78	0.66
1:C:572:LEU:HB3	1:C:640:GLN:HE22	1.60	0.66
1:C:304:THR:HG22	1:C:306:LYS:H	1.61	0.66
1:A:643:ASN:HB3	1:A:924:VAL:HG12	1.78	0.66
1:D:470:ASN:O	1:D:471:PHE:C	2.37	0.66
1:E:419:VAL:HG21	1:E:452:ARG:HB2	1.77	0.66
1:L:921:VAL:HG12	1:L:943:PRO:HB2	1.78	0.66
4:S:7:ASP:OD1	4:S:7:ASP:N	2.25	0.66
1:B:721:ALA:HB3	1:B:903:THR:HB	1.77	0.66
1:I:754:ASN:OD1	1:I:754:ASN:N	2.28	0.66
1:E:372:LEU:HD12	1:E:645:TYR:HB2	1.77	0.66
1:H:429:LYS:N	1:H:439:GLU:O	2.29	0.66
1:H:686:GLU:HG2	1:H:700:TYR:CZ	2.30	0.65
1:D:170:GLN:O	1:F:839:GLN:NE2	2.29	0.65
1:K:446:SER:O	1:K:449:ASN:ND2	2.29	0.65
1:E:231:PRO:HG3	1:E:318:SER:HB2	1.77	0.65
1:F:89:ASP:OD1	1:F:932:ARG:NH1	2.29	0.65
1:J:120:TYR:HE1	1:L:846:PRO:HB2	1.61	0.65
1:K:950:THR:HA	5:U:1:MET:HB3	1.77	0.65
1:A:733:ASN:O	1:A:734:ASP:C	2.37	0.65
1:B:686:GLU:HG2	1:B:700:TYR:CE2	2.32	0.65
1:D:379:ARG:HE	1:D:390:VAL:HB	1.61	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:195:ALA:HB1	1:I:200:GLN:HB3	1.79	0.65
1:L:250:VAL:O	1:L:260:GLN:NE2	2.29	0.65
6:3:24:ASP:O	6:3:25:ILE:HG13	1.97	0.65
1:C:788:ASP:O	1:C:795:ARG:NH1	2.29	0.65
1:E:572:LEU:O	1:E:929:ARG:NH1	2.28	0.65
1:I:419:VAL:HG21	1:I:452:ARG:HB2	1.79	0.65
1:J:218:ALA:HB3	1:J:283:VAL:HG22	1.78	0.65
1:J:329:ARG:HE	1:J:593:GLN:HB2	1.61	0.65
1:L:331:ASN:OD1	1:L:379:ARG:NH2	2.29	0.65
2:N:205:ASP:OD1	2:N:205:ASP:N	2.30	0.65
1:D:304:THR:HG22	1:D:306:LYS:H	1.62	0.65
1:F:391:ASP:HB3	1:F:539:ASN:HD21	1.62	0.65
1:J:304:THR:HG22	1:J:306:LYS:H	1.61	0.65
1:L:405:THR:HG21	1:L:465:ALA:HA	1.77	0.65
1:A:646:LEU:HG	1:A:648:ALA:HB2	1.79	0.65
1:D:839:GLN:NE2	1:E:170:GLN:O	2.29	0.65
1:A:237:ALA:HB3	1:A:246:GLN:NE2	2.12	0.65
1:H:429:LYS:HG3	1:H:441:ASP:HB2	1.78	0.65
1:D:759:ASN:N	1:D:759:ASN:OD1	2.28	0.64
1:D:916:TYR:CZ	1:D:918:LEU:HD21	2.32	0.64
1:I:680:THR:OG1	1:I:681:ARG:N	2.26	0.64
1:K:681:ARG:NH2	1:K:909:MET:SD	2.70	0.64
4:P:58:GLU:HA	4:P:61:ALA:CB	2.27	0.64
1:B:823:ASN:OD1	1:B:824:ASN:ND2	2.30	0.64
1:E:66:ARG:NH2	1:E:613:CYS:SG	2.70	0.64
1:A:758:CYS:SG	1:A:759:ASN:N	2.69	0.64
1:B:164:LYS:HE2	1:C:446:SER:HA	1.79	0.64
1:H:920:GLU:HG2	6:1:30:MET:HE1	1.79	0.64
1:A:411:ASN:ND2	1:B:466:ASN:OD1	2.31	0.64
1:A:803:GLN:HE22	1:B:550:GLY:HA3	1.63	0.64
1:B:18:ASP:N	1:B:18:ASP:OD1	2.31	0.64
1:B:304:THR:HG22	1:B:306:LYS:H	1.62	0.64
1:E:485:LYS:HG2	1:E:508:VAL:HB	1.78	0.64
1:A:440:LYS:HE2	1:A:442:ALA:HB2	1.78	0.64
1:A:754:ASN:OD1	1:A:754:ASN:N	2.28	0.64
1:H:221:ARG:NH1	1:H:288:GLU:OE2	2.31	0.64
1:J:589:ASN:OD1	1:J:601:ARG:NE	2.30	0.64
1:J:940:LEU:HD23	1:K:12:MET:HG3	1.80	0.64
1:I:487:SER:OG	1:I:506:ARG:NH1	2.30	0.64
3:M:327:GLN:HA	5:U:147:ARG:HH21	1.60	0.64
1:E:378:ASP:OD1	1:E:379:ARG:N	2.32	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:635:ASN:OD1	1:B:635:ASN:N	2.30	0.63
1:J:121:ASN:ND2	1:J:232:CYS:SG	2.68	0.63
1:L:95:MET:HE1	1:L:573:LEU:HD22	1.79	0.63
1:E:752:GLY:HA2	1:F:103:ARG:HH21	1.62	0.63
1:G:178:ILE:HG12	1:G:183:ILE:HG22	1.81	0.63
1:G:825:SER:OG	1:G:840:ALA:HA	1.97	0.63
1:I:485:LYS:HG2	1:I:508:VAL:HB	1.80	0.63
1:J:137:ALA:HB2	1:J:163:GLN:HG2	1.80	0.63
1:H:196:ASP:H	1:H:200:GLN:HB2	1.63	0.63
1:A:32:ARG:HD2	6:W:22:TRP:HA	1.80	0.63
1:C:35:GLU:OE2	1:C:41:ASN:ND2	2.31	0.63
1:J:839:GLN:NE2	1:K:170:GLN:O	2.32	0.63
1:A:298:HIS:HE2	1:A:319:MET:HE2	1.64	0.63
1:C:322:ARG:NH1	1:C:478:LEU:O	2.32	0.63
1:D:683:LYS:NZ	1:D:712:TYR:OH	2.31	0.63
1:J:929:ARG:HD2	1:J:935:ILE:HG12	1.80	0.63
1:B:218:ALA:HB3	1:B:283:VAL:HG22	1.81	0.63
1:E:348:ALA:HB2	1:E:355:ASN:HA	1.80	0.63
1:K:121:ASN:ND2	1:K:232:CYS:SG	2.71	0.63
1:K:339:ASN:HD21	1:K:365:THR:H	1.46	0.63
1:A:254:ASN:OD1	1:A:254:ASN:N	2.30	0.63
1:C:482:ASP:OD2	1:C:506:ARG:NH1	2.32	0.63
1:E:639:ASP:N	1:E:639:ASP:OD1	2.32	0.63
1:J:196:ASP:H	1:J:200:GLN:HB2	1.64	0.63
1:F:500:TYR:HB2	1:F:598:ASN:HD22	1.64	0.62
1:F:789:ARG:N	1:F:792:SER:OG	2.31	0.62
1:I:916:TYR:CZ	1:I:918:LEU:HD21	2.33	0.62
1:K:401:GLU:OE2	6:3:68:ARG:NH2	2.32	0.62
1:L:485:LYS:HG2	1:L:508:VAL:HB	1.81	0.62
1:A:634:ARG:NH1	1:A:931:HIS:O	2.31	0.62
1:D:366:GLU:HG3	1:D:707:LEU:HD22	1.81	0.62
1:D:446:SER:O	1:D:449:ASN:ND2	2.32	0.62
1:I:809:LYS:NZ	4:R:55:THR:OG1	2.31	0.62
1:B:730:TRP:O	1:B:731:PRO:C	2.38	0.62
1:C:58:ASP:N	1:C:58:ASP:OD1	2.31	0.62
1:D:739:PRO:HG2	1:L:341:THR:HB	1.80	0.62
1:L:130:ASN:ND2	1:L:230:LYS:O	2.32	0.62
2:N:133:ASN:ND2	2:N:430:VAL:O	2.32	0.62
1:K:407:ASP:O	1:L:126:LYS:NZ	2.32	0.62
1:A:514:ASP:OD1	1:A:515:CYS:N	2.28	0.62
1:C:587:ASP:OD2	1:C:601:ARG:NH2	2.30	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:598:ASN:ND2	1:H:603:ASP:OD2	2.32	0.62
1:I:234:GLY:HA3	1:I:297:THR:HG21	1.80	0.62
1:C:339:ASN:ND2	1:C:359:ASP:OD1	2.30	0.62
1:D:522:ARG:NH2	1:D:798:GLN:OE1	2.32	0.62
1:K:680:THR:HG21	1:K:711:PHE:HB3	1.81	0.62
1:A:589:ASN:OD1	1:A:601:ARG:NE	2.33	0.62
1:B:835:MET:HE1	1:C:210:TRP:HB3	1.82	0.62
1:C:502:TYR:CZ	1:C:506:ARG:HD2	2.34	0.62
1:D:487:SER:OG	1:D:506:ARG:NH1	2.32	0.62
1:J:210:TRP:HB3	1:L:835:MET:HE1	1.82	0.62
2:N:211:ASP:OD1	2:N:212:THR:N	2.33	0.62
6:W:30:MET:O	6:W:32:GLY:N	2.32	0.62
1:A:172:PRO:HG3	1:C:839:GLN:HB3	1.80	0.62
1:B:792:SER:O	1:B:796:ASN:ND2	2.32	0.62
1:D:229:MET:HE1	1:D:314:MET:HA	1.81	0.62
1:J:635:ASN:ND2	5:V:171:LEU:O	2.33	0.62
1:L:758:CYS:SG	1:L:759:ASN:N	2.72	0.62
1:E:790:MET:SD	1:E:867:ARG:NH2	2.73	0.62
1:H:18:ASP:OD1	1:H:19:ALA:N	2.33	0.62
1:L:391:ASP:HB3	1:L:539:ASN:HD21	1.63	0.62
1:F:736:LEU:HD22	1:F:763:ASP:HB3	1.81	0.61
1:G:446:SER:O	1:G:449:ASN:ND2	2.32	0.61
1:G:572:LEU:O	1:G:929:ARG:NH2	2.33	0.61
1:J:587:ASP:OD1	1:J:601:ARG:NH1	2.33	0.61
1:K:759:ASN:ND2	1:K:861:LYS:O	2.33	0.61
1:L:401:GLU:HG3	1:L:522:ARG:HG3	1.82	0.61
6:Y:39:SER:HB3	6:Y:41:TRP:O	1.99	0.61
1:A:183:ILE:HG21	1:A:219:ALA:HB2	1.80	0.61
1:E:921:VAL:HB	1:E:943:PRO:HD2	1.83	0.61
1:J:339:ASN:ND2	1:J:363:ARG:O	2.33	0.61
1:L:573:LEU:HD12	1:L:929:ARG:HH12	1.65	0.61
1:D:619:PHE:HD2	1:D:621:MET:HG3	1.65	0.61
1:K:733:ASN:ND2	1:L:58:ASP:O	2.34	0.61
4:Q:33:SER:OG	4:Q:37:ARG:N	2.33	0.61
1:E:339:ASN:HD21	1:E:365:THR:HG23	1.64	0.61
1:F:250:VAL:O	1:F:260:GLN:NE2	2.33	0.61
1:H:647:SER:OG	1:H:675:ARG:NH2	2.33	0.61
1:K:678:ALA:HB3	1:K:918:LEU:HG	1.81	0.61
4:R:28:ASN:ND2	4:R:43:ASN:OD1	2.27	0.61
1:D:822:HIS:O	1:D:822:HIS:ND1	2.34	0.61
1:F:102:ILE:HA	1:F:612:ILE:HG22	1.81	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:630:GLU:OE2	1:L:634:ARG:NH1	2.33	0.61
1:I:55:VAL:HG12	1:I:56:THR:HG23	1.83	0.61
1:J:17:GLN:HB3	1:J:21:GLU:HB2	1.83	0.61
1:A:796:ASN:ND2	1:A:866:ASP:O	2.30	0.61
1:E:165:THR:N	1:F:444:GLU:O	2.34	0.61
1:I:754:ASN:ND2	4:R:50:GLU:OE1	2.34	0.61
1:D:821:GLN:HG2	1:D:845:PHE:HB2	1.83	0.61
1:F:759:ASN:N	1:F:759:ASN:OD1	2.31	0.61
1:L:598:ASN:ND2	1:L:603:ASP:OD2	2.34	0.61
1:D:411:ASN:HD22	1:D:463:LEU:H	1.48	0.60
1:F:836:ARG:NE	1:F:836:ARG:O	2.32	0.60
1:I:202:GLU:OE1	1:I:204:GLN:NE2	2.32	0.60
1:I:250:VAL:O	1:I:260:GLN:NE2	2.33	0.60
1:K:407:ASP:N	1:K:407:ASP:OD1	2.34	0.60
1:J:455:ASN:ND2	1:L:207:GLU:O	2.34	0.60
1:K:227:THR:O	1:K:309:ASN:ND2	2.32	0.60
1:H:940:LEU:HD23	1:I:12:MET:HG3	1.83	0.60
1:K:104:GLY:HA2	1:K:610:ASP:HB2	1.83	0.60
1:A:730:TRP:O	1:A:731:PRO:C	2.33	0.60
1:E:18:ASP:OD1	1:E:19:ALA:N	2.31	0.60
1:F:717:PHE:HB3	1:F:744:ILE:HD13	1.83	0.60
1:K:647:SER:HB2	1:K:675:ARG:NH2	2.16	0.60
4:Q:28:ASN:ND2	4:Q:43:ASN:OD1	2.30	0.60
1:B:39:SER:N	1:C:778:GLN:OE1	2.32	0.60
1:H:456:ASN:O	1:I:836:ARG:NH2	2.33	0.60
1:H:814:GLN:NE2	1:I:240:THR:O	2.34	0.60
1:K:231:PRO:O	1:K:235:SER:OG	2.20	0.60
1:L:419:VAL:HG21	1:L:452:ARG:HB2	1.81	0.60
1:F:201:PRO:HG2	1:F:286:TYR:CE2	2.36	0.60
1:K:183:ILE:HG21	1:K:219:ALA:HB2	1.83	0.60
3:M:153:ASN:HA	3:M:158:GLN:HE22	1.65	0.60
6:X:80:VAL:C	6:X:82:ASP:H	2.10	0.60
1:A:589:ASN:HD22	1:A:600:LEU:HB2	1.66	0.60
1:C:598:ASN:ND2	1:C:603:ASP:OD2	2.34	0.60
1:G:137:ALA:HB2	1:G:163:GLN:HG2	1.83	0.60
1:J:806:ASP:OD1	1:J:809:LYS:N	2.28	0.60
1:B:390:VAL:HG11	1:B:790:MET:HE1	1.84	0.60
1:E:391:ASP:N	1:E:391:ASP:OD1	2.34	0.60
1:F:225:LYS:O	1:F:309:ASN:ND2	2.35	0.60
1:H:758:CYS:SG	1:H:759:ASN:N	2.75	0.60
1:G:250:VAL:HB	1:G:260:GLN:HE21	1.67	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:350:GLN:O	1:J:351:ALA:C	2.44	0.60
1:J:400:ILE:HD11	1:J:476:ILE:HG12	1.83	0.60
1:G:538:ARG:HA	1:G:543:ARG:HH21	1.67	0.60
1:G:754:ASN:OD1	1:G:754:ASN:N	2.32	0.60
1:I:73:GLU:OE2	1:J:66:ARG:NH2	2.30	0.60
1:I:866:ASP:N	1:I:866:ASP:OD1	2.35	0.60
1:K:569:LYS:NZ	1:K:570:ASN:OD1	2.34	0.60
2:N:51:GLY:N	2:N:54:SER:OG	2.35	0.60
2:N:295:SER:CB	2:N:377:PRO:HD2	2.32	0.60
2:N:130:ASN:ND2	2:N:130:ASN:O	2.35	0.59
5:V:165:ARG:O	5:V:169:LEU:HB2	2.02	0.59
1:B:403:HIS:ND1	1:C:325:TYR:OH	2.32	0.59
1:C:329:ARG:NH1	1:C:702:GLY:O	2.27	0.59
1:D:68:ILE:HD13	1:D:68:ILE:H	1.65	0.59
1:D:689:SER:OG	4:R:26:ARG:NH1	2.35	0.59
1:J:183:ILE:HG21	1:J:219:ALA:HB2	1.83	0.59
1:J:317:GLN:HE22	1:J:834:THR:HB	1.67	0.59
1:J:755:VAL:HG13	1:J:762:LYS:HG2	1.84	0.59
1:K:518:ASN:HB3	1:K:521:ALA:HB3	1.84	0.59
1:L:251:LYS:HG3	1:L:253:GLN:H	1.68	0.59
1:K:61:GLN:OE1	1:K:91:ARG:NH1	2.35	0.59
1:K:420:ILE:HD12	1:K:421:ASN:H	1.67	0.59
1:L:66:ARG:HE	1:L:68:ILE:HD11	1.67	0.59
1:H:743:GLU:OE1	1:H:746:ARG:NH1	2.35	0.59
1:L:790:MET:SD	1:L:867:ARG:NH2	2.75	0.59
5:V:139:SER:HB3	5:V:164:PRO:CD	2.32	0.59
1:B:921:VAL:HB	1:B:943:PRO:HD2	1.85	0.59
1:I:946:ALA:HA	1:L:728:VAL:HG22	1.84	0.59
1:L:646:LEU:O	1:L:647:SER:C	2.45	0.59
1:L:806:ASP:OD1	1:L:808:THR:N	2.35	0.59
3:M:234:LEU:HD22	5:U:198:PHE:HD2	1.66	0.59
4:P:58:GLU:O	4:P:62:SER:N	2.35	0.59
1:E:440:LYS:HE2	1:E:442:ALA:HB2	1.84	0.59
1:G:400:ILE:HD11	1:G:476:ILE:HG12	1.84	0.59
1:H:588:VAL:HG12	1:H:607:ILE:HG22	1.83	0.59
1:H:803:GLN:HE21	1:I:550:GLY:HA3	1.66	0.59
1:I:684:THR:O	4:Q:26:ARG:NH2	2.36	0.59
6:W:39:SER:HB3	6:X:82:ASP:HB2	1.85	0.59
1:A:79:TYR:HE1	1:A:584:PHE:HB2	1.68	0.59
1:A:718:LYS:HB3	1:A:905:GLU:HG3	1.85	0.59
1:C:553:ARG:NH2	1:C:554:TYR:OH	2.35	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:348:ALA:HB2	1:G:355:ASN:HA	1.84	0.59
1:I:921:VAL:HB	1:I:943:PRO:HD2	1.83	0.59
1:A:535:ASN:ND2	1:A:535:ASN:O	2.34	0.59
1:C:343:ASN:N	1:C:343:ASN:OD1	2.33	0.59
1:G:37:TYR:HB2	1:H:879:MET:HE3	1.85	0.59
1:H:836:ARG:NH1	1:H:836:ARG:O	2.36	0.59
1:A:493:ILE:HD11	1:A:502:TYR:CD1	2.37	0.59
1:B:403:HIS:HE1	1:C:543:ARG:HB3	1.68	0.59
1:F:207:GLU:OE1	1:F:208:SER:N	2.36	0.59
1:G:529:ASP:OD1	1:G:715:HIS:NE2	2.36	0.59
1:J:37:TYR:HB2	1:K:879:MET:HE3	1.83	0.59
1:A:538:ARG:HA	1:A:543:ARG:HH11	1.66	0.59
1:B:362:ASP:OD1	1:B:941:ARG:NH2	2.31	0.59
1:B:407:ASP:OD2	1:B:462:ASN:ND2	2.36	0.59
1:D:400:ILE:HD11	1:D:476:ILE:HG12	1.85	0.59
1:H:298:HIS:ND1	1:H:321:ASN:OD1	2.27	0.59
1:C:792:SER:O	1:C:796:ASN:ND2	2.36	0.58
1:H:883:ALA:H	1:I:48:THR:HG1	1.49	0.58
1:J:105:VAL:HG11	4:Q:57:LEU:HA	1.85	0.58
2:N:135:ASN:HD21	2:N:138:MET:HB2	1.67	0.58
3:M:70:HIS:CE1	3:M:99:LEU:HD21	2.38	0.58
1:B:135:ASP:HA	1:B:165:THR:HA	1.85	0.58
1:C:278:ASN:N	1:C:278:ASN:OD1	2.35	0.58
1:F:678:ALA:HB3	1:F:918:LEU:HG	1.84	0.58
1:L:112:PHE:HD1	1:L:326:ILE:HB	1.68	0.58
1:C:749:ASP:OD1	1:C:749:ASP:N	2.36	0.58
1:E:313:LEU:O	1:E:316:GLN:NE2	2.36	0.58
1:H:113:LYS:NZ	1:H:321:ASN:O	2.30	0.58
1:I:927:VAL:HG22	1:I:937:THR:HG22	1.85	0.58
1:F:178:ILE:HG12	1:F:183:ILE:HG22	1.85	0.58
2:N:122:ASP:OD1	2:N:564:ARG:NH1	2.36	0.58
3:M:47:GLN:HB2	6:W:8:SER:HB3	1.86	0.58
4:Q:20:PRO:HG2	4:Q:25:VAL:HG11	1.85	0.58
4:R:110:LEU:HA	4:R:114:LEU:HD23	1.85	0.58
1:A:639:ASP:OD2	1:A:926:ARG:NH1	2.36	0.58
1:B:355:ASN:ND2	1:B:357:VAL:O	2.35	0.58
1:E:792:SER:O	1:E:796:ASN:ND2	2.36	0.58
1:G:130:ASN:OD1	1:G:130:ASN:N	2.34	0.58
1:G:252:GLN:CD	1:G:258:GLU:HG2	2.29	0.58
1:I:436:ASN:N	1:I:436:ASN:OD1	2.35	0.58
1:J:130:ASN:ND2	1:J:230:LYS:O	2.37	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:487:SER:OG	1:J:506:ARG:NH1	2.37	0.58
1:B:647:SER:HB3	1:B:675:ARG:HH21	1.68	0.58
1:G:518:ASN:HB3	1:G:521:ALA:HB3	1.84	0.58
1:G:841:TYR:CZ	1:H:221:ARG:HB3	2.39	0.58
1:J:170:GLN:O	1:L:839:GLN:NE2	2.36	0.58
1:C:569:LYS:NZ	1:C:570:ASN:OD1	2.35	0.58
1:D:24:SER:OG	1:F:638:ASN:ND2	2.36	0.58
1:J:113:LYS:NZ	1:J:321:ASN:O	2.36	0.58
1:J:231:PRO:O	1:J:235:SER:OG	2.20	0.58
1:J:425:LEU:HD12	1:J:451:ILE:HD12	1.85	0.58
1:D:378:ASP:OD1	1:D:379:ARG:N	2.37	0.58
1:L:475:ASN:OD1	1:L:538:ARG:NE	2.37	0.58
1:C:24:SER:OG	3:M:16:SER:O	2.20	0.58
1:B:231:PRO:HG3	1:B:318:SER:HB2	1.85	0.58
1:B:371:LEU:O	1:B:372:LEU:C	2.45	0.58
1:C:371:LEU:HD13	6:W:30:MET:HE2	1.86	0.58
1:C:789:ARG:HD3	6:X:76:PHE:HZ	1.68	0.58
1:G:648:ALA:HA	1:G:921:VAL:HG22	1.85	0.58
1:H:268:THR:HG22	1:H:270:GLU:H	1.68	0.58
1:K:53:HIS:ND1	1:K:54:ASP:OD2	2.36	0.58
2:N:146:ARG:HB2	2:N:165:TRP:CD2	2.38	0.58
4:S:33:SER:OG	4:S:37:ARG:N	2.31	0.58
1:A:237:ALA:HB3	1:A:246:GLN:CD	2.29	0.57
1:G:218:ALA:HB3	1:G:283:VAL:HG22	1.85	0.57
1:L:574:LEU:H	1:L:929:ARG:NH1	2.01	0.57
4:S:111:THR:O	4:S:115:ASN:ND2	2.36	0.57
1:A:137:ALA:HA	1:A:163:GLN:HA	1.84	0.57
1:A:325:TYR:N	1:A:595:SER:OG	2.36	0.57
1:B:485:LYS:HG2	1:B:508:VAL:HB	1.85	0.57
1:D:730:TRP:O	1:D:731:PRO:C	2.39	0.57
4:R:110:LEU:O	4:R:114:LEU:HB2	2.05	0.57
1:D:391:ASP:HB3	1:D:539:ASN:HD21	1.69	0.57
1:J:910:ASP:OD1	1:J:910:ASP:N	2.35	0.57
5:U:221:ASP:N	5:U:221:ASP:OD1	2.37	0.57
1:A:632:MET:HG3	5:U:170:THR:HG22	1.87	0.57
1:B:889:GLN:HA	1:B:892:LEU:HD23	1.87	0.57
1:D:403:HIS:NE2	1:E:547:MET:SD	2.77	0.57
1:F:797:PHE:O	1:F:798:GLN:NE2	2.37	0.57
1:G:274:GLY:HA3	1:G:279:LEU:HB2	1.86	0.57
1:I:560:GLN:OE1	1:I:560:GLN:N	2.38	0.57
3:M:270:VAL:HA	3:M:273:HIS:CE1	2.40	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:871:ARG:NH2	6:X:30:MET:SD	2.77	0.57
1:C:251:LYS:HG3	1:C:252:GLN:H	1.69	0.57
1:F:531:VAL:O	1:F:532:ASN:C	2.48	0.57
1:H:534:PHE:HE2	1:H:867:ARG:HH21	1.53	0.57
1:I:694:TYR:HE2	1:I:696:PRO:HA	1.70	0.57
1:K:910:ASP:OD1	1:K:910:ASP:N	2.30	0.57
1:I:845:PHE:O	1:I:846:PRO:C	2.38	0.57
1:K:170:GLN:HG3	1:L:452:ARG:HB3	1.86	0.57
2:N:254:ARG:C	2:N:256:SER:N	2.60	0.57
6:3:65:GLN:HG2	6:3:68:ARG:HB2	1.86	0.57
1:C:674:PHE:HA	1:C:943:PRO:HG2	1.87	0.57
1:D:639:ASP:OD1	1:D:639:ASP:N	2.36	0.57
1:E:268:THR:HG22	1:E:270:GLU:H	1.69	0.57
1:I:350:GLN:OE1	1:I:577:SER:OG	2.22	0.57
2:N:386:SER:C	2:N:388:LYS:H	2.12	0.57
1:D:669:ARG:HB3	1:D:669:ARG:HH11	1.69	0.57
1:E:317:GLN:HE22	1:E:835:MET:H	1.52	0.57
1:E:529:ASP:OD1	1:E:715:HIS:NE2	2.37	0.57
1:E:650:ASN:HB3	1:E:916:TYR:HE1	1.69	0.57
1:I:669:ARG:NH2	1:I:945:SER:H	2.03	0.57
1:J:325:TYR:N	1:J:595:SER:OG	2.36	0.57
1:K:135:ASP:OD1	1:K:165:THR:OG1	2.22	0.57
1:K:675:ARG:HD3	1:K:922:PHE:HE1	1.70	0.57
1:L:274:GLY:HA2	1:L:277:ASP:HB3	1.87	0.57
1:F:252:GLN:O	1:F:256:LYS:HB3	2.05	0.57
1:G:520:GLY:HA3	1:H:114:PRO:HG2	1.87	0.57
1:J:103:ARG:NH1	1:L:750:GLY:O	2.36	0.57
1:J:639:ASP:OD2	1:J:926:ARG:NH2	2.37	0.57
1:L:210:TRP:CZ3	1:L:417:GLY:HA3	2.40	0.57
1:L:446:SER:O	1:L:449:ASN:ND2	2.37	0.57
1:G:126:LYS:NZ	1:I:407:ASP:O	2.34	0.57
1:H:553:ARG:NH1	1:H:554:TYR:OH	2.38	0.57
1:H:846:PRO:HB2	1:I:120:TYR:HE1	1.69	0.57
2:N:283:ILE:HD12	2:N:403:TYR:HB3	1.86	0.57
4:P:61:ALA:O	4:P:64:ALA:HB2	2.05	0.57
1:K:940:LEU:HD13	5:U:31:ILE:HG12	1.87	0.56
1:L:334:GLY:N	1:L:366:GLU:OE2	2.35	0.56
2:N:76:SER:O	2:N:77:THR:C	2.44	0.56
1:D:589:ASN:ND2	1:D:599:ASP:OD1	2.38	0.56
1:I:574:LEU:HG	1:I:929:ARG:HH11	1.70	0.56
1:A:79:TYR:CE1	1:A:584:PHE:HB2	2.40	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:330:ASP:OD1	1:A:331:ASN:ND2	2.35	0.56
1:A:589:ASN:HD21	1:A:601:ARG:HG3	1.70	0.56
1:A:686:GLU:OE1	1:A:712:TYR:OH	2.23	0.56
1:C:475:ASN:OD1	1:C:538:ARG:NE	2.38	0.56
1:D:921:VAL:HG12	1:D:943:PRO:HG2	1.86	0.56
1:E:110:PRO:HD3	1:E:553:ARG:HH21	1.70	0.56
1:E:669:ARG:HH12	1:E:944:PHE:HA	1.70	0.56
1:F:523:TRP:CD1	1:F:802:ARG:HD3	2.41	0.56
1:G:910:ASP:OD1	1:G:910:ASP:N	2.31	0.56
1:I:905:GLU:OE1	4:R:22:TRP:NE1	2.30	0.56
1:J:389:ALA:HB3	1:J:545:ARG:HE	1.69	0.56
2:N:282:ASN:HA	2:N:404:ARG:HG2	1.88	0.56
1:B:407:ASP:O	1:C:126:LYS:NZ	2.34	0.56
1:E:183:ILE:HG21	1:E:219:ALA:HB2	1.86	0.56
5:U:59:ALA:HB2	5:U:193:VAL:HG21	1.87	0.56
1:G:24:SER:HB3	1:I:638:ASN:HD21	1.69	0.56
1:G:675:ARG:NH2	1:G:920:GLU:OE1	2.39	0.56
1:H:792:SER:O	1:H:796:ASN:ND2	2.38	0.56
1:K:82:ARG:NH1	1:K:581:GLU:OE2	2.39	0.56
4:P:20:PRO:HB2	4:P:25:VAL:HG21	1.86	0.56
1:B:422:THR:HG22	1:B:452:ARG:HB2	1.88	0.56
1:D:735:ARG:HB3	1:E:63:LEU:HG	1.88	0.56
1:D:835:MET:HE1	1:E:210:TRP:HB3	1.86	0.56
1:G:664:ILE:HD11	1:G:902:MET:HE3	1.86	0.56
1:J:547:MET:SD	1:L:403:HIS:NE2	2.79	0.56
1:K:403:HIS:HE1	1:L:543:ARG:HB3	1.70	0.56
4:Q:67:ALA:O	4:Q:71:THR:OG1	2.21	0.56
5:V:164:PRO:O	5:V:168:ILE:HB	2.06	0.56
1:C:363:ARG:NE	1:C:923:ASP:OD2	2.39	0.56
1:D:946:ALA:HA	1:I:728:VAL:HG12	1.87	0.56
1:H:327:ALA:HB2	1:H:546:SER:HA	1.86	0.56
1:I:526:ASP:OD1	1:I:526:ASP:N	2.38	0.56
1:J:35:GLU:OE2	1:J:41:ASN:ND2	2.39	0.56
1:K:456:ASN:O	1:L:836:ARG:NH2	2.37	0.56
5:V:80:TYR:HE1	5:V:195:SER:HB2	1.70	0.56
1:D:294:THR:HB	1:D:297:THR:HG23	1.86	0.56
1:E:364:ASN:HB2	1:E:650:ASN:ND2	2.21	0.56
1:E:387:ASN:HB3	1:E:545:ARG:HD2	1.86	0.56
1:F:196:ASP:O	1:F:197:LYS:C	2.49	0.56
1:F:526:ASP:C	1:F:528:MET:N	2.60	0.56
1:I:573:LEU:HA	1:I:929:ARG:NH2	2.20	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:936:GLU:HB3	5:V:157:ALA:HA	1.87	0.56
1:K:735:ARG:NH2	1:L:57:THR:O	2.36	0.56
1:K:773:TYR:HH	1:K:794:PHE:H	1.50	0.56
1:B:948:ASN:OD1	1:B:948:ASN:N	2.39	0.56
1:G:406:GLU:OE1	1:H:475:ASN:ND2	2.39	0.56
1:J:126:LYS:NZ	1:L:407:ASP:O	2.29	0.56
1:K:346:VAL:HA	1:K:355:ASN:HD21	1.70	0.56
1:E:176:ILE:O	1:E:217:HIS:ND1	2.32	0.56
1:H:807:ASP:N	1:H:807:ASP:OD1	2.37	0.56
1:I:19:ALA:HA	1:I:22:TYR:CE2	2.41	0.56
1:I:113:LYS:NZ	1:I:321:ASN:O	2.34	0.56
1:I:356:ALA:HA	5:V:156:GLY:H	1.71	0.56
1:L:421:ASN:OD1	1:L:421:ASN:N	2.38	0.56
1:A:405:THR:HG21	1:A:465:ALA:HA	1.88	0.55
1:A:813:TYR:O	1:A:814:GLN:NE2	2.39	0.55
1:A:883:ALA:H	1:B:48:THR:HG1	1.54	0.55
1:B:732:GLY:O	1:B:734:ASP:N	2.38	0.55
1:C:645:TYR:CZ	6:W:30:MET:HA	2.41	0.55
1:E:209:GLN:OE1	1:E:209:GLN:N	2.39	0.55
5:U:148:PRO:HD3	5:U:154:ILE:HD12	1.88	0.55
1:A:133:GLU:HG2	1:A:167:VAL:HG13	1.89	0.55
1:A:532:ASN:ND2	1:A:535:ASN:OD1	2.39	0.55
1:A:856:ASP:N	1:A:856:ASP:OD1	2.38	0.55
1:F:790:MET:SD	1:F:867:ARG:NH2	2.79	0.55
1:G:394:ASP:OD2	1:G:397:VAL:N	2.37	0.55
1:H:714:ASN:ND2	1:H:868:THR:O	2.39	0.55
1:I:379:ARG:HE	1:I:390:VAL:HB	1.72	0.55
1:I:523:TRP:CD1	1:I:802:ARG:HD3	2.41	0.55
1:J:585:ARG:HD3	1:J:590:MET:HE3	1.88	0.55
1:K:35:GLU:OE2	1:K:41:ASN:ND2	2.39	0.55
1:C:137:ALA:HA	1:C:163:GLN:HB3	1.88	0.55
1:C:532:ASN:OD1	1:C:535:ASN:N	2.37	0.55
1:C:772:ASN:HA	6:W:35:PHE:CE2	2.41	0.55
1:D:408:GLU:OE1	1:D:408:GLU:N	2.37	0.55
1:F:251:LYS:HG2	1:F:258:GLU:HB3	1.88	0.55
1:F:339:ASN:ND2	1:F:359:ASP:OD1	2.36	0.55
1:G:543:ARG:HG2	1:G:547:MET:HE2	1.88	0.55
1:H:455:ASN:HD22	1:I:837:GLU:HA	1.71	0.55
1:I:354:LEU:HD23	1:J:91:ARG:HH21	1.69	0.55
5:V:3:LYS:HB3	5:V:200:PRO:HD2	1.88	0.55
1:A:407:ASP:OD2	1:A:462:ASN:ND2	2.33	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:337:TYR:CZ	1:B:585:ARG:HG3	2.42	0.55
1:C:18:ASP:OD1	1:C:18:ASP:N	2.31	0.55
1:D:574:LEU:H	1:D:929:ARG:NH1	2.00	0.55
1:F:587:ASP:OD2	1:F:601:ARG:NH2	2.40	0.55
5:U:179:ARG:HH22	5:U:182:GLY:N	2.04	0.55
1:A:545:ARG:NH2	1:A:593:GLN:OE1	2.39	0.55
1:B:134:TRP:HB2	1:B:309:ASN:HB3	1.89	0.55
1:E:756:ALA:O	1:E:757:GLN:C	2.48	0.55
1:F:644:ASP:O	1:F:647:SER:OG	2.20	0.55
1:J:391:ASP:OD1	1:J:545:ARG:NH2	2.38	0.55
1:J:635:ASN:OD1	1:J:636:ASP:N	2.39	0.55
1:K:733:ASN:HB3	1:L:60:SER:HA	1.87	0.55
1:B:408:GLU:OE1	1:B:408:GLU:N	2.35	0.55
1:C:261:VAL:HG13	1:C:287:SER:O	2.06	0.55
1:C:893:TYR:OH	1:E:948:ASN:ND2	2.39	0.55
1:E:598:ASN:ND2	1:E:603:ASP:OD2	2.39	0.55
1:H:372:LEU:HD12	1:H:645:TYR:HB2	1.88	0.55
1:I:639:ASP:OD1	1:I:639:ASP:N	2.38	0.55
1:J:924:VAL:HG11	1:K:12:MET:HB3	1.88	0.55
1:K:207:GLU:O	1:L:455:ASN:ND2	2.39	0.55
1:D:425:LEU:HD12	1:D:451:ILE:HD12	1.88	0.55
1:D:529:ASP:OD2	1:D:715:HIS:NE2	2.40	0.55
1:D:820:HIS:HA	1:E:204:GLN:HE22	1.72	0.55
1:E:573:LEU:HA	1:E:929:ARG:HH22	1.72	0.55
1:E:795:ARG:HH22	6:Y:41:TRP:C	2.13	0.55
1:K:210:TRP:CZ3	1:K:417:GLY:HA3	2.41	0.55
1:K:587:ASP:OD2	1:K:601:ARG:NH2	2.40	0.55
1:B:803:GLN:OE1	1:C:552:GLY:N	2.39	0.55
1:C:334:GLY:N	1:C:366:GLU:OE2	2.35	0.55
1:C:813:TYR:O	1:C:814:GLN:NE2	2.37	0.55
1:C:929:ARG:HG2	1:C:935:ILE:HG12	1.87	0.55
1:D:814:GLN:NE2	1:E:240:THR:O	2.39	0.55
1:E:102:ILE:HD13	1:E:609:PHE:HE2	1.72	0.55
1:E:805:VAL:HG13	1:E:855:VAL:HG21	1.89	0.55
1:F:740:ASN:HB3	1:F:741:GLU:HG3	1.89	0.55
1:J:444:GLU:HA	1:L:164:LYS:HG2	1.89	0.55
1:L:675:ARG:HH22	6:4:30:MET:HB3	1.72	0.55
1:A:207:GLU:HB2	1:B:455:ASN:HD21	1.71	0.55
1:D:764:TRP:HZ2	1:D:870:TRP:HB3	1.72	0.55
1:E:42:ASN:OD1	1:E:42:ASN:N	2.36	0.55
1:E:929:ARG:HH21	1:E:935:ILE:HD11	1.72	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:682:LEU:HD22	1:H:705:PRO:HB2	1.87	0.55
1:L:371:LEU:O	1:L:372:LEU:C	2.49	0.55
2:N:207:GLY:HA2	2:N:243:LEU:HB2	1.89	0.55
3:M:14:LEU:HD21	3:M:74:LEU:HB3	1.88	0.55
1:C:680:THR:OG1	1:C:681:ARG:N	2.40	0.55
1:E:514:ASP:OD1	1:E:515:CYS:N	2.32	0.55
1:G:733:ASN:HB3	1:H:60:SER:HA	1.89	0.55
1:G:812:ASP:OD2	1:H:238:LYS:NZ	2.37	0.55
1:G:927:VAL:HG22	1:G:937:THR:HG22	1.89	0.55
1:I:758:CYS:SG	1:I:759:ASN:N	2.79	0.55
1:J:452:ARG:HB3	1:L:170:GLN:HB3	1.90	0.55
4:P:61:ALA:O	4:P:62:SER:C	2.47	0.55
1:A:733:ASN:OD1	1:A:733:ASN:N	2.39	0.54
1:D:416:LEU:HD21	1:E:412:TYR:HE1	1.72	0.54
1:E:174:SER:OG	1:E:207:GLU:OE2	2.25	0.54
1:F:496:ASN:OD1	1:F:499:THR:N	2.41	0.54
1:G:130:ASN:HD22	1:I:842:PRO:HD3	1.73	0.54
2:N:536:GLY:H	2:N:539:GLN:HE21	1.55	0.54
1:F:195:ALA:HB1	1:F:200:GLN:HB3	1.89	0.54
1:F:274:GLY:HA3	1:F:279:LEU:HD21	1.89	0.54
1:G:758:CYS:HB3	1:G:799:PRO:HB3	1.90	0.54
1:J:227:THR:OG1	1:J:289:ASP:OD1	2.25	0.54
1:J:394:ASP:OD1	1:J:397:VAL:N	2.36	0.54
1:K:500:TYR:HB2	1:K:598:ASN:HD22	1.71	0.54
1:K:764:TRP:HZ2	1:K:870:TRP:HB3	1.72	0.54
1:L:386:TRP:HB2	1:L:388:GLN:HG3	1.89	0.54
1:B:88:GLY:HA3	1:B:91:ARG:NH1	2.22	0.54
1:B:391:ASP:HB3	1:B:539:ASN:HD21	1.73	0.54
1:D:866:ASP:N	1:D:866:ASP:OD1	2.39	0.54
1:I:556:PRO:HG3	4:S:54:GLY:HA3	1.89	0.54
1:I:573:LEU:HA	1:I:929:ARG:HH22	1.71	0.54
2:N:468:LEU:HD12	2:N:469:PRO:HD2	1.89	0.54
1:B:74:ASP:OD1	1:B:586:LYS:NZ	2.39	0.54
1:B:268:THR:C	1:B:270:GLU:H	2.14	0.54
1:B:469:ARG:NH2	1:B:828:VAL:HG21	2.22	0.54
1:G:650:ASN:HB3	1:G:916:TYR:HE1	1.71	0.54
1:H:61:GLN:OE1	1:H:91:ARG:NH1	2.41	0.54
5:V:13:TYR:OH	5:V:184:GLY:O	2.25	0.54
6:4:32:GLY:O	6:4:33:GLY:C	2.50	0.54
1:A:598:ASN:ND2	1:A:603:ASP:OD2	2.41	0.54
1:A:806:ASP:OD1	1:A:809:LYS:N	2.32	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:14:ILE:HG22	1:B:15:SER:H	1.72	0.54
1:C:111:THR:O	1:C:324:ASN:ND2	2.39	0.54
1:E:573:LEU:HA	1:E:929:ARG:NH2	2.23	0.54
1:H:718:LYS:HB2	1:H:905:GLU:HB3	1.89	0.54
1:I:218:ALA:HB3	1:I:283:VAL:HG22	1.90	0.54
1:A:391:ASP:HB3	1:A:539:ASN:HD21	1.72	0.54
1:A:919:PHE:O	1:A:921:VAL:HG13	2.07	0.54
1:B:942:THR:HG21	1:C:9:TRP:HH2	1.72	0.54
1:C:330:ASP:OD2	1:C:370:GLN:NE2	2.36	0.54
1:D:444:GLU:HB3	1:F:164:LYS:HA	1.89	0.54
1:G:196:ASP:H	1:G:200:GLN:HB2	1.72	0.54
1:H:636:ASP:HA	1:H:928:HIS:HE1	1.72	0.54
1:J:385:MET:HE1	1:L:780:PHE:HD2	1.72	0.54
1:J:789:ARG:NH2	6:3:35:PHE:O	2.40	0.54
1:A:893:TYR:OH	5:U:226:TYR:HA	2.08	0.54
1:E:425:LEU:HD12	1:E:451:ILE:HD12	1.90	0.54
1:G:500:TYR:HB2	1:G:598:ASN:HD22	1.72	0.54
1:I:650:ASN:HB3	1:I:916:TYR:HE1	1.73	0.54
1:K:178:ILE:HG22	1:K:183:ILE:HG22	1.89	0.54
1:K:391:ASP:HB3	1:K:539:ASN:HD21	1.72	0.54
1:K:500:TYR:HB2	1:K:598:ASN:ND2	2.23	0.54
2:N:115:ASP:N	2:N:115:ASP:OD1	2.37	0.54
1:C:639:ASP:N	1:C:639:ASP:OD1	2.40	0.54
1:D:635:ASN:OD1	1:D:636:ASP:N	2.41	0.54
1:E:201:PRO:HG2	1:E:286:TYR:CG	2.42	0.54
1:E:346:VAL:HG13	1:E:355:ASN:HB3	1.90	0.54
1:E:795:ARG:NH2	6:Y:41:TRP:HA	2.17	0.54
1:J:231:PRO:HG2	1:J:318:SER:HB2	1.88	0.54
1:K:167:VAL:N	1:L:449:ASN:OD1	2.40	0.54
1:K:529:ASP:OD1	1:K:862:LYS:NZ	2.40	0.54
2:N:83:ASN:HB2	2:N:86:ASN:HB2	1.89	0.54
1:A:229:MET:HE1	1:A:314:MET:HA	1.88	0.54
1:B:680:THR:HG22	1:B:681:ARG:H	1.72	0.54
1:F:830:TYR:N	1:F:837:GLU:OE2	2.35	0.54
1:J:201:PRO:HG2	1:J:286:TYR:CD1	2.42	0.54
1:L:391:ASP:OD1	1:L:545:ARG:NH1	2.41	0.54
5:V:126:LEU:N	5:V:137:ASP:OD1	2.41	0.54
1:C:929:ARG:HB2	1:C:929:ARG:HH11	1.73	0.53
1:H:407:ASP:O	1:I:126:LYS:NZ	2.40	0.53
1:I:469:ARG:HH12	1:I:828:VAL:HG11	1.72	0.53
3:M:143:LEU:HD22	3:M:172:VAL:HG21	1.89	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:362:ASP:OD2	1:A:948:ASN:ND2	2.41	0.53
1:A:673:ALA:HB2	1:B:9:TRP:CZ2	2.43	0.53
1:D:615:TYR:CZ	1:F:762:LYS:HE3	2.43	0.53
1:G:485:LYS:HG2	1:G:508:VAL:HB	1.91	0.53
1:G:523:TRP:CD1	1:G:802:ARG:HD3	2.43	0.53
1:K:340:SER:OG	1:K:343:ASN:O	2.25	0.53
1:L:825:SER:O	1:L:827:PHE:CD2	2.61	0.53
2:N:218:GLY:HA3	2:N:226:VAL:HG13	1.90	0.53
1:B:565:PHE:HD1	1:B:567:ALA:H	1.57	0.53
1:E:429:LYS:O	1:E:439:GLU:N	2.34	0.53
1:I:651:MET:SD	4:Q:18:ARG:NH1	2.81	0.53
1:I:916:TYR:CE2	1:I:918:LEU:HD21	2.44	0.53
1:J:669:ARG:N	1:J:898:HIS:O	2.37	0.53
1:K:895:ASN:HB3	5:U:194:PRO:HD3	1.89	0.53
1:L:231:PRO:O	1:L:235:SER:OG	2.26	0.53
1:E:341:THR:OG1	1:E:361:GLN:NE2	2.32	0.53
1:E:429:LYS:N	1:E:439:GLU:O	2.29	0.53
1:H:487:SER:OG	1:H:506:ARG:NH1	2.38	0.53
1:I:737:LEU:N	1:I:763:ASP:OD2	2.29	0.53
1:J:812:ASP:OD2	1:K:238:LYS:NZ	2.34	0.53
2:N:193:LEU:O	2:N:197:ARG:NH1	2.42	0.53
1:C:277:ASP:OD1	1:C:278:ASN:N	2.42	0.53
1:F:485:LYS:HG2	1:F:508:VAL:HB	1.91	0.53
1:I:734:ASP:HA	1:I:739:PRO:HB3	1.91	0.53
1:L:125:PRO:HG2	1:L:128:ALA:HB2	1.89	0.53
5:V:36:ALA:HB1	5:V:40:MET:HB3	1.89	0.53
1:D:669:ARG:HB3	1:D:669:ARG:NH1	2.24	0.53
1:G:413:CYS:HA	1:H:461:ILE:HB	1.90	0.53
1:G:922:PHE:O	1:G:941:ARG:HA	2.08	0.53
1:A:218:ALA:HB3	1:A:283:VAL:HG22	1.90	0.53
1:B:744:ILE:HG12	1:B:764:TRP:CD2	2.44	0.53
1:D:732:GLY:O	1:D:733:ASN:C	2.49	0.53
1:E:452:ARG:NH2	1:E:455:ASN:O	2.40	0.53
1:F:446:SER:O	1:F:449:ASN:ND2	2.42	0.53
1:J:198:THR:HB	1:J:241:ASN:CG	2.34	0.53
1:K:312:GLU:OE2	1:L:209:GLN:NE2	2.42	0.53
1:A:493:ILE:HD11	1:A:502:TYR:HD1	1.74	0.53
1:D:598:ASN:ND2	1:D:603:ASP:OD2	2.42	0.53
1:J:572:LEU:O	1:J:929:ARG:NH2	2.41	0.53
1:L:235:SER:HB3	1:L:292:ILE:HD11	1.90	0.53
1:B:29:GLN:NE2	6:X:5:ASN:OD1	2.42	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:482:ASP:OD2	1:F:506:ARG:NH2	2.42	0.53
1:G:724:PHE:CE1	1:G:900:LEU:HD13	2.44	0.53
1:H:829:GLY:HA2	1:H:837:GLU:HG2	1.91	0.53
1:I:598:ASN:ND2	1:I:603:ASP:OD2	2.41	0.53
4:Q:28:ASN:N	4:Q:28:ASN:OD1	2.42	0.53
1:A:170:GLN:O	1:C:839:GLN:NE2	2.42	0.53
1:A:675:ARG:NH1	1:A:920:GLU:OE1	2.40	0.53
1:A:789:ARG:NH2	6:X:35:PHE:O	2.37	0.53
1:G:304:THR:HG22	1:G:306:LYS:H	1.72	0.53
1:H:200:GLN:O	1:H:201:PRO:C	2.46	0.53
1:H:225:LYS:O	1:H:309:ASN:ND2	2.42	0.53
1:H:522:ARG:NH2	1:H:798:GLN:OE1	2.42	0.53
1:I:500:TYR:HB2	1:I:598:ASN:HD22	1.74	0.53
1:L:195:ALA:HB1	1:L:200:GLN:HB3	1.91	0.53
4:P:43:ASN:ND2	4:P:43:ASN:O	2.41	0.53
1:C:588:VAL:HG12	1:C:592:LEU:HD12	1.90	0.52
1:C:836:ARG:NE	1:C:836:ARG:O	2.40	0.52
1:D:598:ASN:O	1:D:701:SER:OG	2.27	0.52
1:E:390:VAL:HG21	1:E:790:MET:HE1	1.90	0.52
6:W:28:SER:HB3	6:X:84:LEU:HD22	1.91	0.52
1:D:871:ARG:HH12	6:O:30:MET:HG2	1.74	0.52
1:G:823:ASN:O	1:G:824:ASN:C	2.51	0.52
1:I:441:ASP:N	1:I:441:ASP:OD1	2.43	0.52
1:J:518:ASN:HB3	1:J:521:ALA:HB3	1.91	0.52
1:J:737:LEU:HD13	1:J:753:TYR:CD1	2.44	0.52
1:K:724:PHE:HE1	1:K:900:LEU:HD13	1.74	0.52
5:V:126:LEU:N	5:V:137:ASP:H	2.07	0.52
1:B:396:ASP:OD1	6:X:65:GLN:HB2	2.08	0.52
1:D:410:PRO:HB2	1:D:412:TYR:CE1	2.44	0.52
1:E:279:LEU:HB3	1:F:438:TRP:HB2	1.92	0.52
1:I:410:PRO:HB2	1:I:412:TYR:CE2	2.45	0.52
1:I:587:ASP:OD2	1:I:601:ARG:NH1	2.42	0.52
2:N:547:ARG:HD3	2:N:549:ARG:HD3	1.90	0.52
1:A:329:ARG:HG2	1:A:593:GLN:HB2	1.92	0.52
1:A:639:ASP:OD1	1:A:639:ASP:N	2.42	0.52
1:B:253:GLN:HG3	1:B:254:ASN:H	1.74	0.52
1:B:325:TYR:HE2	1:B:543:ARG:HG2	1.73	0.52
1:D:115:TYR:HE2	1:F:850:ILE:HD13	1.73	0.52
1:F:636:ASP:OD1	1:F:636:ASP:N	2.42	0.52
1:F:714:ASN:HB3	1:F:870:TRP:NE1	2.24	0.52
1:G:103:ARG:NH2	1:I:751:GLU:O	2.41	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:565:PHE:HD1	1:G:567:ALA:H	1.55	0.52
1:L:355:ASN:ND2	1:L:357:VAL:O	2.42	0.52
4:P:33:SER:O	4:P:36:GLY:N	2.43	0.52
4:S:50:GLU:HG2	4:S:52:VAL:HG23	1.90	0.52
1:C:789:ARG:HD3	6:X:76:PHE:CZ	2.44	0.52
1:D:759:ASN:ND2	1:D:861:LYS:O	2.36	0.52
1:F:513:VAL:HG13	1:F:517:ILE:HG21	1.91	0.52
1:J:422:THR:OG1	1:J:450:GLU:OE1	2.21	0.52
1:L:301:TYR:CZ	1:L:303:PRO:HG3	2.45	0.52
1:L:897:ALA:O	1:L:898:HIS:ND1	2.42	0.52
3:M:104:ARG:HG3	3:M:105:TYR:HD1	1.74	0.52
1:B:369:TYR:O	1:B:370:GLN:C	2.49	0.52
1:G:744:ILE:HG12	1:G:764:TRP:CD2	2.44	0.52
1:L:176:ILE:O	1:L:217:HIS:ND1	2.43	0.52
1:A:178:ILE:HG12	1:A:183:ILE:HG22	1.92	0.52
1:B:886:ASP:OD1	1:B:886:ASP:N	2.43	0.52
1:D:211:TYR:HE1	1:F:311:ARG:HH21	1.55	0.52
1:G:113:LYS:HE2	1:G:296:ASP:HB2	1.92	0.52
1:G:825:SER:O	1:G:827:PHE:CD2	2.62	0.52
4:Q:125:ARG:HG3	4:Q:126:GLN:N	2.23	0.52
1:A:355:ASN:OD1	1:A:357:VAL:N	2.37	0.52
1:A:758:CYS:HG	1:A:760:MET:H	1.55	0.52
1:B:212:GLU:H	1:B:212:GLU:CD	2.16	0.52
1:C:95:MET:HE1	1:C:573:LEU:HD22	1.92	0.52
1:G:734:ASP:N	1:G:734:ASP:OD1	2.43	0.52
1:K:686:GLU:HG3	1:K:700:TYR:CE2	2.44	0.52
1:K:744:ILE:HG12	1:K:764:TRP:CD2	2.44	0.52
1:L:121:ASN:ND2	1:L:232:CYS:SG	2.79	0.52
1:L:359:ASP:OD1	1:L:360:LEU:N	2.42	0.52
3:M:243:THR:O	3:M:262:ARG:NH2	2.40	0.52
1:D:655:ILE:HD11	1:D:915:LEU:HB2	1.92	0.52
1:D:789:ARG:N	1:D:792:SER:OG	2.43	0.52
1:G:363:ARG:NE	1:G:923:ASP:OD2	2.40	0.52
1:G:724:PHE:HE1	1:G:900:LEU:HD13	1.75	0.52
1:H:921:VAL:HG12	1:H:943:PRO:HG2	1.92	0.52
1:K:19:ALA:HA	1:K:22:TYR:CE2	2.45	0.52
1:K:21:GLU:O	5:V:176:SER:OG	2.21	0.52
1:L:669:ARG:N	1:L:898:HIS:O	2.40	0.52
2:N:238:PRO:HB2	2:N:259:LEU:O	2.10	0.52
1:A:675:ARG:HH22	6:X:30:MET:HB3	1.75	0.52
1:B:545:ARG:NH2	1:B:593:GLN:OE1	2.42	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:928:HIS:NE2	1:D:930:PRO:HG3	2.25	0.52
1:E:229:MET:HG3	1:E:309:ASN:ND2	2.24	0.52
1:H:199:PHE:HA	1:H:221:ARG:NH2	2.25	0.52
1:H:409:LEU:HD11	1:I:473:TYR:HB3	1.92	0.52
1:J:327:ALA:HB2	1:J:546:SER:HA	1.92	0.52
5:U:11:TRP:HA	5:U:23:ALA:HB2	1.92	0.52
1:A:66:ARG:NH2	1:E:73:GLU:OE1	2.41	0.51
1:D:18:ASP:OD1	1:D:18:ASP:N	2.43	0.51
1:F:58:ASP:N	1:F:58:ASP:OD1	2.43	0.51
1:J:298:HIS:ND1	1:J:321:ASN:OD1	2.29	0.51
1:J:648:ALA:HA	1:J:921:VAL:HG22	1.92	0.51
1:K:921:VAL:HB	1:K:943:PRO:HD2	1.91	0.51
1:L:133:GLU:HG2	1:L:167:VAL:HG13	1.91	0.51
1:L:241:ASN:OD1	1:L:241:ASN:N	2.42	0.51
1:L:298:HIS:ND1	1:L:321:ASN:OD1	2.34	0.51
1:L:829:GLY:HA2	1:L:837:GLU:HG2	1.92	0.51
2:N:99:ASN:H	2:N:99:ASN:HD22	1.57	0.51
3:M:106:ASN:OD1	3:M:107:SER:N	2.43	0.51
6:X:40:LEU:H	6:X:40:LEU:HD23	1.74	0.51
1:B:406:GLU:OE2	1:C:538:ARG:NH2	2.43	0.51
1:C:131:PRO:HB3	1:C:169:GLY:HA2	1.93	0.51
1:D:699:THR:O	1:D:699:THR:OG1	2.23	0.51
1:E:201:PRO:HG2	1:E:286:TYR:CD1	2.45	0.51
1:E:734:ASP:HA	1:E:739:PRO:HB3	1.92	0.51
2:N:196:GLY:O	2:N:197:ARG:C	2.51	0.51
1:A:120:TYR:HE1	1:C:846:PRO:HB2	1.75	0.51
1:H:806:ASP:HB2	1:H:858:ILE:HG23	1.93	0.51
1:I:341:THR:HB	1:L:739:PRO:HG2	1.93	0.51
1:J:246:GLN:HE21	1:L:822:HIS:CE1	2.28	0.51
1:K:298:HIS:ND1	1:K:321:ASN:OD1	2.32	0.51
1:L:234:GLY:HA3	1:L:297:THR:HG21	1.91	0.51
2:N:128:HIS:HD2	2:N:521:PRO:HB3	1.76	0.51
5:U:215:ASN:N	5:U:215:ASN:OD1	2.44	0.51
1:A:3:PRO:HG3	3:M:355:MET:HE1	1.93	0.51
1:B:400:ILE:HG12	1:B:524:SER:HA	1.93	0.51
1:C:355:ASN:ND2	1:C:357:VAL:O	2.43	0.51
1:D:108:ARG:HH12	1:D:549:LEU:HB3	1.75	0.51
1:D:241:ASN:HD21	1:D:245:GLY:HA3	1.75	0.51
1:E:475:ASN:OD1	1:E:538:ARG:NE	2.44	0.51
1:J:845:PHE:O	1:J:846:PRO:C	2.44	0.51
1:K:230:LYS:HB2	1:K:292:ILE:HD11	1.93	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:332:PHE:HB3	1:K:335:LEU:HD12	1.92	0.51
1:K:574:LEU:HG	1:K:929:ARG:NH1	2.25	0.51
2:N:171:PRO:HD2	2:N:183:LEU:HD21	1.91	0.51
4:P:40:LEU:HD12	4:P:46:THR:HG21	1.93	0.51
1:D:572:LEU:O	1:D:929:ARG:NH2	2.44	0.51
1:F:52:THR:OG1	1:F:53:HIS:N	2.43	0.51
1:F:829:GLY:HA2	1:F:837:GLU:HG2	1.91	0.51
1:G:48:THR:HB	1:I:883:ALA:H	1.75	0.51
1:G:574:LEU:H	1:G:929:ARG:NH1	2.09	0.51
1:I:339:ASN:OD1	1:I:365:THR:N	2.33	0.51
1:I:697:TYR:O	4:Q:26:ARG:NH1	2.43	0.51
1:L:825:SER:O	1:L:827:PHE:N	2.44	0.51
2:N:72:VAL:HG23	2:N:558:LEU:HD13	1.93	0.51
1:B:212:GLU:OE1	1:B:212:GLU:N	2.41	0.51
1:B:704:ILE:N	1:B:708:ASP:OD2	2.43	0.51
1:G:845:PHE:O	1:G:846:PRO:C	2.41	0.51
1:J:768:GLN:O	1:J:772:ASN:ND2	2.35	0.51
1:J:918:LEU:O	1:J:919:PHE:C	2.49	0.51
2:N:301:GLU:O	2:N:302:GLN:C	2.54	0.51
1:D:237:ALA:HB3	1:D:246:GLN:CD	2.36	0.51
1:D:499:THR:HG22	1:D:501:ASP:H	1.76	0.51
1:D:538:ARG:HD3	6:Y:66:MET:HE2	1.92	0.51
1:E:472:LEU:O	1:E:473:TYR:C	2.53	0.51
1:E:942:THR:HB	1:E:943:PRO:HD3	1.92	0.51
1:F:754:ASN:OD1	1:F:754:ASN:N	2.38	0.51
1:H:337:TYR:CZ	1:H:585:ARG:HG2	2.46	0.51
1:H:650:ASN:HB3	1:H:916:TYR:HE1	1.74	0.51
1:I:574:LEU:HD13	1:I:630:GLU:HG3	1.93	0.51
1:J:378:ASP:OD1	1:J:380:THR:N	2.43	0.51
1:K:355:ASN:OD1	1:K:356:ALA:N	2.43	0.51
1:L:582:TRP:HB3	1:L:584:PHE:HE1	1.75	0.51
2:N:142:LYS:O	2:N:253:SER:OG	2.20	0.51
5:V:169:LEU:O	5:V:173:THR:OG1	2.29	0.51
1:A:304:THR:HG22	1:A:306:LYS:H	1.75	0.51
1:A:730:TRP:O	1:A:730:TRP:CG	2.62	0.51
1:D:224:LYS:HG2	1:D:287:SER:HB2	1.93	0.51
1:D:824:ASN:ND2	1:D:824:ASN:O	2.43	0.51
1:E:871:ARG:CZ	6:Y:30:MET:HE1	2.40	0.51
1:G:950:THR:O	1:G:951:THR:OG1	2.27	0.51
1:H:650:ASN:OD1	1:H:916:TYR:OH	2.20	0.51
1:I:298:HIS:ND1	1:I:321:ASN:OD1	2.35	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:563:GLN:OE1	1:I:564:LYS:N	2.44	0.51
1:I:919:PHE:O	1:I:921:VAL:HG13	2.10	0.51
1:K:330:ASP:OD1	1:K:379:ARG:NH2	2.44	0.51
1:B:470:ASN:O	1:B:471:PHE:C	2.51	0.51
1:C:330:ASP:OD1	1:C:331:ASN:ND2	2.43	0.51
1:F:715:HIS:CD2	1:F:716:THR:HG23	2.46	0.51
1:H:871:ARG:HH11	6:1:31:SER:HB3	1.75	0.51
1:K:113:LYS:NZ	1:K:321:ASN:O	2.35	0.51
1:K:452:ARG:NE	1:K:455:ASN:O	2.39	0.51
1:L:19:ALA:N	1:L:46:ASN:OD1	2.43	0.51
1:L:746:ARG:HB3	1:L:749:ASP:HB2	1.93	0.51
1:L:942:THR:HB	1:L:943:PRO:HD3	1.92	0.51
5:V:215:ASN:OD1	5:V:215:ASN:N	2.43	0.51
1:B:2:THR:HG22	1:B:4:SER:H	1.75	0.51
1:C:789:ARG:N	1:C:792:SER:OG	2.44	0.51
1:G:18:ASP:OD1	1:G:18:ASP:N	2.41	0.51
1:K:195:ALA:HB1	1:K:200:GLN:HB3	1.93	0.51
2:N:133:ASN:H	2:N:175:TYR:HE1	1.59	0.51
1:B:299:ILE:HG21	1:B:302:MET:HE2	1.92	0.50
1:B:482:ASP:OD1	1:B:506:ARG:NH1	2.43	0.50
1:G:133:GLU:HG2	1:G:167:VAL:HG13	1.93	0.50
1:I:45:ARG:HH11	1:I:45:ARG:HG3	1.76	0.50
1:K:496:ASN:OD1	1:K:499:THR:N	2.44	0.50
3:M:200:ASN:HB2	5:U:199:ASN:ND2	2.27	0.50
5:V:19:LEU:HD11	5:V:88:THR:HG21	1.93	0.50
1:C:187:VAL:HG12	1:C:192:PRO:HA	1.92	0.50
1:C:307:GLU:OE1	1:C:307:GLU:N	2.39	0.50
1:C:402:ASN:ND2	1:C:517:ILE:O	2.35	0.50
1:F:398:ARG:NH2	1:F:866:ASP:OD2	2.37	0.50
1:F:425:LEU:HD12	1:F:451:ILE:HD12	1.93	0.50
1:G:822:HIS:HE1	1:H:246:GLN:NE2	2.09	0.50
1:H:821:GLN:HB2	1:H:845:PHE:HB2	1.91	0.50
1:K:413:CYS:SG	1:K:459:MET:HB2	2.51	0.50
2:N:297:LYS:O	2:N:300:THR:HB	2.11	0.50
1:C:921:VAL:CB	1:C:943:PRO:HD2	2.38	0.50
1:D:363:ARG:NE	1:D:923:ASP:OD2	2.44	0.50
1:D:434:GLN:HG3	1:D:437:GLY:N	2.25	0.50
1:E:900:LEU:HD11	1:E:902:MET:HG2	1.92	0.50
1:J:598:ASN:O	1:J:701:SER:OG	2.23	0.50
1:J:650:ASN:HB3	1:J:916:TYR:HE1	1.77	0.50
2:N:396:ASN:OD1	2:N:396:ASN:N	2.39	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:M:313:SER:O	3:M:314:LEU:HB2	2.10	0.50
6:W:32:GLY:O	6:W:34:ALA:N	2.43	0.50
1:A:753:TYR:O	1:A:762:LYS:HG3	2.12	0.50
1:B:325:TYR:CE2	1:B:543:ARG:HG2	2.47	0.50
1:B:372:LEU:O	1:B:373:LEU:C	2.54	0.50
1:B:730:TRP:C	1:B:732:GLY:N	2.60	0.50
1:E:113:LYS:NZ	1:E:321:ASN:O	2.29	0.50
1:E:297:THR:OG1	1:E:318:SER:OG	2.28	0.50
1:F:113:LYS:NZ	1:F:321:ASN:O	2.27	0.50
1:F:227:THR:OG1	1:F:289:ASP:OD1	2.25	0.50
1:G:221:ARG:HH12	1:G:288:GLU:CD	2.20	0.50
1:H:135:ASP:OD2	1:H:225:LYS:NZ	2.29	0.50
1:I:708:ASP:HB3	1:I:710:THR:HG23	1.94	0.50
1:I:812:ASP:N	1:I:812:ASP:OD1	2.44	0.50
1:J:389:ALA:O	1:J:545:ARG:NH2	2.44	0.50
1:A:113:LYS:HE2	1:A:296:ASP:HB2	1.93	0.50
1:A:646:LEU:HG	1:A:648:ALA:CB	2.41	0.50
1:C:130:ASN:N	1:C:130:ASN:OD1	2.41	0.50
1:C:200:GLN:O	1:C:201:PRO:C	2.53	0.50
1:D:133:GLU:HG2	1:D:167:VAL:HG22	1.94	0.50
1:G:203:PRO:HD3	1:G:221:ARG:HD2	1.92	0.50
1:I:307:GLU:OE1	1:I:307:GLU:N	2.44	0.50
1:I:391:ASP:OD1	1:I:539:ASN:ND2	2.42	0.50
1:J:529:ASP:OD1	1:J:715:HIS:NE2	2.45	0.50
1:K:724:PHE:CE1	1:K:900:LEU:HD13	2.47	0.50
1:A:744:ILE:HG12	1:A:764:TRP:CD2	2.47	0.50
1:A:789:ARG:NH2	6:X:36:SER:O	2.40	0.50
1:B:17:GLN:NE2	5:U:177:GLU:O	2.39	0.50
1:B:165:THR:N	1:C:444:GLU:O	2.25	0.50
1:C:18:ASP:HA	1:C:47:PRO:HD2	1.94	0.50
1:C:426:THR:HG21	1:C:440:LYS:HE3	1.92	0.50
1:E:673:ALA:HB2	1:F:9:TRP:CZ2	2.47	0.50
1:F:35:GLU:OE1	1:F:41:ASN:ND2	2.44	0.50
1:F:447:ASP:OD1	1:F:447:ASP:N	2.43	0.50
1:G:121:ASN:ND2	1:G:232:CYS:SG	2.82	0.50
1:H:425:LEU:HD12	1:H:451:ILE:HD13	1.93	0.50
1:H:588:VAL:HG11	1:H:606:SER:HA	1.93	0.50
1:J:72:ARG:HD3	1:J:79:TYR:OH	2.10	0.50
1:K:892:LEU:HD13	5:U:189:ILE:HD11	1.93	0.50
2:N:80:ALA:O	2:N:81:SER:C	2.53	0.50
3:M:236:LEU:HD22	3:M:258:LEU:HD21	1.94	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:P:28:ASN:OD1	4:P:28:ASN:N	2.44	0.50
1:A:24:SER:O	1:A:25:PRO:C	2.54	0.50
1:B:669:ARG:HH22	2:N:101:TYR:HE1	1.60	0.50
1:B:725:ASP:N	1:B:725:ASP:OD1	2.42	0.50
1:C:224:LYS:HG3	1:C:288:GLU:O	2.11	0.50
1:E:936:GLU:HG2	5:U:157:ALA:HA	1.94	0.50
1:G:921:VAL:HA	1:G:943:PRO:HG2	1.93	0.50
1:H:680:THR:HG21	1:H:711:PHE:HB3	1.93	0.50
1:H:844:ASN:HB3	1:I:246:GLN:HE21	1.77	0.50
1:I:677:TRP:NE1	1:I:902:MET:SD	2.84	0.50
1:J:43:LYS:NZ	1:L:94:ASP:OD2	2.37	0.50
1:J:355:ASN:OD1	1:J:356:ALA:N	2.44	0.50
1:J:714:ASN:OD1	1:J:714:ASN:N	2.43	0.50
1:J:754:ASN:N	1:J:754:ASN:OD1	2.44	0.50
1:K:196:ASP:H	1:K:200:GLN:HB2	1.77	0.50
5:U:179:ARG:NH2	5:U:182:GLY:O	2.44	0.50
1:C:910:ASP:OD1	1:C:910:ASP:N	2.30	0.50
1:E:327:ALA:HB2	1:E:546:SER:HA	1.94	0.50
1:E:518:ASN:HB3	1:E:521:ALA:HB3	1.94	0.50
1:E:865:CYS:SG	1:E:868:THR:HG21	2.52	0.50
1:G:380:THR:HG21	6:1:72:LYS:HG2	1.94	0.50
1:I:694:TYR:HH	4:Q:33:SER:C	2.20	0.50
1:J:207:GLU:HB3	1:K:455:ASN:HD21	1.77	0.50
1:K:669:ARG:HD3	5:U:28:SER:HB3	1.93	0.50
2:N:459:ASN:O	2:N:460:PHE:C	2.55	0.50
1:A:90:ASN:OD1	1:A:90:ASN:N	2.45	0.50
1:D:732:GLY:O	1:D:734:ASP:N	2.45	0.50
1:F:51:PRO:HD3	6:Z:11:PRO:HA	1.94	0.50
1:G:839:GLN:HG2	1:H:172:PRO:HG3	1.93	0.50
1:H:368:SER:HG	1:H:644:ASP:CG	2.18	0.50
1:J:200:GLN:O	1:J:201:PRO:C	2.47	0.50
1:J:447:ASP:N	1:J:447:ASP:OD1	2.43	0.50
1:K:39:SER:O	1:L:778:GLN:NE2	2.45	0.50
1:K:644:ASP:OD1	1:K:645:TYR:N	2.43	0.50
4:Q:71:THR:HG22	4:Q:75:ILE:HG23	1.94	0.50
1:A:823:ASN:O	1:A:824:ASN:C	2.52	0.49
1:B:514:ASP:OD1	1:B:515:CYS:N	2.40	0.49
1:D:338:TYR:OH	1:D:564:LYS:N	2.31	0.49
1:E:90:ASN:N	1:E:90:ASN:OD1	2.45	0.49
1:F:253:GLN:H	1:F:253:GLN:CD	2.20	0.49
1:G:238:LYS:NZ	1:I:812:ASP:OD2	2.35	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:532:ASN:HD21	1:I:703:SER:HB3	1.76	0.49
1:J:830:TYR:N	1:J:837:GLU:OE1	2.35	0.49
1:K:401:GLU:HG2	1:K:403:HIS:CD2	2.46	0.49
2:N:189:VAL:O	2:N:193:LEU:HG	2.12	0.49
2:N:274:THR:H	2:N:277:ASP:CG	2.20	0.49
5:U:13:TYR:CE2	5:U:15:PRO:HA	2.46	0.49
1:A:456:ASN:O	1:B:836:ARG:NH1	2.45	0.49
1:E:413:CYS:HA	1:F:461:ILE:HB	1.94	0.49
1:H:329:ARG:HB2	1:H:333:ILE:H	1.77	0.49
1:H:475:ASN:OD1	1:H:538:ARG:NE	2.44	0.49
1:J:92:VAL:HG21	1:J:629:LEU:HD23	1.94	0.49
1:J:650:ASN:ND2	1:J:650:ASN:H	2.10	0.49
1:K:412:TYR:OH	1:L:835:MET:HA	2.12	0.49
1:K:839:GLN:NE2	1:L:170:GLN:O	2.45	0.49
1:C:572:LEU:HB3	1:C:640:GLN:NE2	2.26	0.49
1:H:655:ILE:HD11	1:H:915:LEU:HB2	1.94	0.49
1:I:121:ASN:ND2	1:I:232:CYS:SG	2.68	0.49
1:I:469:ARG:HG2	1:I:515:CYS:HB3	1.95	0.49
1:J:225:LYS:O	1:J:309:ASN:ND2	2.45	0.49
6:X:80:VAL:C	6:X:82:ASP:N	2.71	0.49
1:B:41:ASN:N	1:B:41:ASN:OD1	2.46	0.49
1:B:724:PHE:CE1	1:B:900:LEU:HD13	2.48	0.49
1:E:733:ASN:HB3	1:F:60:SER:HA	1.95	0.49
1:E:902:MET:HE3	1:E:904:PHE:HE1	1.78	0.49
1:G:455:ASN:HD21	1:I:207:GLU:HB3	1.78	0.49
1:H:700:TYR:CZ	1:H:702:GLY:HA3	2.47	0.49
1:I:500:TYR:HB2	1:I:598:ASN:ND2	2.27	0.49
1:J:929:ARG:NH1	1:J:929:ARG:HB2	2.27	0.49
1:A:237:ALA:O	1:A:238:LYS:C	2.56	0.49
1:B:500:TYR:HB2	1:B:598:ASN:HD22	1.77	0.49
1:C:251:LYS:HB3	1:C:256:LYS:HA	1.95	0.49
1:D:405:THR:HG21	1:D:465:ALA:HA	1.93	0.49
1:D:551:ASN:HB3	1:F:521:ALA:HB2	1.94	0.49
1:D:803:GLN:OE1	1:E:552:GLY:N	2.45	0.49
1:E:99:TYR:HE2	1:E:560:GLN:HE21	1.59	0.49
1:G:237:ALA:HB3	1:G:246:GLN:HG2	1.94	0.49
1:G:900:LEU:HD21	1:G:902:MET:HE2	1.93	0.49
1:H:339:ASN:HD21	1:H:365:THR:HG23	1.78	0.49
1:H:482:ASP:OD2	1:H:502:TYR:OH	2.31	0.49
1:K:677:TRP:NE1	1:K:902:MET:SD	2.85	0.49
2:N:51:GLY:HA2	2:N:116:ARG:HH22	1.75	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:636:ASP:HA	1:A:928:HIS:HE1	1.78	0.49
1:A:784:GLU:CD	1:A:784:GLU:H	2.17	0.49
1:B:430:PRO:HA	1:B:438:TRP:CD1	2.47	0.49
1:C:210:TRP:CZ3	1:C:417:GLY:HA3	2.48	0.49
1:C:473:TYR:O	1:C:477:ALA:HB3	2.12	0.49
1:G:789:ARG:O	1:G:792:SER:OG	2.31	0.49
1:H:112:PHE:CD1	1:H:326:ILE:HB	2.48	0.49
1:I:710:THR:O	1:I:710:THR:OG1	2.31	0.49
1:J:764:TRP:HZ2	1:J:870:TRP:HB3	1.78	0.49
1:J:789:ARG:O	1:J:792:SER:OG	2.30	0.49
1:A:796:ASN:OD1	1:A:796:ASN:N	2.46	0.49
1:C:819:LEU:HD21	4:P:78:ASP:HB3	1.94	0.49
1:D:731:PRO:HG3	1:D:742:PHE:CE1	2.48	0.49
1:G:552:GLY:N	1:I:803:GLN:OE1	2.44	0.49
1:G:678:ALA:HB3	1:G:918:LEU:HG	1.95	0.49
1:H:669:ARG:HH22	1:H:945:SER:H	1.59	0.49
1:K:337:TYR:CZ	1:K:585:ARG:HG2	2.48	0.49
1:L:587:ASP:OD2	1:L:601:ARG:NH2	2.46	0.49
3:M:14:LEU:HD23	3:M:74:LEU:HD22	1.93	0.49
5:V:179:ARG:H	5:V:179:ARG:NE	2.09	0.49
6:Y:10:ALA:O	6:Y:11:PRO:C	2.54	0.49
1:A:115:TYR:CG	1:C:519:LEU:HG	2.48	0.49
1:A:251:LYS:HB2	1:A:256:LYS:HG2	1.95	0.49
1:B:197:LYS:HB3	1:B:261:VAL:HG11	1.94	0.49
1:B:400:ILE:HD12	1:B:476:ILE:HD13	1.95	0.49
1:B:587:ASP:OD2	1:B:601:ARG:NH2	2.40	0.49
1:E:574:LEU:HG	1:E:929:ARG:HH11	1.76	0.49
1:F:429:LYS:HZ1	1:F:443:THR:HG1	1.53	0.49
1:F:573:LEU:HD11	1:F:578:TYR:CZ	2.48	0.49
1:G:539:ASN:OD1	1:G:542:LEU:N	2.38	0.49
1:H:928:HIS:HD2	1:H:930:PRO:HD3	1.78	0.49
1:I:678:ALA:O	1:I:918:LEU:N	2.41	0.49
1:K:714:ASN:ND2	1:K:868:THR:O	2.42	0.49
4:P:55:THR:C	4:P:57:LEU:HB2	2.38	0.49
1:A:495:ASP:OD1	1:A:495:ASP:N	2.46	0.49
1:B:196:ASP:O	1:B:197:LYS:C	2.56	0.49
1:C:379:ARG:HB2	1:C:790:MET:HE1	1.94	0.49
1:F:66:ARG:HG3	1:F:615:TYR:CZ	2.48	0.49
1:H:522:ARG:N	1:I:547:MET:HE2	2.28	0.49
1:J:686:GLU:HG2	1:J:700:TYR:CZ	2.47	0.49
1:K:57:THR:HG21	1:K:61:GLN:HG3	1.93	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:200:GLN:O	1:K:201:PRO:C	2.50	0.49
1:L:299:ILE:HG21	1:L:302:MET:HB2	1.94	0.49
1:L:329:ARG:HD3	1:L:593:GLN:HB2	1.93	0.49
2:N:212:THR:HG22	2:N:238:PRO:HA	1.95	0.49
2:N:478:ASP:C	2:N:480:ALA:N	2.65	0.49
1:A:865:CYS:SG	1:A:868:THR:HG21	2.52	0.49
1:G:73:GLU:HB2	1:G:80:LYS:HE2	1.95	0.49
1:G:327:ALA:HB2	1:G:546:SER:HA	1.95	0.49
1:H:407:ASP:OD1	1:H:407:ASP:N	2.42	0.49
1:I:594:SER:OG	1:I:701:SER:OG	2.28	0.49
1:J:178:ILE:HG12	1:J:183:ILE:HG22	1.94	0.49
1:K:428:VAL:HG12	1:K:440:LYS:HA	1.95	0.49
4:S:46:THR:O	4:S:46:THR:OG1	2.31	0.49
1:C:628:THR:HG22	1:C:632:MET:HE2	1.95	0.48
1:C:805:VAL:HG13	1:C:855:VAL:HG21	1.95	0.48
1:D:90:ASN:HD22	1:D:623:HIS:HB3	1.77	0.48
1:D:940:LEU:HD23	1:E:12:MET:HG3	1.94	0.48
1:H:403:HIS:ND1	1:I:325:TYR:OH	2.35	0.48
1:H:747:SER:OG	1:H:748:VAL:N	2.46	0.48
1:L:754:ASN:ND2	4:Q:50:GLU:OE1	2.46	0.48
1:L:803:GLN:NE2	1:L:859:THR:OG1	2.38	0.48
3:M:275:PHE:O	3:M:276:GLN:C	2.56	0.48
4:P:55:THR:O	4:P:56:PRO:C	2.53	0.48
1:A:420:ILE:HG13	1:A:421:ASN:OD1	2.14	0.48
1:B:178:ILE:HD13	1:B:284:VAL:HG23	1.95	0.48
1:F:337:TYR:HA	1:F:585:ARG:HH21	1.78	0.48
1:I:327:ALA:HB2	1:I:546:SER:HA	1.95	0.48
1:I:667:PRO:O	1:I:669:ARG:N	2.46	0.48
1:K:727:SER:HB2	5:U:16:GLN:HE21	1.78	0.48
1:L:201:PRO:HG3	1:L:286:TYR:CG	2.49	0.48
4:P:99:LYS:HD3	4:P:100:LEU:HG	1.93	0.48
5:U:217:ASP:HB3	5:U:220:LYS:O	2.12	0.48
5:V:87:THR:O	5:V:88:THR:C	2.56	0.48
1:A:524:SER:O	1:A:862:LYS:NZ	2.36	0.48
1:C:108:ARG:NH1	1:C:550:GLY:O	2.34	0.48
1:C:397:VAL:HG11	1:C:536:HIS:CD2	2.48	0.48
1:C:486:TYR:O	1:C:506:ARG:NE	2.44	0.48
1:D:74:ASP:OD2	1:D:586:LYS:NZ	2.36	0.48
1:F:61:GLN:HE22	1:F:91:ARG:HB3	1.78	0.48
1:H:210:TRP:CE3	1:H:417:GLY:HA3	2.47	0.48
1:J:75:THR:HG22	1:J:76:ALA:H	1.79	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:436:ASN:N	1:L:436:ASN:OD1	2.46	0.48
1:L:513:VAL:HG13	1:L:517:ILE:HG21	1.94	0.48
1:B:200:GLN:O	1:B:202:GLU:N	2.46	0.48
1:C:587:ASP:O	1:C:591:VAL:HG22	2.13	0.48
1:D:36:THR:HG21	6:Z:11:PRO:HG3	1.95	0.48
1:D:329:ARG:HB2	1:D:333:ILE:H	1.78	0.48
1:G:755:VAL:HG12	1:G:762:LYS:HE2	1.95	0.48
1:G:795:ARG:HH21	6:1:73:GLU:C	2.22	0.48
1:H:19:ALA:HA	1:H:22:TYR:CE2	2.49	0.48
1:I:118:THR:OG1	1:I:119:ALA:N	2.46	0.48
1:K:714:ASN:OD1	1:K:714:ASN:N	2.45	0.48
1:A:585:ARG:HD2	1:A:590:MET:HG2	1.94	0.48
1:B:856:ASP:OD1	1:B:856:ASP:N	2.42	0.48
1:D:207:GLU:OE2	1:D:213:THR:OG1	2.31	0.48
1:D:541:GLY:O	1:D:545:ARG:HG3	2.13	0.48
1:D:871:ARG:CZ	6:0:30:MET:HE2	2.43	0.48
1:E:357:VAL:HG13	1:E:565:PHE:CE2	2.48	0.48
1:E:377:GLY:HA2	6:Y:37:TRP:HZ3	1.79	0.48
1:G:929:ARG:HB3	1:G:934:VAL:O	2.14	0.48
1:H:23:LEU:HD22	1:H:27:LEU:HD23	1.94	0.48
1:H:686:GLU:HG2	1:H:700:TYR:CE1	2.48	0.48
1:J:330:ASP:HB2	1:J:545:ARG:NH2	2.29	0.48
1:K:646:LEU:O	1:K:647:SER:C	2.52	0.48
2:N:261:ILE:HG23	2:N:406:TRP:CZ2	2.48	0.48
1:A:72:ARG:HE	1:A:79:TYR:HD2	1.61	0.48
1:B:666:ILE:HB	1:B:900:LEU:HB3	1.95	0.48
1:D:262:GLU:O	1:D:287:SER:OG	2.28	0.48
1:E:330:ASP:OD2	1:E:379:ARG:NH2	2.46	0.48
1:G:202:GLU:O	1:G:203:PRO:C	2.55	0.48
1:J:329:ARG:NH2	1:J:592:LEU:O	2.47	0.48
1:J:444:GLU:HB3	1:L:164:LYS:HA	1.95	0.48
1:K:410:PRO:HB2	1:K:412:TYR:CE1	2.49	0.48
1:L:845:PHE:O	1:L:846:PRO:C	2.46	0.48
2:N:478:ASP:C	2:N:480:ALA:H	2.17	0.48
1:B:89:ASP:OD1	1:B:89:ASP:N	2.43	0.48
1:D:717:PHE:HB3	1:D:744:ILE:HD13	1.96	0.48
1:D:883:ALA:H	1:E:48:THR:HG1	1.61	0.48
1:F:754:ASN:HA	1:F:761:THR:HA	1.95	0.48
1:H:379:ARG:HD2	1:H:379:ARG:HA	1.71	0.48
1:J:43:LYS:HG2	1:L:570:ASN:O	2.14	0.48
2:N:193:LEU:HB3	2:N:197:ARG:HH22	1.79	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:186:GLY:O	1:A:193:LYS:N	2.39	0.48
1:B:88:GLY:HA3	1:B:91:ARG:HH11	1.79	0.48
1:B:924:VAL:HG21	1:C:12:MET:HB3	1.96	0.48
1:C:378:ASP:OD1	1:C:378:ASP:N	2.47	0.48
1:D:351:ALA:HB1	1:G:932:ARG:HH12	1.79	0.48
1:D:412:TYR:OH	1:E:835:MET:HA	2.14	0.48
1:E:358:VAL:HG23	1:E:939:TYR:CZ	2.49	0.48
1:F:373:LEU:HD13	1:F:379:ARG:HH12	1.79	0.48
1:G:235:SER:HB2	1:I:842:PRO:HB3	1.95	0.48
1:G:329:ARG:HD3	1:G:333:ILE:HG22	1.95	0.48
1:I:796:ASN:O	1:I:865:CYS:HA	2.14	0.48
1:K:520:GLY:HA3	1:L:114:PRO:HG2	1.96	0.48
1:K:881:MET:HE1	1:L:55:VAL:HG11	1.96	0.48
1:L:809:LYS:NZ	4:Q:55:THR:OG1	2.32	0.48
1:A:538:ARG:NH2	1:C:406:GLU:OE2	2.37	0.48
1:B:839:GLN:NE2	1:C:170:GLN:O	2.47	0.48
1:C:574:LEU:HB2	1:C:929:ARG:HD2	1.95	0.48
1:C:821:GLN:NE2	1:C:845:PHE:CG	2.81	0.48
1:D:298:HIS:O	1:D:299:ILE:C	2.53	0.48
1:E:255:GLY:O	1:E:256:LYS:HG2	2.13	0.48
1:F:313:LEU:O	1:F:316:GLN:HG2	2.14	0.48
1:G:9:TRP:CZ2	1:I:673:ALA:HB2	2.49	0.48
1:H:201:PRO:HG3	1:H:286:TYR:CD1	2.49	0.48
1:L:563:GLN:OE1	1:L:565:PHE:N	2.40	0.48
5:V:144:LEU:HD13	5:V:144:LEU:HA	1.72	0.48
1:C:918:LEU:O	1:C:919:PHE:C	2.54	0.48
1:F:572:LEU:O	1:F:929:ARG:NH2	2.47	0.48
1:F:639:ASP:OD1	1:F:639:ASP:N	2.46	0.48
1:F:807:ASP:N	1:F:807:ASP:OD1	2.46	0.48
1:H:490:ASN:OD1	1:H:490:ASN:N	2.47	0.48
1:J:118:THR:OG1	1:J:119:ALA:N	2.46	0.48
1:J:407:ASP:OD2	1:J:462:ASN:ND2	2.31	0.48
1:L:372:LEU:O	1:L:373:LEU:C	2.55	0.48
1:L:601:ARG:HH12	1:L:696:PRO:HA	1.78	0.48
3:M:23:SER:OG	3:M:24:THR:N	2.46	0.48
1:A:406:GLU:OE2	1:B:538:ARG:NH2	2.47	0.47
1:B:329:ARG:HB2	1:B:333:ILE:H	1.79	0.47
1:B:786:TYR:HD1	6:X:93:ASP:CB	2.27	0.47
1:D:46:ASN:H	6:Z:27:THR:CG2	2.27	0.47
1:G:378:ASP:OD1	1:G:380:THR:N	2.47	0.47
1:G:560:GLN:OE1	1:G:560:GLN:N	2.47	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:679:PHE:HB3	1:G:917:VAL:HG22	1.95	0.47
1:I:225:LYS:O	1:I:309:ASN:ND2	2.46	0.47
1:J:560:GLN:OE1	1:J:560:GLN:N	2.47	0.47
1:K:425:LEU:HD12	1:K:451:ILE:HD13	1.96	0.47
1:K:664:ILE:HD11	1:K:902:MET:HE2	1.96	0.47
1:K:738:THR:HG22	1:K:739:PRO:HD2	1.94	0.47
1:L:113:LYS:HZ3	1:L:321:ASN:C	2.22	0.47
2:N:476:TYR:HD1	2:N:512:THR:O	1.97	0.47
6:X:76:PHE:N	6:X:76:PHE:CD1	2.82	0.47
1:A:826:GLY:HA2	1:A:838:GLY:C	2.39	0.47
1:B:676:GLY:O	1:B:920:GLU:HB2	2.13	0.47
1:C:565:PHE:HD1	1:C:567:ALA:H	1.61	0.47
1:D:337:TYR:OH	1:D:693:GLY:O	2.21	0.47
1:F:200:GLN:HB3	1:F:201:PRO:HD3	1.94	0.47
1:F:675:ARG:HH21	1:F:920:GLU:HB3	1.78	0.47
1:H:204:GLN:H	1:H:204:GLN:HG2	1.38	0.47
1:H:865:CYS:SG	1:H:868:THR:HG21	2.54	0.47
1:J:234:GLY:HA3	1:J:297:THR:HG21	1.96	0.47
1:J:446:SER:HG	1:L:166:HIS:CE1	2.29	0.47
1:K:482:ASP:OD2	1:K:502:TYR:OH	2.29	0.47
2:N:127:LEU:HD11	2:N:554:VAL:HG13	1.97	0.47
3:M:200:ASN:HB2	5:U:199:ASN:HD21	1.79	0.47
4:P:33:SER:O	4:P:34:ILE:C	2.55	0.47
6:W:39:SER:O	6:W:40:LEU:C	2.55	0.47
1:A:236:TYR:CZ	1:C:848:PRO:HD3	2.49	0.47
1:A:817:GLY:O	1:A:821:GLN:HG3	2.13	0.47
1:D:754:ASN:OD1	1:D:754:ASN:N	2.45	0.47
1:E:133:GLU:HB3	1:E:167:VAL:HG13	1.96	0.47
1:E:619:PHE:O	1:E:621:MET:N	2.46	0.47
1:E:777:TYR:O	1:E:778:GLN:NE2	2.35	0.47
1:F:475:ASN:OD1	1:F:538:ARG:NE	2.31	0.47
1:I:675:ARG:HH21	1:I:920:GLU:HB3	1.79	0.47
1:K:411:ASN:ND2	1:L:466:ASN:OD1	2.39	0.47
1:A:762:LYS:HE2	1:B:615:TYR:CE2	2.50	0.47
1:B:487:SER:N	1:B:506:ARG:HE	2.11	0.47
1:C:594:SER:OG	1:C:701:SER:O	2.28	0.47
1:D:232:CYS:O	1:D:233:TYR:C	2.53	0.47
1:F:41:ASN:HB2	6:Y:25:ILE:HA	1.95	0.47
1:F:121:ASN:ND2	1:F:232:CYS:SG	2.87	0.47
1:F:921:VAL:HG21	1:F:941:ARG:HD3	1.96	0.47
1:G:807:ASP:OD1	1:G:807:ASP:N	2.46	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:835:MET:HE1	1:H:210:TRP:N	2.30	0.47
1:H:737:LEU:HB2	1:H:763:ASP:OD1	2.14	0.47
1:L:746:ARG:HD3	1:L:749:ASP:CB	2.44	0.47
2:N:154:THR:OG1	2:N:158:GLN:O	2.25	0.47
1:A:337:TYR:CZ	1:A:585:ARG:HG2	2.50	0.47
1:A:689:SER:OG	1:A:695:ASP:OD2	2.27	0.47
1:B:724:PHE:HE1	1:B:900:LEU:HD13	1.80	0.47
1:C:178:ILE:HG13	1:C:217:HIS:HB3	1.96	0.47
1:D:645:TYR:HD1	6:O:28:SER:O	1.97	0.47
1:H:472:LEU:O	1:H:473:TYR:C	2.57	0.47
1:J:673:ALA:HB2	1:K:9:TRP:CZ2	2.49	0.47
1:K:545:ARG:NH2	1:K:593:GLN:OE1	2.47	0.47
1:K:836:ARG:NE	1:K:836:ARG:O	2.48	0.47
1:L:297:THR:OG1	1:L:318:SER:OG	2.25	0.47
1:L:789:ARG:N	1:L:792:SER:OG	2.46	0.47
1:L:825:SER:C	1:L:827:PHE:H	2.22	0.47
2:N:445:MET:HE3	2:N:529:LEU:HB2	1.97	0.47
3:M:234:LEU:HD22	5:U:198:PHE:CD2	2.47	0.47
6:Z:25:ILE:HG12	6:Z:26:GLY:H	1.79	0.47
1:A:416:LEU:HD21	1:B:412:TYR:HE1	1.80	0.47
1:A:646:LEU:O	1:A:647:SER:C	2.57	0.47
1:B:327:ALA:HB2	1:B:546:SER:HA	1.96	0.47
1:C:163:GLN:O	1:C:163:GLN:NE2	2.48	0.47
1:F:216:ASN:OD1	1:F:216:ASN:N	2.46	0.47
1:F:522:ARG:NH2	1:F:798:GLN:OE1	2.47	0.47
1:H:881:MET:HE1	1:I:55:VAL:HG11	1.95	0.47
1:I:351:ALA:HA	1:J:932:ARG:HH22	1.80	0.47
1:I:543:ARG:O	1:I:547:MET:HG3	2.15	0.47
1:J:24:SER:HB3	1:L:638:ASN:HD21	1.80	0.47
1:J:733:ASN:HB3	1:K:60:SER:HA	1.96	0.47
2:N:135:ASN:OD1	2:N:138:MET:N	2.37	0.47
2:N:385:ASP:OD2	2:N:502:ASN:HB2	2.15	0.47
5:U:59:ALA:O	5:U:60:ALA:C	2.56	0.47
6:3:9:LEU:HD23	6:3:9:LEU:H	1.79	0.47
1:A:241:ASN:ND2	1:A:243:ASN:H	2.13	0.47
1:A:678:ALA:O	1:A:918:LEU:N	2.41	0.47
1:B:918:LEU:O	1:B:919:PHE:C	2.55	0.47
1:C:636:ASP:OD1	1:C:636:ASP:N	2.46	0.47
1:D:646:LEU:O	1:D:647:SER:C	2.57	0.47
1:D:842:PRO:HG3	1:E:130:ASN:ND2	2.29	0.47
1:E:574:LEU:HB3	1:E:575:PRO:HD2	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:5:MET:HE1	3:M:378:PRO:HB3	1.97	0.47
1:G:90:ASN:OD1	1:G:90:ASN:N	2.47	0.47
1:G:120:TYR:CD2	1:G:236:TYR:HB2	2.49	0.47
1:G:251:LYS:HE2	1:G:256:LYS:HD2	1.97	0.47
1:H:165:THR:N	1:I:444:GLU:O	2.46	0.47
1:I:278:ASN:N	1:I:278:ASN:OD1	2.47	0.47
1:I:513:VAL:HG13	1:I:517:ILE:HG21	1.97	0.47
1:I:539:ASN:HB3	1:I:542:LEU:HB3	1.95	0.47
1:I:541:GLY:O	1:I:545:ARG:HD3	2.15	0.47
1:J:330:ASP:OD2	1:J:379:ARG:NH2	2.45	0.47
1:L:712:TYR:HA	1:L:866:ASP:HB3	1.97	0.47
2:N:51:GLY:CA	2:N:116:ARG:HH21	2.23	0.47
2:N:148:MET:HG2	2:N:163:TYR:CE1	2.50	0.47
2:N:262:ARG:HG2	2:N:263:LYS:H	1.80	0.47
4:Q:73:ARG:NH2	4:Q:76:VAL:HG21	2.30	0.47
5:V:10:MET:HG2	5:V:26:ASP:HB2	1.97	0.47
5:V:84:PRO:C	5:V:86:PRO:HD3	2.39	0.47
6:W:39:SER:HB3	6:X:82:ASP:CB	2.44	0.47
1:A:643:ASN:ND2	6:X:29:ASN:OD1	2.48	0.47
1:D:449:ASN:OD1	1:F:167:VAL:N	2.46	0.47
1:F:234:GLY:HA3	1:F:297:THR:HG21	1.97	0.47
1:H:619:PHE:O	1:H:621:MET:N	2.45	0.47
1:I:387:ASN:OD1	1:I:545:ARG:HG2	2.14	0.47
1:I:650:ASN:ND2	1:I:650:ASN:H	2.12	0.47
1:I:714:ASN:ND2	1:I:868:THR:O	2.48	0.47
1:J:254:ASN:O	1:J:254:ASN:ND2	2.48	0.47
1:K:90:ASN:N	1:K:90:ASN:OD1	2.47	0.47
1:K:519:LEU:HD13	1:L:115:TYR:CD2	2.50	0.47
1:K:749:ASP:OD1	1:K:749:ASP:N	2.48	0.47
1:L:695:ASP:O	1:L:697:TYR:N	2.48	0.47
2:N:535:ILE:HG22	2:N:536:GLY:H	1.79	0.47
6:Y:30:MET:HE3	6:Y:31:SER:N	2.30	0.47
1:B:372:LEU:O	1:B:375:SER:N	2.48	0.47
1:D:274:GLY:HA2	1:D:279:LEU:HD11	1.96	0.47
1:D:823:ASN:OD1	1:D:824:ASN:N	2.48	0.47
1:E:643:ASN:N	1:E:643:ASN:OD1	2.48	0.47
1:F:865:CYS:SG	1:F:868:THR:HG21	2.55	0.47
1:G:411:ASN:OD1	1:G:411:ASN:N	2.47	0.47
1:G:788:ASP:OD1	1:G:792:SER:OG	2.24	0.47
1:I:918:LEU:O	1:I:919:PHE:C	2.57	0.47
1:I:942:THR:HB	1:I:943:PRO:HD3	1.97	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:209:GLN:CD	1:J:211:TYR:HB3	2.40	0.47
1:J:299:ILE:HG21	1:J:302:MET:HB2	1.97	0.47
1:J:541:GLY:O	1:J:545:ARG:HG3	2.15	0.47
1:K:950:THR:HB	5:U:33:TYR:OH	2.14	0.47
6:3:66:MET:HG2	6:3:70:LYS:HE3	1.97	0.47
1:A:578:TYR:CZ	1:A:933:GLY:HA2	2.50	0.47
1:A:638:ASN:ND2	1:B:24:SER:OG	2.48	0.47
1:B:700:TYR:CZ	1:B:702:GLY:HA3	2.50	0.47
1:B:876:SER:HB2	1:C:56:THR:HG21	1.97	0.47
1:C:658:ASN:N	1:C:909:MET:O	2.39	0.47
1:D:500:TYR:HB2	1:D:598:ASN:ND2	2.30	0.47
1:E:61:GLN:HE22	1:E:91:ARG:HG2	1.79	0.47
1:F:19:ALA:HB3	6:Y:25:ILE:HB	1.97	0.47
1:F:203:PRO:O	1:F:204:GLN:C	2.57	0.47
1:I:210:TRP:CZ3	1:I:417:GLY:HA3	2.50	0.47
1:I:325:TYR:CE2	1:I:543:ARG:HG2	2.50	0.47
1:I:745:LYS:NZ	4:R:48:THR:O	2.39	0.47
1:J:621:MET:HE2	1:J:621:MET:HB2	1.82	0.47
1:J:714:ASN:HB3	1:J:870:TRP:NE1	2.30	0.47
1:J:819:LEU:HD12	1:J:819:LEU:H	1.79	0.47
1:K:619:PHE:O	1:K:621:MET:N	2.48	0.47
1:L:82:ARG:NH2	1:L:353:GLN:OE1	2.48	0.47
1:L:265:PHE:HD1	1:L:284:VAL:HG22	1.80	0.47
1:L:389:ALA:HB3	1:L:545:ARG:HD2	1.97	0.47
2:N:535:ILE:H	2:N:535:ILE:HG12	1.41	0.47
1:A:598:ASN:OD1	1:A:598:ASN:N	2.45	0.46
1:B:486:TYR:C	1:B:506:ARG:HE	2.23	0.46
1:C:328:PHE:CE2	1:C:549:LEU:HD11	2.51	0.46
1:D:733:ASN:O	1:D:734:ASP:C	2.58	0.46
1:D:797:PHE:CZ	1:D:799:PRO:HG3	2.50	0.46
1:E:812:ASP:OD1	1:E:812:ASP:N	2.48	0.46
1:F:207:GLU:OE1	1:F:209:GLN:N	2.48	0.46
1:F:391:ASP:OD1	1:F:391:ASP:N	2.48	0.46
1:G:299:ILE:HG21	1:G:302:MET:HB2	1.96	0.46
1:G:737:LEU:HD13	1:G:753:TYR:CE1	2.50	0.46
1:H:134:TRP:HB3	1:H:229:MET:HE3	1.97	0.46
1:H:312:GLU:OE1	1:H:312:GLU:N	2.31	0.46
1:H:669:ARG:N	1:H:898:HIS:O	2.46	0.46
1:I:661:ASN:O	4:Q:12:SER:HB3	2.15	0.46
2:N:97:GLN:H	2:N:97:GLN:HG2	1.61	0.46
3:M:204:ALA:HB2	3:M:231:ASN:HD21	1.80	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:Y:68:ARG:O	6:Y:69:ASP:C	2.57	0.46
6:1:25:ILE:H	6:1:25:ILE:HG12	1.35	0.46
1:B:792:SER:OG	1:B:793:PHE:N	2.48	0.46
1:C:54:ASP:N	1:C:54:ASP:OD1	2.48	0.46
1:E:277:ASP:O	1:E:279:LEU:N	2.48	0.46
1:E:927:VAL:HG22	1:E:937:THR:HG22	1.98	0.46
1:F:327:ALA:HB2	1:F:546:SER:HA	1.97	0.46
1:G:51:PRO:HD3	6:2:11:PRO:HA	1.98	0.46
1:G:89:ASP:OD2	1:G:932:ARG:NH2	2.45	0.46
1:G:131:PRO:HB2	1:G:222:VAL:HA	1.97	0.46
1:G:229:MET:HE2	1:G:229:MET:HB3	1.69	0.46
1:G:466:ASN:O	1:G:470:ASN:ND2	2.42	0.46
1:H:329:ARG:HG3	1:H:333:ILE:O	2.16	0.46
1:J:818:ILE:H	1:J:818:ILE:HD12	1.80	0.46
1:K:423:GLU:O	1:K:450:GLU:HA	2.14	0.46
1:K:475:ASN:OD1	1:K:538:ARG:NE	2.48	0.46
1:K:681:ARG:HH21	1:K:913:THR:HG21	1.79	0.46
1:K:797:PHE:CE2	1:K:799:PRO:HG3	2.51	0.46
3:M:199:VAL:HG11	3:M:235:LEU:HD23	1.97	0.46
6:Y:5:ASN:C	6:Y:7:ALA:H	2.22	0.46
6:4:30:MET:HE2	6:4:30:MET:HB2	1.47	0.46
1:D:419:VAL:HG21	1:D:452:ARG:HB2	1.97	0.46
1:D:778:GLN:OE1	1:F:39:SER:N	2.48	0.46
1:E:724:PHE:CE1	1:E:900:LEU:HD13	2.50	0.46
1:E:843:ALA:HB3	1:F:120:TYR:HD2	1.80	0.46
1:F:468:TRP:O	1:F:469:ARG:C	2.58	0.46
1:F:472:LEU:HA	1:F:472:LEU:HD23	1.73	0.46
1:H:744:ILE:HG12	1:H:764:TRP:CE2	2.50	0.46
1:J:302:MET:HE2	1:J:491:VAL:HG22	1.96	0.46
2:N:86:ASN:HB3	2:N:90:ASN:O	2.16	0.46
1:A:551:ASN:CG	1:C:521:ALA:HB2	2.41	0.46
1:C:120:TYR:CD2	1:C:236:TYR:HB2	2.50	0.46
1:C:484:LEU:HD22	4:P:75:ILE:HD11	1.96	0.46
1:E:265:PHE:HB3	1:E:281:PRO:HB3	1.96	0.46
1:E:427:LYS:HD2	1:E:445:PHE:CD2	2.51	0.46
1:F:70:VAL:HG12	1:F:82:ARG:HG2	1.97	0.46
1:F:397:VAL:HG11	1:F:536:HIS:CD2	2.50	0.46
1:H:359:ASP:OD1	1:H:360:LEU:N	2.49	0.46
1:H:596:LEU:HD12	1:H:596:LEU:HA	1.56	0.46
1:J:198:THR:HB	1:J:241:ASN:OD1	2.15	0.46
1:L:134:TRP:CH2	1:L:166:HIS:HB2	2.49	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:M:152:ALA:O	3:M:158:GLN:NE2	2.49	0.46
5:U:55:LEU:HD12	5:U:55:LEU:HA	1.43	0.46
1:B:197:LYS:O	1:B:198:THR:C	2.56	0.46
1:B:830:TYR:N	1:B:837:GLU:OE2	2.35	0.46
1:C:275:ASN:N	1:C:275:ASN:OD1	2.46	0.46
1:D:490:ASN:N	1:D:490:ASN:OD1	2.47	0.46
1:E:235:SER:HB3	1:E:292:ILE:CD1	2.41	0.46
1:E:470:ASN:O	1:E:471:PHE:C	2.55	0.46
1:G:416:LEU:HD23	1:G:416:LEU:H	1.80	0.46
1:G:655:ILE:HD11	1:G:915:LEU:HB2	1.97	0.46
1:J:929:ARG:HB2	1:J:929:ARG:HH11	1.81	0.46
1:K:120:TYR:CD2	1:K:236:TYR:HB2	2.50	0.46
1:K:646:LEU:HD21	1:K:918:LEU:HD22	1.98	0.46
1:L:669:ARG:NH2	1:L:945:SER:H	2.11	0.46
4:P:56:PRO:O	4:P:57:LEU:C	2.56	0.46
1:D:714:ASN:N	1:D:714:ASN:OD1	2.49	0.46
1:F:251:LYS:HD2	1:F:251:LYS:HA	1.67	0.46
1:F:795:ARG:HE	1:F:795:ARG:HB2	1.50	0.46
1:F:845:PHE:O	1:F:846:PRO:C	2.50	0.46
1:G:17:GLN:HB3	1:G:21:GLU:HB2	1.98	0.46
1:H:108:ARG:NH2	1:H:549:LEU:HB2	2.30	0.46
1:H:335:LEU:HD23	1:H:591:VAL:HG11	1.96	0.46
1:H:737:LEU:HD13	1:H:753:TYR:CD1	2.51	0.46
1:I:945:SER:O	1:L:727:SER:OG	2.31	0.46
1:J:77:TYR:O	1:J:586:LYS:N	2.48	0.46
1:K:343:ASN:N	1:K:343:ASN:OD1	2.48	0.46
1:K:598:ASN:ND2	1:K:603:ASP:OD2	2.48	0.46
1:L:201:PRO:HG3	1:L:286:TYR:CD1	2.51	0.46
1:L:695:ASP:O	1:L:696:PRO:C	2.55	0.46
1:B:744:ILE:HG23	1:B:764:TRP:CD1	2.51	0.46
1:B:932:ARG:HH12	3:M:93:LEU:HA	1.80	0.46
1:D:714:ASN:HB3	1:D:870:TRP:NE1	2.30	0.46
1:E:87:VAL:HB	1:E:575:PRO:HA	1.96	0.46
1:H:413:CYS:SG	1:H:459:MET:HB2	2.55	0.46
1:I:133:GLU:HG2	1:I:167:VAL:HG13	1.98	0.46
1:J:90:ASN:HD22	1:J:623:HIS:HB3	1.80	0.46
1:J:456:ASN:O	1:K:836:ARG:NH1	2.48	0.46
1:J:744:ILE:HG12	1:J:764:TRP:CE2	2.51	0.46
1:L:887:LEU:HD12	1:L:887:LEU:HA	1.74	0.46
2:N:76:SER:C	2:N:78:ASP:N	2.68	0.46
4:P:61:ALA:O	4:P:63:ALA:N	2.49	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:89:ASP:OD1	1:A:932:ARG:NH1	2.48	0.46
1:B:14:ILE:O	1:B:15:SER:C	2.58	0.46
1:B:350:GLN:HE21	1:B:350:GLN:HB3	1.47	0.46
1:C:236:TYR:CG	1:C:237:ALA:N	2.83	0.46
1:D:921:VAL:HB	1:D:943:PRO:HD2	1.98	0.46
1:F:138:ALA:HB3	1:F:164:LYS:HD2	1.97	0.46
1:F:572:LEU:HB3	1:F:640:GLN:HE22	1.81	0.46
1:G:402:ASN:ND2	1:G:515:CYS:O	2.42	0.46
1:G:921:VAL:HB	1:G:943:PRO:HD2	1.97	0.46
1:I:574:LEU:HD12	1:I:634:ARG:HE	1.80	0.46
1:J:473:TYR:CD2	1:L:409:LEU:HD21	2.50	0.46
1:J:632:MET:HE2	5:V:170:THR:HG21	1.98	0.46
1:K:549:LEU:HD23	1:K:549:LEU:HA	1.75	0.46
1:K:754:ASN:O	1:K:762:LYS:HE2	2.16	0.46
1:K:821:GLN:HB2	1:K:845:PHE:HB2	1.98	0.46
1:L:340:SER:OG	1:L:690:LEU:O	2.22	0.46
2:N:407:TYR:O	2:N:408:LEU:C	2.56	0.46
4:R:112:ARG:HD3	4:R:112:ARG:HA	1.71	0.46
1:B:942:THR:HB	1:B:943:PRO:HD3	1.97	0.46
1:C:113:LYS:NZ	1:C:321:ASN:O	2.31	0.46
1:D:484:LEU:HD11	1:D:527:TYR:CD1	2.51	0.46
1:D:835:MET:HA	1:F:412:TYR:OH	2.16	0.46
1:E:463:LEU:O	1:E:464:ASN:C	2.53	0.46
1:E:594:SER:OG	1:E:701:SER:OG	2.26	0.46
1:E:747:SER:O	1:E:749:ASP:N	2.48	0.46
1:F:518:ASN:ND2	1:F:523:TRP:HD1	2.14	0.46
1:H:82:ARG:HG3	1:H:581:GLU:HG2	1.98	0.46
1:H:196:ASP:H	1:H:200:GLN:CB	2.27	0.46
1:I:479:TYR:OH	1:I:537:HIS:ND1	2.27	0.46
1:J:551:ASN:HB3	1:L:521:ALA:HB2	1.98	0.46
1:K:573:LEU:HA	1:K:929:ARG:NH2	2.30	0.46
1:K:917:VAL:O	1:K:918:LEU:C	2.53	0.46
1:A:534:PHE:HZ	1:A:867:ARG:HG3	1.81	0.46
1:B:573:LEU:HD11	1:B:578:TYR:CE2	2.51	0.46
1:B:836:ARG:O	1:B:836:ARG:NE	2.49	0.46
1:C:922:PHE:O	1:C:941:ARG:HA	2.16	0.46
1:D:330:ASP:HB2	1:D:545:ARG:HH21	1.81	0.46
1:D:845:PHE:O	1:D:846:PRO:C	2.56	0.46
1:E:830:TYR:N	1:E:837:GLU:OE2	2.40	0.46
1:F:201:PRO:CD	1:F:286:TYR:HE2	2.29	0.46
1:J:500:TYR:HB2	1:J:598:ASN:HD22	1.81	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:500:TYR:HB2	1:L:598:ASN:ND2	2.31	0.46
2:N:479:GLN:O	2:N:480:ALA:C	2.58	0.46
3:M:14:LEU:HD11	3:M:71:GLU:HG3	1.98	0.46
5:V:7:THR:OG1	5:V:25:GLN:OE1	2.24	0.46
1:A:19:ALA:HA	1:A:22:TYR:CE2	2.51	0.45
1:B:805:VAL:HG21	1:B:847:TYR:HD2	1.81	0.45
1:C:364:ASN:HB2	1:C:650:ASN:ND2	2.32	0.45
1:C:739:PRO:HG2	1:E:341:THR:HB	1.98	0.45
1:C:874:PHE:CE1	1:C:887:LEU:HB3	2.51	0.45
1:D:730:TRP:O	1:D:730:TRP:CG	2.67	0.45
1:E:68:ILE:HD13	1:E:68:ILE:HA	1.84	0.45
1:E:941:ARG:O	1:E:945:SER:HA	2.16	0.45
1:F:3:PRO:HB2	1:F:4:SER:H	1.56	0.45
1:F:724:PHE:HE2	1:F:893:TYR:HE2	1.64	0.45
1:G:229:MET:HE1	1:G:314:MET:HG3	1.97	0.45
1:G:379:ARG:HB3	1:G:790:MET:HE3	1.98	0.45
1:H:178:ILE:HG22	1:H:183:ILE:HA	1.97	0.45
1:H:329:ARG:HB2	1:H:333:ILE:N	2.32	0.45
1:I:529:ASP:OD1	1:I:715:HIS:NE2	2.27	0.45
1:I:724:PHE:CE1	1:I:900:LEU:HD13	2.51	0.45
1:J:271:ALA:HB3	1:J:279:LEU:HD13	1.98	0.45
1:K:430:PRO:HA	1:K:438:TRP:CD1	2.51	0.45
1:K:490:ASN:N	1:K:490:ASN:OD1	2.48	0.45
1:K:646:LEU:HD11	1:K:918:LEU:HD21	1.97	0.45
1:L:327:ALA:HB2	1:L:546:SER:HA	1.98	0.45
1:L:572:LEU:O	1:L:929:ARG:NH2	2.49	0.45
2:N:179:MET:HE3	2:N:179:MET:HB3	1.61	0.45
1:A:490:ASN:N	1:A:490:ASN:OD1	2.49	0.45
1:A:728:VAL:HG21	5:U:226:TYR:CE2	2.51	0.45
1:A:932:ARG:HH22	1:E:351:ALA:HA	1.80	0.45
1:B:764:TRP:HZ2	1:B:870:TRP:HB3	1.81	0.45
1:C:188:GLU:HB3	1:C:191:THR:HB	1.98	0.45
1:E:596:LEU:HA	1:E:596:LEU:HD12	1.76	0.45
1:E:876:SER:HB2	1:F:56:THR:HG21	1.99	0.45
1:F:619:PHE:O	1:F:621:MET:N	2.47	0.45
1:G:213:THR:C	1:G:214:GLU:HG3	2.41	0.45
1:H:744:ILE:HG12	1:H:764:TRP:CD2	2.52	0.45
1:K:181:GLU:HB2	1:K:194:TYR:CD1	2.52	0.45
1:L:563:GLN:OE1	1:L:564:LYS:N	2.50	0.45
1:L:865:CYS:SG	1:L:868:THR:OG1	2.71	0.45
2:N:189:VAL:HG11	2:N:498:ARG:HD2	1.97	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:M:334:MET:SD	5:U:151:THR:OG1	2.70	0.45
1:D:12:MET:HE1	1:F:926:ARG:HB3	1.99	0.45
1:F:436:ASN:N	1:F:436:ASN:OD1	2.49	0.45
1:F:572:LEU:HB3	1:F:640:GLN:NE2	2.32	0.45
1:H:210:TRP:CZ3	1:H:417:GLY:HA3	2.52	0.45
1:H:595:SER:C	1:H:597:GLY:N	2.73	0.45
1:I:858:ILE:HD12	1:I:858:ILE:HA	1.89	0.45
1:J:252:GLN:HG3	1:J:258:GLU:CD	2.41	0.45
1:K:339:ASN:ND2	1:K:363:ARG:O	2.50	0.45
1:L:348:ALA:HB2	1:L:355:ASN:HA	1.97	0.45
1:L:746:ARG:HD3	1:L:749:ASP:HB2	1.98	0.45
5:V:72:ARG:HG3	5:V:73:SER:N	2.31	0.45
1:A:462:ASN:O	1:A:466:ASN:ND2	2.33	0.45
1:A:473:TYR:O	1:A:477:ALA:HB3	2.16	0.45
1:B:817:GLY:O	1:B:821:GLN:HG3	2.17	0.45
1:C:239:PRO:HA	1:C:246:GLN:HA	1.98	0.45
1:D:391:ASP:OD1	1:D:545:ARG:NH2	2.34	0.45
1:E:829:GLY:HA2	1:E:837:GLU:HG2	1.98	0.45
1:G:201:PRO:HG2	1:G:286:TYR:CE1	2.51	0.45
1:H:121:ASN:ND2	1:H:232:CYS:SG	2.83	0.45
1:H:409:LEU:HD13	1:I:470:ASN:HA	1.99	0.45
1:H:678:ALA:HB3	1:H:918:LEU:HG	1.99	0.45
1:I:126:LYS:HG2	1:I:233:TYR:CD2	2.51	0.45
1:I:251:LYS:HB3	1:I:256:LYS:C	2.42	0.45
1:K:68:ILE:HG22	1:K:69:PRO:HD2	1.98	0.45
1:K:638:ASN:HD21	1:L:24:SER:HB3	1.81	0.45
4:Q:6:PHE:HD1	4:Q:6:PHE:HA	1.69	0.45
6:3:77:GLN:O	6:3:78:GLN:C	2.59	0.45
1:A:210:TRP:CZ3	1:A:417:GLY:HA3	2.51	0.45
1:A:235:SER:HB2	1:C:842:PRO:HA	1.97	0.45
1:A:733:ASN:O	1:A:735:ARG:HG2	2.17	0.45
1:D:397:VAL:HG11	1:D:536:HIS:CE1	2.51	0.45
1:D:823:ASN:ND2	1:D:846:PRO:HD3	2.30	0.45
1:E:565:PHE:O	1:E:567:ALA:N	2.50	0.45
1:F:133:GLU:HG2	1:F:167:VAL:HG13	1.99	0.45
1:G:120:TYR:HE2	1:G:295:PRO:HG2	1.81	0.45
1:I:204:GLN:H	1:I:204:GLN:HG2	1.56	0.45
1:I:251:LYS:HE3	1:I:253:GLN:HB2	1.99	0.45
1:I:902:MET:HE3	1:I:904:PHE:HE1	1.81	0.45
1:J:640:GLN:NE2	1:J:929:ARG:HH22	2.14	0.45
1:J:789:ARG:NH1	6:3:38:GLY:HA2	2.31	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:865:CYS:SG	1:J:868:THR:HG21	2.57	0.45
1:K:526:ASP:N	1:K:526:ASP:OD1	2.50	0.45
3:M:351:MET:HE2	3:M:351:MET:HB3	1.88	0.45
5:V:19:LEU:HD21	5:V:88:THR:OG1	2.17	0.45
1:B:646:LEU:O	1:B:647:SER:C	2.57	0.45
1:D:552:GLY:N	1:F:803:GLN:OE1	2.40	0.45
1:D:560:GLN:OE1	1:D:560:GLN:N	2.50	0.45
1:D:574:LEU:HB3	1:D:575:PRO:HD2	1.99	0.45
1:E:277:ASP:OD1	1:E:278:ASN:N	2.45	0.45
1:E:922:PHE:CE2	1:F:14:ILE:HG23	2.52	0.45
1:E:936:GLU:OE1	5:U:144:LEU:HB2	2.16	0.45
1:F:118:THR:OG1	1:F:119:ALA:N	2.50	0.45
1:F:721:ALA:HB3	1:F:903:THR:HB	1.98	0.45
1:F:942:THR:OG1	1:F:943:PRO:HD3	2.17	0.45
3:M:77:VAL:HG21	3:M:95:TYR:HA	1.99	0.45
4:Q:88:SER:HB2	4:Q:92:ARG:HH11	1.80	0.45
6:Y:23:GLN:HE21	6:Y:23:GLN:HB2	1.48	0.45
1:C:79:TYR:HB3	1:C:584:PHE:HB2	1.99	0.45
1:D:330:ASP:HB2	1:D:545:ARG:NH2	2.31	0.45
1:E:776:GLY:HA2	1:E:780:PHE:CE1	2.52	0.45
1:F:203:PRO:O	1:F:205:ILE:N	2.49	0.45
1:F:528:MET:HB3	1:F:528:MET:HE3	1.57	0.45
1:F:658:ASN:N	1:F:658:ASN:OD1	2.48	0.45
1:F:823:ASN:O	1:F:824:ASN:C	2.58	0.45
1:F:927:VAL:HG22	1:F:937:THR:HG22	1.98	0.45
1:G:710:THR:O	1:G:710:THR:OG1	2.29	0.45
1:H:703:SER:O	1:H:705:PRO:HD3	2.17	0.45
1:J:523:TRP:CD1	1:J:802:ARG:HD3	2.52	0.45
1:J:948:ASN:OD1	1:J:948:ASN:N	2.49	0.45
1:L:112:PHE:CD1	1:L:326:ILE:HB	2.51	0.45
2:N:416:GLN:O	2:N:421:SER:OG	2.32	0.45
6:Y:77:GLN:HB2	6:Y:78:GLN:H	1.46	0.45
1:A:246:GLN:OE1	1:C:822:HIS:HE1	2.00	0.45
1:A:352:SER:O	1:A:354:LEU:N	2.44	0.45
1:A:469:ARG:NH1	1:A:828:VAL:HG21	2.32	0.45
1:A:615:TYR:CE2	1:C:762:LYS:HE2	2.51	0.45
1:C:676:GLY:HA2	1:C:874:PHE:HB2	1.99	0.45
1:D:200:GLN:O	1:D:201:PRO:C	2.47	0.45
1:D:922:PHE:O	1:D:941:ARG:HA	2.17	0.45
1:E:469:ARG:O	1:E:470:ASN:C	2.55	0.45
1:E:523:TRP:CD1	1:E:802:ARG:HD3	2.52	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:362:ASP:OD2	1:G:941:ARG:NH2	2.44	0.45
1:G:383:PHE:HD1	1:G:384:SER:N	2.14	0.45
1:G:551:ASN:CG	1:I:521:ALA:HB2	2.42	0.45
1:L:769:MET:HE3	1:L:769:MET:HB3	1.85	0.45
2:N:183:LEU:O	2:N:184:MET:C	2.57	0.45
3:M:385:ILE:HD12	3:M:385:ILE:HA	1.84	0.45
4:S:133:ALA:O	4:S:136:PRO:HD2	2.17	0.45
1:A:892:LEU:HD13	5:U:225:GLY:HA3	1.97	0.45
1:D:745:LYS:NZ	4:P:48:THR:O	2.46	0.45
1:E:549:LEU:HD23	1:E:549:LEU:HA	1.82	0.45
1:E:836:ARG:O	1:E:836:ARG:NE	2.44	0.45
1:I:120:TYR:HE2	1:I:295:PRO:HG2	1.82	0.45
1:J:641:SER:OG	1:K:45:ARG:HB2	2.17	0.45
1:L:719:LYS:HE2	1:L:743:GLU:HG2	1.99	0.45
4:R:113:GLU:OE1	4:R:113:GLU:N	2.50	0.45
6:X:64:GLY:C	6:X:66:MET:N	2.72	0.45
6:Y:25:ILE:H	6:Y:25:ILE:HG12	1.32	0.45
6:1:40:LEU:HD22	6:1:40:LEU:HA	1.74	0.45
1:A:563:GLN:OE1	1:A:564:LYS:N	2.50	0.45
1:A:789:ARG:NH1	6:X:38:GLY:HA2	2.32	0.45
1:B:113:LYS:NZ	1:B:321:ASN:O	2.35	0.45
1:B:413:CYS:HA	1:C:461:ILE:HB	1.99	0.45
1:B:883:ALA:H	1:C:48:THR:HG1	1.58	0.45
1:C:392:SER:O	1:C:539:ASN:HA	2.17	0.45
1:D:95:MET:HE2	1:D:573:LEU:HD22	1.99	0.45
1:F:120:TYR:CD2	1:F:236:TYR:HB2	2.51	0.45
1:F:260:GLN:H	1:F:260:GLN:HG2	1.57	0.45
1:F:574:LEU:HD23	1:F:574:LEU:HA	1.80	0.45
1:G:461:ILE:HG13	1:G:463:LEU:HD12	1.98	0.45
1:I:619:PHE:O	1:I:621:MET:N	2.44	0.45
1:I:646:LEU:HG	1:I:648:ALA:HB2	1.98	0.45
1:I:788:ASP:OD2	1:I:795:ARG:HB2	2.16	0.45
1:I:887:LEU:HD12	1:I:887:LEU:HA	1.80	0.45
1:J:45:ARG:HD3	1:L:643:ASN:OD1	2.17	0.45
1:K:839:GLN:HB3	1:L:172:PRO:HD3	1.98	0.45
1:K:868:THR:OG1	1:K:869:LEU:N	2.50	0.45
1:L:120:TYR:HE2	1:L:295:PRO:HG2	1.82	0.45
2:N:133:ASN:HB3	2:N:175:TYR:HD1	1.82	0.45
2:N:545:ASP:CG	2:N:546:ALA:H	2.24	0.45
1:A:607:ILE:HD11	1:A:609:PHE:CE1	2.52	0.44
1:A:724:PHE:CE2	1:A:893:TYR:HE1	2.35	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:828:VAL:HG13	1:A:829:GLY:N	2.31	0.44
1:B:670:ASN:OD1	1:B:672:ALA:N	2.50	0.44
1:C:336:MET:HB2	1:C:338:TYR:CE2	2.52	0.44
1:D:409:LEU:HD23	1:E:833:PRO:HB3	1.99	0.44
1:D:820:HIS:HA	1:E:204:GLN:NE2	2.32	0.44
1:D:836:ARG:O	1:D:836:ARG:NE	2.40	0.44
1:G:52:THR:OG1	1:G:53:HIS:N	2.49	0.44
1:G:229:MET:N	1:G:309:ASN:OD1	2.44	0.44
1:H:254:ASN:N	1:H:254:ASN:OD1	2.50	0.44
1:H:849:LEU:C	1:H:850:ILE:HD12	2.42	0.44
1:J:170:GLN:HG3	1:K:452:ARG:HB3	1.99	0.44
1:J:366:GLU:HG3	1:J:707:LEU:HD22	1.99	0.44
1:J:744:ILE:HG12	1:J:764:TRP:CD2	2.52	0.44
1:K:197:LYS:O	1:K:198:THR:C	2.55	0.44
1:K:328:PHE:CE1	1:K:549:LEU:HD11	2.52	0.44
1:K:681:ARG:HD2	1:K:906:VAL:HG11	1.97	0.44
1:L:297:THR:OG1	1:L:298:HIS:N	2.48	0.44
1:L:402:ASN:OD1	1:L:403:HIS:N	2.50	0.44
2:N:386:SER:C	2:N:388:LYS:N	2.74	0.44
1:A:886:ASP:OD1	1:A:887:LEU:N	2.50	0.44
1:B:266:PHE:HE2	1:C:449:ASN:HD22	1.65	0.44
1:E:647:SER:HB2	1:E:675:ARG:HH12	1.81	0.44
1:E:773:TYR:HH	1:E:792:SER:HG	1.60	0.44
1:F:201:PRO:CD	1:F:286:TYR:CE2	3.01	0.44
1:F:278:ASN:N	1:F:278:ASN:OD1	2.50	0.44
1:F:902:MET:HE3	1:F:904:PHE:HE1	1.82	0.44
1:G:237:ALA:CB	1:G:246:GLN:HG2	2.47	0.44
1:H:253:GLN:OE1	1:H:254:ASN:N	2.47	0.44
1:I:746:ARG:HE	1:I:749:ASP:HB2	1.82	0.44
1:J:416:LEU:HD23	1:J:416:LEU:H	1.81	0.44
1:J:419:VAL:HG21	1:J:452:ARG:HB2	1.99	0.44
1:K:835:MET:HE1	1:L:210:TRP:HB3	1.98	0.44
1:L:196:ASP:OD1	1:L:198:THR:N	2.50	0.44
2:N:439:TRP:CZ3	2:N:543:ILE:HD11	2.52	0.44
5:V:60:ALA:O	5:V:61:ILE:C	2.58	0.44
1:A:9:TRP:CZ2	1:C:673:ALA:HB2	2.52	0.44
1:A:806:ASP:OD1	1:A:808:THR:OG1	2.31	0.44
1:B:821:GLN:HB3	1:B:845:PHE:HB2	2.00	0.44
1:E:130:ASN:OD1	1:E:232:CYS:HA	2.17	0.44
1:G:371:LEU:CD1	6:2:30:MET:HE1	2.47	0.44
1:H:167:VAL:N	1:I:449:ASN:OD1	2.47	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:413:CYS:HA	1:I:461:ILE:HB	1.99	0.44
1:H:724:PHE:CE1	1:H:900:LEU:HD13	2.53	0.44
1:H:941:ARG:HG3	1:H:944:PHE:O	2.18	0.44
1:I:776:GLY:HA2	1:I:780:PHE:CE1	2.52	0.44
1:J:619:PHE:O	1:J:621:MET:N	2.46	0.44
1:K:673:ALA:HB3	1:K:942:THR:HG21	1.99	0.44
1:K:714:ASN:HB3	1:K:870:TRP:NE1	2.32	0.44
6:W:25:ILE:H	6:W:25:ILE:HG12	1.09	0.44
1:A:650:ASN:C	1:A:651:MET:HG2	2.41	0.44
1:C:743:GLU:O	1:C:761:THR:OG1	2.28	0.44
1:D:329:ARG:HG3	1:D:333:ILE:O	2.18	0.44
1:D:481:PRO:HB2	1:D:483:LYS:HG2	1.99	0.44
1:E:747:SER:C	1:E:749:ASP:N	2.75	0.44
1:E:902:MET:HE3	1:E:904:PHE:CE1	2.51	0.44
1:F:434:GLN:HG3	1:F:437:GLY:H	1.81	0.44
1:G:743:GLU:O	1:G:761:THR:OG1	2.21	0.44
1:G:817:GLY:O	1:G:821:GLN:HG3	2.17	0.44
1:H:844:ASN:N	1:H:844:ASN:OD1	2.49	0.44
1:I:563:GLN:OE1	1:I:565:PHE:N	2.37	0.44
1:I:563:GLN:NE2	1:I:568:ILE:HD11	2.33	0.44
1:J:237:ALA:HB3	1:J:246:GLN:OE1	2.18	0.44
1:J:490:ASN:OD1	1:J:490:ASN:N	2.49	0.44
1:K:221:ARG:NH2	1:K:288:GLU:OE2	2.50	0.44
1:L:204:GLN:H	1:L:204:GLN:HG2	1.45	0.44
1:L:389:ALA:HB3	1:L:545:ARG:CD	2.47	0.44
2:N:491:SER:O	2:N:492:LEU:HB2	2.15	0.44
1:A:866:ASP:N	1:A:866:ASP:OD1	2.47	0.44
1:B:598:ASN:N	1:B:598:ASN:OD1	2.49	0.44
1:D:20:SER:HB3	6:Z:23:GLN:HG3	1.99	0.44
1:E:485:LYS:HB3	1:E:506:ARG:HG2	2.00	0.44
1:E:747:SER:C	1:E:749:ASP:H	2.25	0.44
1:F:585:ARG:NH1	1:F:590:MET:HE2	2.32	0.44
1:G:466:ASN:ND2	1:I:411:ASN:OD1	2.44	0.44
1:G:646:LEU:HD12	1:G:646:LEU:HA	1.85	0.44
1:H:85:LEU:HD13	1:H:614:LEU:HD21	1.98	0.44
1:H:485:LYS:O	1:H:506:ARG:NH2	2.51	0.44
1:H:681:ARG:HG3	1:H:717:PHE:CZ	2.53	0.44
1:I:688:PRO:HB3	1:I:698:TYR:CZ	2.53	0.44
1:J:841:TYR:CE1	1:K:221:ARG:HB2	2.53	0.44
5:U:6:PRO:HG2	5:U:196:VAL:HG23	1.99	0.44
1:A:14:ILE:HA	1:A:14:ILE:HD13	1.77	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:232:CYS:O	1:A:233:TYR:C	2.56	0.44
1:A:407:ASP:N	1:A:407:ASP:OD1	2.51	0.44
1:B:516:TYR:HA	1:B:519:LEU:HD21	2.00	0.44
1:B:773:TYR:O	1:B:775:ILE:HG13	2.18	0.44
1:C:497:PRO:HA	1:C:502:TYR:CG	2.52	0.44
1:F:19:ALA:N	1:F:46:ASN:OD1	2.30	0.44
1:F:426:THR:HG23	1:F:447:ASP:HA	1.98	0.44
1:F:440:LYS:HG2	1:F:441:ASP:H	1.83	0.44
1:G:916:TYR:CZ	1:G:918:LEU:HD22	2.52	0.44
1:H:356:ALA:O	1:H:939:TYR:OH	2.24	0.44
1:H:373:LEU:HB3	1:H:379:ARG:NH1	2.32	0.44
1:H:928:HIS:CD2	1:H:930:PRO:HD3	2.53	0.44
1:J:403:HIS:NE2	1:K:547:MET:SD	2.90	0.44
1:L:352:SER:O	1:L:353:GLN:NE2	2.50	0.44
1:L:902:MET:HE3	1:L:904:PHE:HE1	1.83	0.44
2:N:96:ILE:HD12	2:N:96:ILE:HG23	1.71	0.44
5:V:139:SER:HB3	5:V:164:PRO:HD2	1.98	0.44
6:Y:22:TRP:CD1	6:Y:22:TRP:H	2.35	0.44
1:C:355:ASN:OD1	1:C:356:ALA:N	2.50	0.44
1:C:921:VAL:CG1	1:C:943:PRO:HB2	2.44	0.44
1:E:19:ALA:HA	1:E:22:TYR:CE2	2.52	0.44
1:E:744:ILE:HG12	1:E:764:TRP:CD2	2.53	0.44
1:F:650:ASN:ND2	1:F:650:ASN:H	2.13	0.44
1:G:573:LEU:HD12	1:G:929:ARG:HH12	1.82	0.44
1:I:425:LEU:HD12	1:I:451:ILE:HD13	1.99	0.44
1:K:634:ARG:HH22	1:K:932:ARG:HA	1.81	0.44
1:L:523:TRP:CD1	1:L:802:ARG:HD3	2.53	0.44
1:L:608:LYS:NZ	1:L:610:ASP:OD1	2.47	0.44
1:L:634:ARG:NH2	1:L:932:ARG:HA	2.33	0.44
4:S:122:LEU:HD23	4:S:122:LEU:HA	1.87	0.44
5:V:13:TYR:CE2	5:V:15:PRO:HA	2.53	0.44
5:V:166:GLN:O	5:V:170:THR:OG1	2.22	0.44
1:A:460:GLU:HB2	1:C:416:LEU:HD23	1.99	0.44
1:A:569:LYS:HB3	1:A:569:LYS:HE2	1.69	0.44
1:B:66:ARG:HG3	1:B:615:TYR:CZ	2.53	0.44
1:C:563:GLN:OE1	1:C:565:PHE:N	2.38	0.44
1:C:770:LEU:HB3	1:C:878:PHE:O	2.18	0.44
1:D:45:ARG:NH1	6:Z:27:THR:HG22	2.27	0.44
1:D:99:TYR:OH	1:F:762:LYS:NZ	2.43	0.44
1:E:460:GLU:CD	1:F:126:LYS:H	2.26	0.44
1:G:232:CYS:O	1:G:233:TYR:C	2.60	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:737:LEU:HB2	1:G:763:ASP:OD2	2.17	0.44
1:G:789:ARG:HH21	6:1:75:ASN:HB3	1.83	0.44
1:H:640:GLN:HE21	1:H:640:GLN:H	1.66	0.44
1:I:397:VAL:HG11	1:I:536:HIS:NE2	2.32	0.44
1:I:716:THR:HB	1:I:907:ASP:HB2	1.99	0.44
1:I:737:LEU:HD13	1:I:753:TYR:CE2	2.52	0.44
1:J:638:ASN:ND2	1:K:24:SER:OG	2.39	0.44
1:K:46:ASN:HB2	6:3:27:THR:OG1	2.18	0.44
1:K:529:ASP:HB3	1:K:715:HIS:NE2	2.33	0.44
1:K:790:MET:HE2	1:K:790:MET:HB3	1.87	0.44
1:K:883:ALA:H	1:L:48:THR:HG1	1.61	0.44
1:L:922:PHE:O	1:L:941:ARG:HA	2.17	0.44
2:N:170:LEU:O	2:N:171:PRO:C	2.61	0.44
4:P:78:ASP:OD1	4:P:79:PHE:N	2.45	0.44
6:Y:16:ARG:O	6:Y:17:PRO:C	2.54	0.44
1:A:378:ASP:OD1	1:A:379:ARG:N	2.50	0.44
1:B:495:ASP:OD1	1:B:495:ASP:N	2.49	0.44
1:B:774:ASN:N	1:B:774:ASN:OD1	2.51	0.44
1:C:257:LEU:HD23	1:C:257:LEU:HA	1.83	0.44
1:C:715:HIS:HD2	1:C:716:THR:HG23	1.83	0.44
1:E:409:LEU:HD21	1:F:473:TYR:CG	2.53	0.44
1:E:724:PHE:HE1	1:E:900:LEU:HD13	1.82	0.44
1:F:797:PHE:HD1	1:F:798:GLN:N	2.15	0.44
1:H:222:VAL:O	1:H:287:SER:HA	2.18	0.44
1:H:789:ARG:NH2	6:1:35:PHE:O	2.51	0.44
1:H:790:MET:HE2	1:H:790:MET:HB3	1.87	0.44
1:I:695:ASP:O	1:I:696:PRO:C	2.55	0.44
1:K:522:ARG:N	1:L:547:MET:HE2	2.33	0.44
1:K:734:ASP:O	1:L:62:ARG:HG2	2.18	0.44
5:V:80:TYR:CE1	5:V:195:SER:HB2	2.51	0.44
1:A:325:TYR:HD2	1:A:543:ARG:HA	1.83	0.43
1:A:325:TYR:HE2	1:A:543:ARG:HG3	1.82	0.43
1:A:558:HIS:O	1:A:558:HIS:ND1	2.51	0.43
1:A:678:ALA:HB3	1:A:918:LEU:HB2	1.99	0.43
1:B:784:GLU:H	1:B:784:GLU:CD	2.25	0.43
1:C:232:CYS:O	1:C:233:TYR:C	2.60	0.43
1:D:327:ALA:HB2	1:D:546:SER:HA	1.99	0.43
1:D:542:LEU:HA	1:D:545:ARG:NH1	2.32	0.43
1:D:619:PHE:O	1:D:621:MET:N	2.49	0.43
1:D:844:ASN:OD1	1:D:844:ASN:N	2.50	0.43
1:H:178:ILE:HD12	1:H:284:VAL:HG23	1.99	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:690:LEU:HD12	1:J:706:TYR:HE2	1.82	0.43
1:L:55:VAL:HG12	1:L:56:THR:HG23	1.99	0.43
1:L:512:LEU:HD23	1:L:818:ILE:HG12	1.99	0.43
1:L:695:ASP:C	1:L:697:TYR:N	2.75	0.43
1:L:724:PHE:CE1	1:L:900:LEU:HD13	2.53	0.43
5:U:61:ILE:O	5:U:62:THR:C	2.58	0.43
5:V:146:LEU:HD12	5:V:152:PHE:CE2	2.53	0.43
1:A:178:ILE:HD13	1:A:284:VAL:HG12	2.01	0.43
1:A:425:LEU:HD12	1:A:451:ILE:HB	2.01	0.43
1:B:183:ILE:HG21	1:B:219:ALA:HB2	2.00	0.43
1:B:231:PRO:CG	1:B:318:SER:HB2	2.48	0.43
1:B:574:LEU:HB3	1:B:575:PRO:HD2	2.00	0.43
1:E:379:ARG:HD2	1:E:379:ARG:HA	1.72	0.43
1:F:231:PRO:HG3	1:F:318:SER:HB2	1.99	0.43
1:F:315:GLY:O	1:F:316:GLN:C	2.59	0.43
1:G:328:PHE:CD2	1:G:549:LEU:HD11	2.53	0.43
1:G:490:ASN:OD1	1:G:490:ASN:N	2.51	0.43
1:J:45:ARG:HH12	6:4:27:THR:HG23	1.83	0.43
1:J:132:CYS:SG	1:J:229:MET:HE3	2.59	0.43
1:J:177:ASN:H	1:J:184:GLN:HB3	1.83	0.43
1:J:475:ASN:OD1	1:J:538:ARG:NE	2.51	0.43
1:K:80:LYS:HE2	1:K:581:GLU:OE1	2.18	0.43
1:L:57:THR:OG1	1:L:58:ASP:N	2.52	0.43
1:L:392:SER:O	1:L:539:ASN:HA	2.18	0.43
1:L:818:ILE:H	1:L:818:ILE:HD12	1.83	0.43
6:Y:8:SER:O	6:Y:10:ALA:N	2.51	0.43
1:A:325:TYR:HH	1:C:403:HIS:CE1	2.36	0.43
1:A:921:VAL:HB	1:A:943:PRO:HD2	1.99	0.43
1:B:254:ASN:OD1	1:B:254:ASN:N	2.51	0.43
1:B:426:THR:HG21	1:B:440:LYS:HE3	1.99	0.43
1:B:518:ASN:HB3	1:B:521:ALA:HB3	1.99	0.43
1:C:202:GLU:O	1:C:203:PRO:C	2.57	0.43
1:D:414:PHE:HB2	1:F:125:PRO:HG3	2.01	0.43
1:E:788:ASP:OD2	1:E:795:ARG:HB2	2.17	0.43
1:F:463:LEU:O	1:F:464:ASN:C	2.60	0.43
1:F:666:ILE:HD11	1:F:919:PHE:CZ	2.52	0.43
1:G:227:THR:O	1:G:309:ASN:ND2	2.41	0.43
1:H:166:HIS:CE1	1:I:446:SER:HB2	2.53	0.43
1:H:332:PHE:CE2	1:H:387:ASN:HB2	2.53	0.43
1:H:643:ASN:OD1	1:I:45:ARG:HD3	2.18	0.43
1:I:917:VAL:C	1:I:918:LEU:HD23	2.43	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:181:GLU:HB2	1:J:194:TYR:CD2	2.54	0.43
1:L:541:GLY:O	1:L:545:ARG:HD3	2.18	0.43
1:L:634:ARG:HG3	1:L:929:ARG:O	2.18	0.43
3:M:31:MET:SD	3:M:34:ILE:HD11	2.59	0.43
6:1:74:GLN:HE21	6:1:74:GLN:HB2	1.70	0.43
1:A:197:LYS:O	1:A:198:THR:C	2.59	0.43
1:A:288:GLU:OE2	1:C:841:TYR:OH	2.25	0.43
1:A:523:TRP:CD1	1:A:802:ARG:HD3	2.53	0.43
1:B:759:ASN:OD1	1:B:759:ASN:N	2.43	0.43
1:B:782:ILE:HD11	1:C:383:PHE:HB2	2.00	0.43
1:C:71:ASP:OD1	1:C:72:ARG:N	2.52	0.43
1:C:327:ALA:HB2	1:C:546:SER:HA	2.00	0.43
1:E:164:LYS:HD3	1:F:444:GLU:HA	2.00	0.43
1:E:197:LYS:O	1:E:221:ARG:NH2	2.51	0.43
1:G:317:GLN:OE1	1:G:835:MET:HB3	2.18	0.43
1:G:886:ASP:OD1	1:G:886:ASP:N	2.49	0.43
1:H:419:VAL:HG21	1:H:452:ARG:HB2	1.99	0.43
1:H:660:THR:O	1:H:660:THR:OG1	2.26	0.43
1:I:247:GLY:O	1:I:248:ILE:C	2.59	0.43
1:I:248:ILE:HG22	1:I:250:VAL:H	1.84	0.43
1:I:724:PHE:HE1	1:I:900:LEU:HD13	1.82	0.43
1:K:366:GLU:HG3	1:K:707:LEU:HD22	2.01	0.43
1:L:590:MET:HE1	1:L:688:PRO:HG3	1.99	0.43
2:N:148:MET:HG2	2:N:163:TYR:HE1	1.83	0.43
1:A:257:LEU:HD12	1:A:257:LEU:H	1.82	0.43
1:A:332:PHE:HB3	1:A:335:LEU:HD12	2.00	0.43
1:A:650:ASN:HB3	1:A:916:TYR:HE1	1.83	0.43
1:A:655:ILE:HB	1:A:913:THR:O	2.18	0.43
1:B:90:ASN:OD1	1:B:90:ASN:N	2.52	0.43
1:B:170:GLN:HG3	1:C:452:ARG:HB3	1.99	0.43
1:C:23:LEU:HD22	1:C:27:LEU:HD23	2.00	0.43
1:C:373:LEU:HB3	1:C:379:ARG:HD3	2.01	0.43
1:C:389:ALA:O	1:C:545:ARG:NH1	2.51	0.43
1:C:480:LEU:HD23	1:C:528:MET:SD	2.58	0.43
1:C:495:ASP:OD1	1:C:495:ASP:N	2.51	0.43
1:D:923:ASP:HA	1:D:941:ARG:HB3	1.99	0.43
1:E:403:HIS:HE1	1:F:543:ARG:HB3	1.84	0.43
1:F:773:TYR:O	1:F:775:ILE:HG13	2.19	0.43
1:G:472:LEU:HD23	1:G:472:LEU:HA	1.78	0.43
1:H:408:GLU:HG3	1:I:474:SER:HB2	2.00	0.43
1:H:479:TYR:OH	1:H:537:HIS:ND1	2.41	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:563:GLN:NE2	1:H:580:TYR:OH	2.33	0.43
1:H:737:LEU:HD13	1:H:753:TYR:CE1	2.54	0.43
1:I:818:ILE:HD12	1:I:818:ILE:H	1.83	0.43
1:I:825:SER:O	1:I:827:PHE:N	2.51	0.43
1:J:565:PHE:O	1:J:567:ALA:N	2.52	0.43
1:K:363:ARG:NE	1:K:923:ASP:OD2	2.41	0.43
6:Y:76:PHE:HD1	6:Y:77:GLN:H	1.64	0.43
1:A:73:GLU:O	1:A:79:TYR:HB2	2.19	0.43
1:A:788:ASP:OD2	1:A:795:ARG:NE	2.51	0.43
1:C:401:GLU:HG2	1:C:522:ARG:HG3	2.01	0.43
1:C:500:TYR:HB2	1:C:598:ASN:ND2	2.34	0.43
1:D:373:LEU:HD23	1:D:373:LEU:HA	1.74	0.43
1:E:737:LEU:HB2	1:E:763:ASP:OD2	2.18	0.43
1:E:830:TYR:CZ	1:E:831:LEU:HD13	2.53	0.43
1:F:417:GLY:C	1:F:419:VAL:H	2.26	0.43
1:F:828:VAL:HG12	1:F:829:GLY:N	2.32	0.43
1:G:541:GLY:O	1:G:545:ARG:HG3	2.18	0.43
1:H:232:CYS:O	1:H:233:TYR:C	2.60	0.43
1:H:368:SER:HG	1:H:646:LEU:H	1.65	0.43
1:H:421:ASN:N	1:H:421:ASN:OD1	2.50	0.43
1:H:432:THR:HG22	1:H:437:GLY:C	2.43	0.43
1:I:83:PHE:N	1:I:580:TYR:O	2.44	0.43
1:J:371:LEU:HB3	1:J:645:TYR:HE2	1.84	0.43
1:J:392:SER:N	1:J:539:ASN:OD1	2.40	0.43
1:J:425:LEU:O	1:J:449:ASN:ND2	2.39	0.43
1:J:601:ARG:NH2	1:J:698:TYR:O	2.52	0.43
1:L:113:LYS:NZ	1:L:321:ASN:O	2.46	0.43
4:Q:73:ARG:NH1	4:Q:73:ARG:HB3	2.34	0.43
1:B:409:LEU:HD23	1:B:409:LEU:HA	1.90	0.43
1:B:647:SER:HB3	1:B:675:ARG:NH2	2.32	0.43
1:C:681:ARG:O	1:C:713:LEU:HB2	2.18	0.43
1:D:431:LYS:HE2	1:D:434:GLN:HB3	2.01	0.43
1:F:480:LEU:HD23	1:F:528:MET:SD	2.59	0.43
1:G:256:LYS:C	1:G:258:GLU:H	2.26	0.43
1:H:702:GLY:O	1:H:703:SER:C	2.59	0.43
1:K:241:ASN:OD1	1:K:243:ASN:N	2.51	0.43
1:K:792:SER:OG	1:K:793:PHE:N	2.52	0.43
1:L:492:LYS:HA	1:L:492:LYS:HD2	1.82	0.43
2:N:188:ILE:O	2:N:189:VAL:C	2.57	0.43
2:N:220:ASP:OD2	2:N:223:THR:N	2.44	0.43
4:R:103:LEU:HD23	4:R:103:LEU:HA	1.82	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:W:31:SER:HB2	6:W:33:GLY:N	2.28	0.43
1:A:342:GLY:HA2	1:K:749:ASP:HB3	2.00	0.43
1:A:746:ARG:HD3	1:A:749:ASP:CG	2.44	0.43
1:A:788:ASP:OD2	1:A:795:ARG:HB2	2.19	0.43
1:B:131:PRO:HB3	1:B:169:GLY:HA2	2.00	0.43
1:B:396:ASP:OD2	6:X:62:SER:HB3	2.17	0.43
1:B:521:ALA:HB2	1:C:551:ASN:CG	2.44	0.43
1:B:526:ASP:N	1:B:526:ASP:OD1	2.51	0.43
1:B:565:PHE:O	1:B:569:LYS:HB3	2.19	0.43
1:B:639:ASP:OD2	1:B:926:ARG:NH1	2.52	0.43
1:C:619:PHE:O	1:C:621:MET:N	2.49	0.43
1:D:528:MET:HE3	1:D:528:MET:HB3	1.90	0.43
1:D:564:LYS:O	1:D:565:PHE:C	2.61	0.43
1:D:760:MET:HG2	1:D:765:PHE:HB2	2.01	0.43
1:G:373:LEU:HD23	1:G:373:LEU:HA	1.81	0.43
1:G:789:ARG:HH21	6:1:75:ASN:CB	2.32	0.43
1:H:85:LEU:N	1:H:578:TYR:O	2.52	0.43
1:H:332:PHE:CZ	1:H:387:ASN:HB2	2.54	0.43
1:I:55:VAL:O	1:I:622:ALA:N	2.46	0.43
1:I:373:LEU:HD13	1:I:379:ARG:HH12	1.83	0.43
1:K:409:LEU:HD21	1:L:473:TYR:CG	2.54	0.43
1:L:93:LEU:HB2	1:L:618:PHE:CE2	2.54	0.43
1:L:859:THR:O	4:Q:51:THR:HA	2.19	0.43
3:M:17:GLN:HB2	3:M:18:PRO:HD3	2.00	0.43
4:P:96:ARG:HD3	4:P:96:ARG:HA	1.84	0.43
4:S:18:ARG:H	4:S:18:ARG:HG2	1.67	0.43
5:U:127:THR:HG22	5:U:136:ASN:OD1	2.19	0.43
1:A:79:TYR:HB3	1:A:586:LYS:HE3	2.01	0.43
1:A:632:MET:HE2	5:U:170:THR:HG21	2.00	0.43
1:A:635:ASN:OD1	5:U:171:LEU:O	2.37	0.43
1:A:737:LEU:HB2	1:A:763:ASP:OD2	2.19	0.43
1:B:196:ASP:H	1:B:200:GLN:HB2	1.84	0.43
1:B:436:ASN:OD1	1:B:436:ASN:N	2.51	0.43
1:B:635:ASN:ND2	3:M:18:PRO:HB3	2.19	0.43
1:C:891:LEU:HD11	3:M:324:TYR:HD1	1.83	0.43
1:G:634:ARG:NH2	1:G:932:ARG:HA	2.34	0.43
1:G:871:ARG:NH1	6:2:30:MET:SD	2.92	0.43
1:H:229:MET:N	1:H:309:ASN:OD1	2.51	0.43
1:H:373:LEU:HD23	1:H:373:LEU:HA	1.76	0.43
1:H:856:ASP:OD1	1:H:856:ASP:N	2.50	0.43
1:I:34:THR:O	1:I:34:THR:OG1	2.35	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:797:PHE:CE2	1:J:799:PRO:HG3	2.53	0.43
1:L:66:ARG:HB2	1:L:615:TYR:CE2	2.54	0.43
1:L:472:LEU:HA	1:L:472:LEU:HD23	1.77	0.43
1:L:490:ASN:N	1:L:490:ASN:OD1	2.50	0.43
1:L:634:ARG:NH2	1:L:931:HIS:O	2.52	0.43
3:M:315:ASN:O	3:M:316:SER:C	2.60	0.43
6:Y:62:SER:O	6:Y:65:GLN:HB3	2.18	0.43
1:A:730:TRP:N	1:A:731:PRO:HD2	2.34	0.43
1:A:921:VAL:HG12	1:A:943:PRO:HB2	2.01	0.43
1:D:275:ASN:OD1	1:D:275:ASN:N	2.52	0.43
1:E:19:ALA:HB2	1:E:46:ASN:HB3	2.00	0.43
1:E:383:PHE:HB3	1:E:388:GLN:HB3	2.00	0.43
1:E:410:PRO:HB2	1:E:412:TYR:CE2	2.53	0.43
1:E:490:ASN:OD1	1:E:490:ASN:N	2.49	0.43
1:E:598:ASN:O	1:E:701:SER:OG	2.27	0.43
1:F:490:ASN:OD1	1:F:490:ASN:N	2.50	0.43
1:F:900:LEU:HD11	1:F:902:MET:HG2	2.00	0.43
1:G:53:HIS:ND1	1:G:54:ASP:OD1	2.52	0.43
1:H:589:ASN:HB2	1:H:601:ARG:HE	1.84	0.43
1:H:708:ASP:HB3	1:H:710:THR:HG23	2.01	0.43
1:I:390:VAL:HG21	1:I:790:MET:HE1	2.00	0.43
1:I:650:ASN:C	1:I:651:MET:HG2	2.44	0.43
1:J:177:ASN:HA	1:J:217:HIS:CD2	2.54	0.43
1:J:811:LYS:HG2	1:J:812:ASP:OD1	2.18	0.43
1:K:683:LYS:HA	1:K:913:THR:HG22	2.00	0.43
1:L:317:GLN:HE22	1:L:835:MET:H	1.65	0.43
1:L:825:SER:C	1:L:827:PHE:N	2.75	0.43
2:N:53:ASN:OD1	2:N:53:ASN:N	2.50	0.43
6:W:32:GLY:HA2	6:W:35:PHE:CD2	2.54	0.43
1:A:472:LEU:HD23	1:A:472:LEU:HA	1.85	0.42
1:D:444:GLU:O	1:F:165:THR:N	2.52	0.42
1:F:398:ARG:HH12	1:F:529:ASP:HA	1.84	0.42
1:G:221:ARG:NH2	1:G:288:GLU:OE2	2.46	0.42
1:G:412:TYR:OH	1:H:835:MET:HA	2.19	0.42
1:G:673:ALA:HB2	1:H:9:TRP:CZ2	2.53	0.42
1:H:534:PHE:CZ	1:H:710:THR:HB	2.54	0.42
1:I:196:ASP:N	1:I:196:ASP:OD1	2.51	0.42
1:J:389:ALA:HB1	1:J:541:GLY:HA2	2.01	0.42
1:J:470:ASN:O	1:J:471:PHE:C	2.60	0.42
1:K:111:THR:HG21	1:K:603:ASP:OD2	2.19	0.42
1:K:332:PHE:CZ	1:K:387:ASN:HB2	2.53	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:560:GLN:OE1	1:L:560:GLN:N	2.52	0.42
1:L:737:LEU:HD13	1:L:753:TYR:CE2	2.54	0.42
2:N:81:SER:HA	2:N:84:TYR:CE2	2.54	0.42
2:N:438:TYR:HB3	2:N:462:VAL:HG13	2.00	0.42
3:M:169:ARG:HB2	3:M:169:ARG:HH11	1.83	0.42
6:Y:73:GLU:HB3	6:Y:74:GLN:H	1.70	0.42
1:B:95:MET:HE3	1:B:95:MET:HB3	1.85	0.42
1:B:740:ASN:HB2	1:B:741:GLU:HG3	2.00	0.42
1:C:66:ARG:HG3	1:C:615:TYR:CZ	2.54	0.42
1:D:27:LEU:O	1:D:28:VAL:C	2.59	0.42
1:D:521:ALA:HB2	1:E:551:ASN:HB3	2.01	0.42
1:D:664:ILE:CG1	1:D:902:MET:HB3	2.49	0.42
1:D:788:ASP:OD2	1:D:795:ARG:HB2	2.18	0.42
1:D:887:LEU:HD23	1:D:887:LEU:HA	1.72	0.42
1:E:746:ARG:HB2	1:E:761:THR:HG22	2.00	0.42
1:H:178:ILE:HD11	1:H:281:PRO:O	2.19	0.42
1:I:865:CYS:SG	1:I:868:THR:OG1	2.64	0.42
1:J:589:ASN:HD21	1:J:600:LEU:H	1.67	0.42
1:J:744:ILE:HG23	1:J:764:TRP:CD1	2.54	0.42
1:K:329:ARG:HG3	1:K:333:ILE:O	2.19	0.42
1:L:905:GLU:HG3	4:Q:22:TRP:HZ2	1.84	0.42
6:W:37:TRP:HB2	6:W:38:GLY:H	1.70	0.42
6:X:74:GLN:HE21	6:X:74:GLN:HB2	1.59	0.42
1:A:201:PRO:HG2	1:A:286:TYR:CD1	2.54	0.42
1:A:332:PHE:CZ	1:A:387:ASN:HB2	2.54	0.42
1:B:786:TYR:CD1	6:X:93:ASP:CB	3.01	0.42
1:C:138:ALA:H	1:C:163:GLN:HA	1.83	0.42
1:E:118:THR:OG1	1:E:119:ALA:N	2.52	0.42
1:E:921:VAL:HG12	1:E:943:PRO:HB2	2.00	0.42
1:G:234:GLY:HA3	1:G:297:THR:HG21	2.00	0.42
1:G:519:LEU:HD23	1:G:519:LEU:HA	1.86	0.42
1:H:710:THR:O	1:H:710:THR:OG1	2.35	0.42
1:J:643:ASN:OD1	1:K:45:ARG:HD2	2.19	0.42
1:K:770:LEU:HD23	1:K:770:LEU:HA	1.92	0.42
1:L:85:LEU:N	1:L:578:TYR:O	2.53	0.42
2:N:183:LEU:O	2:N:186:ASN:HB3	2.18	0.42
2:N:217:LEU:HD23	2:N:232:THR:HG21	2.02	0.42
2:N:393:LEU:HA	2:N:401:THR:HA	2.00	0.42
4:Q:113:GLU:O	4:Q:116:VAL:HG22	2.19	0.42
1:A:413:CYS:HA	1:B:461:ILE:HB	2.02	0.42
1:B:646:LEU:HA	1:B:646:LEU:HD12	1.53	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:17:GLN:HB3	1:C:21:GLU:HB2	2.02	0.42
1:C:649:ALA:O	1:C:651:MET:HG2	2.19	0.42
1:D:519:LEU:HA	1:D:519:LEU:HD23	1.77	0.42
1:E:138:ALA:HB3	1:E:164:LYS:HG3	2.00	0.42
1:E:167:VAL:N	1:F:449:ASN:OD1	2.46	0.42
1:E:232:CYS:O	1:E:233:TYR:C	2.60	0.42
1:E:363:ARG:NH1	1:E:566:PHE:HE1	2.17	0.42
1:E:414:PHE:CE1	1:F:827:PHE:HD1	2.37	0.42
1:E:751:GLU:H	1:E:751:GLU:HG3	1.69	0.42
1:F:330:ASP:OD2	1:F:370:GLN:NE2	2.33	0.42
1:G:65:LEU:HD12	1:G:618:PHE:CE2	2.54	0.42
1:G:120:TYR:HE1	1:I:846:PRO:HB2	1.83	0.42
1:G:514:ASP:O	1:G:517:ILE:HG22	2.19	0.42
1:I:653:TYR:CD1	1:I:664:ILE:HD11	2.54	0.42
1:I:678:ALA:HB3	1:I:918:LEU:HB2	2.02	0.42
1:I:684:THR:C	1:I:686:GLU:H	2.27	0.42
1:I:825:SER:C	1:I:827:PHE:H	2.27	0.42
1:K:514:ASP:O	1:K:517:ILE:HG22	2.19	0.42
1:L:337:TYR:CE2	1:L:585:ARG:HG2	2.54	0.42
1:L:619:PHE:O	1:L:621:MET:N	2.48	0.42
3:M:11:ARG:HD3	3:M:122:ARG:NH1	2.34	0.42
5:V:137:ASP:OD1	5:V:137:ASP:N	2.52	0.42
1:A:366:GLU:HG3	1:A:707:LEU:HD22	2.01	0.42
1:A:412:TYR:HE2	1:B:836:ARG:H	1.67	0.42
1:A:589:ASN:ND2	1:A:600:LEU:HB2	2.34	0.42
1:A:942:THR:HB	1:A:943:PRO:HD3	2.00	0.42
1:B:650:ASN:HD22	1:B:650:ASN:N	2.18	0.42
1:D:409:LEU:HB2	1:E:470:ASN:OD1	2.19	0.42
1:D:737:LEU:HD13	1:D:753:TYR:CD1	2.55	0.42
1:D:812:ASP:OD1	1:D:812:ASP:N	2.52	0.42
1:E:514:ASP:O	1:E:517:ILE:HG22	2.19	0.42
1:F:542:LEU:HA	1:F:542:LEU:HD12	1.74	0.42
1:G:331:ASN:O	1:G:332:PHE:C	2.63	0.42
1:G:782:ILE:HD11	1:H:383:PHE:HB2	2.00	0.42
1:H:75:THR:HG22	1:H:76:ALA:H	1.85	0.42
1:J:329:ARG:HH21	1:J:593:GLN:HA	1.83	0.42
1:J:669:ARG:O	1:J:898:HIS:N	2.47	0.42
3:M:33:ARG:HG3	3:M:38:THR:HG21	2.01	0.42
4:Q:100:LEU:HD22	4:Q:100:LEU:HA	1.84	0.42
5:U:131:ARG:HH21	5:U:171:LEU:HD21	1.84	0.42
6:Y:5:ASN:O	6:Y:6:PHE:HB2	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:97:SER:HB3	1:C:777:TYR:O	2.20	0.42
1:A:330:ASP:CG	1:A:331:ASN:HD22	2.27	0.42
1:B:389:ALA:O	1:B:545:ARG:NH1	2.53	0.42
1:C:324:ASN:HA	1:C:595:SER:OG	2.20	0.42
1:C:822:HIS:H	1:C:844:ASN:HD21	1.68	0.42
1:C:884:LEU:HD13	1:C:922:PHE:HE2	1.85	0.42
1:E:333:ILE:HD11	1:E:370:GLN:HE21	1.85	0.42
1:F:253:GLN:O	1:F:255:GLY:N	2.53	0.42
1:F:724:PHE:CE2	1:F:893:TYR:HE2	2.38	0.42
1:H:74:ASP:OD1	1:H:586:LYS:NZ	2.45	0.42
1:H:371:LEU:HD12	1:H:646:LEU:HD13	2.01	0.42
1:I:298:HIS:NE2	1:I:319:MET:SD	2.92	0.42
1:I:318:SER:OG	1:I:319:MET:N	2.52	0.42
1:J:572:LEU:HA	1:J:572:LEU:HD12	1.78	0.42
1:J:760:MET:HB2	1:J:760:MET:HE2	1.76	0.42
1:K:299:ILE:HD12	1:K:302:MET:HE1	2.00	0.42
1:K:573:LEU:HA	1:K:929:ARG:HH22	1.84	0.42
1:L:382:TYR:HD1	1:L:389:ALA:HA	1.84	0.42
2:N:243:LEU:HD23	2:N:243:LEU:HA	1.92	0.42
2:N:406:TRP:CH2	2:N:425:LEU:HD12	2.54	0.42
5:V:55:LEU:HD21	5:V:194:PRO:HB2	2.01	0.42
6:X:64:GLY:O	6:X:65:GLN:C	2.62	0.42
1:B:484:LEU:HD11	1:B:527:TYR:CD1	2.55	0.42
1:C:366:GLU:HG3	1:C:707:LEU:HD22	2.02	0.42
1:C:373:LEU:HD23	1:C:373:LEU:HA	1.83	0.42
1:D:285:LEU:HD23	1:D:285:LEU:HA	1.88	0.42
1:E:93:LEU:HB2	1:E:618:PHE:CE1	2.54	0.42
1:E:110:PRO:HD2	1:E:603:ASP:O	2.19	0.42
1:E:724:PHE:CE2	1:E:893:TYR:HE2	2.37	0.42
1:E:776:GLY:HA2	1:E:780:PHE:HE1	1.83	0.42
1:F:46:ASN:ND2	6:Y:25:ILE:O	2.53	0.42
1:F:788:ASP:OD2	1:F:795:ARG:HB2	2.19	0.42
1:G:480:LEU:HD23	1:G:528:MET:SD	2.59	0.42
1:G:573:LEU:HD12	1:G:929:ARG:NH1	2.34	0.42
1:H:770:LEU:HD23	1:H:770:LEU:HA	1.90	0.42
1:J:825:SER:C	1:J:827:PHE:H	2.28	0.42
1:J:835:MET:HA	1:L:412:TYR:OH	2.19	0.42
1:K:339:ASN:OD1	1:K:339:ASN:N	2.53	0.42
1:K:542:LEU:HA	1:K:545:ARG:HH21	1.84	0.42
1:K:823:ASN:OD1	1:K:824:ASN:N	2.53	0.42
1:L:301:TYR:CE2	1:L:303:PRO:HG3	2.55	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:337:TYR:CZ	1:L:585:ARG:HG2	2.55	0.42
1:L:817:GLY:O	1:L:821:GLN:HG3	2.19	0.42
1:A:305:ILE:H	1:A:305:ILE:HG13	1.63	0.42
1:A:338:TYR:CZ	1:A:564:LYS:HB2	2.54	0.42
1:A:773:TYR:O	1:A:775:ILE:HG13	2.20	0.42
1:B:95:MET:HE1	1:B:580:TYR:HE2	1.85	0.42
1:B:178:ILE:HG12	1:B:183:ILE:HG22	2.01	0.42
1:D:12:MET:HB3	1:F:924:VAL:HG11	2.02	0.42
1:D:41:ASN:HA	6:Z:24:ASP:O	2.20	0.42
1:D:438:TRP:HH2	1:F:179:THR:HA	1.84	0.42
1:D:534:PHE:CE1	1:D:710:THR:HB	2.55	0.42
1:E:251:LYS:HG3	1:E:256:LYS:HA	2.01	0.42
1:F:32:ARG:HG3	6:Y:20:GLY:O	2.20	0.42
1:G:887:LEU:HA	1:G:887:LEU:HD23	1.78	0.42
1:I:251:LYS:HB2	1:I:258:GLU:H	1.84	0.42
1:I:368:SER:OG	1:I:644:ASP:OD1	2.28	0.42
1:I:525:LEU:HD23	1:I:525:LEU:HA	1.86	0.42
1:I:731:PRO:HG3	1:I:742:PHE:CE1	2.55	0.42
1:I:786:TYR:CE1	1:I:787:LYS:HG3	2.55	0.42
1:J:463:LEU:O	1:J:464:ASN:C	2.56	0.42
1:J:690:LEU:HD23	1:J:690:LEU:HA	1.79	0.42
2:N:217:LEU:HD12	2:N:217:LEU:HA	1.66	0.42
2:N:255:LEU:HA	2:N:255:LEU:HD23	1.74	0.42
1:A:61:GLN:HE21	1:A:91:ARG:HE	1.67	0.42
1:A:667:PRO:HG3	1:K:663:PRO:HG3	2.02	0.42
1:B:391:ASP:OD1	1:B:391:ASP:N	2.39	0.42
1:B:717:PHE:HB3	1:B:744:ILE:HD12	2.02	0.42
1:D:34:THR:O	1:D:35:GLU:C	2.63	0.42
1:D:724:PHE:CE1	1:D:900:LEU:HD13	2.55	0.42
1:D:818:ILE:H	1:D:818:ILE:HD12	1.85	0.42
1:E:724:PHE:HE2	1:E:893:TYR:HE2	1.67	0.42
1:F:333:ILE:HG12	1:F:366:GLU:OE1	2.20	0.42
1:F:370:GLN:HG3	1:F:708:ASP:HA	2.02	0.42
1:G:210:TRP:HB3	1:I:835:MET:HE1	2.02	0.42
1:G:299:ILE:HG21	1:G:302:MET:HE2	2.02	0.42
1:G:571:LEU:HD11	1:G:927:VAL:HG11	2.02	0.42
1:G:646:LEU:O	1:G:647:SER:C	2.60	0.42
1:G:835:MET:HA	1:I:412:TYR:OH	2.20	0.42
1:G:915:LEU:HG	1:G:917:VAL:HG23	2.02	0.42
1:H:100:PHE:HD2	1:H:612:ILE:HD11	1.85	0.42
1:H:681:ARG:NH2	1:H:909:MET:SD	2.93	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:797:PHE:CD1	1:H:799:PRO:HD3	2.55	0.42
1:I:335:LEU:HD23	1:I:561:VAL:HG21	2.02	0.42
1:I:426:THR:OG1	1:I:447:ASP:O	2.33	0.42
1:K:85:LEU:HD13	1:K:614:LEU:HD21	2.02	0.42
1:K:218:ALA:HB3	1:K:283:VAL:HG22	2.01	0.42
1:K:413:CYS:HA	1:L:461:ILE:HB	2.01	0.42
1:L:126:LYS:HE2	1:L:233:TYR:CE2	2.55	0.42
3:M:387:ASN:HA	5:U:145:GLY:O	2.20	0.42
4:P:88:SER:O	4:P:92:ARG:HG2	2.19	0.42
1:A:229:MET:HE2	1:A:229:MET:HB3	1.72	0.42
1:B:702:GLY:O	1:B:703:SER:C	2.62	0.42
1:B:874:PHE:CE2	1:B:887:LEU:HB3	2.55	0.42
1:C:450:GLU:OE1	1:C:450:GLU:N	2.52	0.42
1:D:29:GLN:O	1:D:30:PHE:C	2.61	0.42
1:E:164:LYS:HA	1:F:444:GLU:HB3	2.01	0.42
1:E:177:ASN:OD1	1:E:178:ILE:N	2.50	0.42
1:E:471:PHE:O	1:E:472:LEU:C	2.61	0.42
1:F:633:LEU:HA	1:F:633:LEU:HD23	1.86	0.42
1:F:836:ARG:H	1:F:836:ARG:HG3	1.66	0.42
1:F:887:LEU:HD23	1:F:887:LEU:HA	1.90	0.42
1:G:519:LEU:HD22	1:H:115:TYR:CG	2.55	0.42
1:I:737:LEU:HB2	1:I:763:ASP:OD1	2.19	0.42
1:I:825:SER:C	1:I:827:PHE:N	2.77	0.42
1:J:251:LYS:HA	1:J:256:LYS:HA	2.02	0.42
1:K:72:ARG:HD2	1:K:79:TYR:OH	2.20	0.42
1:K:845:PHE:O	1:K:846:PRO:C	2.52	0.42
3:M:114:LEU:O	3:M:118:VAL:HG13	2.20	0.42
4:P:58:GLU:HA	4:P:61:ALA:H	1.85	0.42
4:Q:35:ASP:OD2	4:Q:37:ARG:NH2	2.48	0.42
5:U:61:ILE:HG13	5:U:62:THR:H	1.84	0.42
5:V:210:ASP:HB3	5:V:216:PHE:CE2	2.55	0.42
6:Y:63:THR:H	6:Y:63:THR:HG22	1.55	0.42
1:A:237:ALA:O	1:A:246:GLN:HG2	2.20	0.41
1:C:587:ASP:CG	1:C:601:ARG:HH21	2.25	0.41
1:D:557:PHE:HD1	1:D:557:PHE:H	1.68	0.41
1:E:93:LEU:HB2	1:E:618:PHE:HE1	1.84	0.41
1:E:773:TYR:O	1:E:775:ILE:HG13	2.20	0.41
1:F:237:ALA:HB3	1:F:246:GLN:HG2	2.01	0.41
1:F:316:GLN:HG2	1:F:316:GLN:H	1.58	0.41
1:G:382:TYR:CE2	6:1:68:ARG:HD3	2.55	0.41
1:G:513:VAL:HG13	1:G:517:ILE:HG21	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:523:TRP:CZ3	1:G:862:LYS:HG2	2.54	0.41
1:G:524:SER:H	1:G:800:MET:HE1	1.85	0.41
1:G:587:ASP:OD2	1:G:601:ARG:NH2	2.53	0.41
1:H:40:LEU:HD12	1:H:40:LEU:HA	1.85	0.41
1:H:472:LEU:HD12	1:H:472:LEU:HA	1.77	0.41
1:I:82:ARG:HG3	1:I:581:GLU:HB2	2.02	0.41
1:I:378:ASP:OD1	1:I:378:ASP:N	2.43	0.41
1:I:950:THR:HA	1:L:890:ASN:HD21	1.85	0.41
1:K:126:LYS:HG2	1:K:233:TYR:CD2	2.55	0.41
1:K:902:MET:HE3	1:K:904:PHE:CE1	2.55	0.41
1:L:333:ILE:HG12	1:L:366:GLU:OE1	2.19	0.41
2:N:276:ASP:OD1	2:N:276:ASP:N	2.53	0.41
2:N:377:PRO:O	2:N:378:VAL:C	2.62	0.41
3:M:26:ASP:OD1	3:M:26:ASP:N	2.43	0.41
1:A:675:ARG:NH2	6:X:30:MET:HB3	2.34	0.41
1:A:803:GLN:OE1	1:B:552:GLY:N	2.50	0.41
1:B:630:GLU:O	1:B:634:ARG:HG3	2.20	0.41
1:B:690:LEU:HD23	1:B:690:LEU:HA	1.84	0.41
1:C:574:LEU:HD23	1:C:574:LEU:HA	1.78	0.41
1:C:635:ASN:OD1	1:C:636:ASP:N	2.54	0.41
1:C:737:LEU:HD13	1:C:753:TYR:CE1	2.55	0.41
1:D:328:PHE:CD1	1:D:549:LEU:HD11	2.55	0.41
1:D:782:ILE:HD11	1:E:383:PHE:HB2	2.01	0.41
1:E:74:ASP:OD1	1:E:586:LYS:NZ	2.38	0.41
1:E:265:PHE:HB2	1:F:428:VAL:O	2.20	0.41
1:E:539:ASN:HB3	1:E:542:LEU:HB3	2.03	0.41
1:E:744:ILE:HG23	1:E:764:TRP:CD1	2.55	0.41
1:E:806:ASP:OD1	1:E:809:LYS:N	2.37	0.41
1:F:174:SER:HB2	1:F:215:ILE:HD13	2.02	0.41
1:F:373:LEU:HD23	1:F:373:LEU:HA	1.83	0.41
1:F:690:LEU:HD12	1:F:690:LEU:HA	1.84	0.41
1:G:549:LEU:HD23	1:G:549:LEU:HA	1.86	0.41
1:G:680:THR:HG21	1:G:711:PHE:HB3	2.01	0.41
1:G:762:LYS:HE3	1:G:762:LYS:HB2	1.87	0.41
1:H:519:LEU:HD13	1:I:115:TYR:CD2	2.55	0.41
1:H:922:PHE:O	1:H:941:ARG:HA	2.20	0.41
1:H:930:PRO:O	1:H:931:HIS:ND1	2.49	0.41
1:I:135:ASP:OD1	1:I:225:LYS:HD2	2.20	0.41
1:I:348:ALA:O	1:I:579:THR:HG22	2.20	0.41
1:J:43:LYS:O	1:J:44:PHE:CG	2.73	0.41
1:K:747:SER:OG	1:K:748:VAL:N	2.52	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:196:ASP:HB3	1:L:200:GLN:HB2	2.02	0.41
1:L:202:GLU:O	1:L:203:PRO:C	2.63	0.41
6:W:29:ASN:O	6:W:30:MET:C	2.63	0.41
1:A:563:GLN:OE1	1:A:565:PHE:N	2.40	0.41
1:B:764:TRP:CZ2	1:B:870:TRP:HB3	2.54	0.41
1:C:95:MET:O	1:C:98:THR:OG1	2.36	0.41
1:C:112:PHE:HE1	1:C:326:ILE:H	1.67	0.41
1:C:413:CYS:SG	1:C:459:MET:HB2	2.60	0.41
1:C:713:LEU:HD23	1:C:713:LEU:HA	1.84	0.41
1:D:237:ALA:O	1:D:238:LYS:C	2.61	0.41
1:E:877:ASN:ND2	1:F:56:THR:OG1	2.52	0.41
1:H:199:PHE:CD2	1:H:243:ASN:HB3	2.55	0.41
1:H:318:SER:OG	1:H:319:MET:N	2.51	0.41
1:H:585:ARG:NH1	1:H:590:MET:HE2	2.35	0.41
1:H:788:ASP:OD2	1:H:795:ARG:NE	2.53	0.41
1:I:397:VAL:HG11	1:I:536:HIS:HE2	1.84	0.41
1:I:408:GLU:H	1:I:408:GLU:HG2	1.60	0.41
1:I:823:ASN:O	1:I:824:ASN:C	2.60	0.41
1:J:737:LEU:HB2	1:J:763:ASP:OD2	2.20	0.41
1:K:210:TRP:CE3	1:K:417:GLY:HA3	2.56	0.41
1:L:135:ASP:OD1	1:L:225:LYS:HD2	2.20	0.41
1:L:202:GLU:HG3	1:L:203:PRO:HD2	2.02	0.41
1:L:335:LEU:HD23	1:L:561:VAL:HG21	2.02	0.41
2:N:129:THR:HG22	2:N:554:VAL:HA	2.02	0.41
2:N:385:ASP:OD2	2:N:389:ARG:HB2	2.20	0.41
3:M:130:ARG:O	3:M:134:GLN:HB2	2.20	0.41
4:S:28:ASN:OD1	4:S:43:ASN:ND2	2.53	0.41
5:V:59:ALA:O	5:V:60:ALA:C	2.58	0.41
1:A:590:MET:HE1	1:A:688:PRO:HB3	2.02	0.41
1:A:650:ASN:OD1	1:A:918:LEU:HD13	2.21	0.41
1:A:675:ARG:HD2	1:A:922:PHE:CE1	2.55	0.41
1:A:928:HIS:HD2	1:A:930:PRO:HD3	1.85	0.41
1:B:420:ILE:O	1:B:422:THR:N	2.53	0.41
1:C:177:ASN:HA	1:C:217:HIS:CD2	2.55	0.41
1:C:463:LEU:HD23	1:C:463:LEU:HA	1.85	0.41
1:C:563:GLN:OE1	1:C:564:LYS:N	2.53	0.41
1:D:136:GLU:OE1	1:D:311:ARG:HB2	2.21	0.41
1:D:162:GLN:HE22	1:D:164:LYS:HG3	1.85	0.41
1:E:818:ILE:HD12	1:E:818:ILE:H	1.86	0.41
1:F:196:ASP:H	1:F:200:GLN:HB2	1.86	0.41
1:F:378:ASP:OD1	1:F:380:THR:N	2.54	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:467:LEU:O	1:F:468:TRP:C	2.60	0.41
1:F:534:PHE:CE2	1:F:710:THR:HB	2.55	0.41
1:F:731:PRO:O	1:F:733:ASN:N	2.54	0.41
1:G:634:ARG:HH22	1:G:932:ARG:HA	1.84	0.41
1:G:900:LEU:HD12	1:G:901:ASP:N	2.35	0.41
1:H:589:ASN:CB	1:H:601:ARG:HE	2.33	0.41
1:I:52:THR:OG1	1:I:53:HIS:N	2.53	0.41
1:I:329:ARG:NH1	1:I:702:GLY:O	2.36	0.41
1:J:372:LEU:HD12	1:J:645:TYR:HB2	2.02	0.41
1:J:408:GLU:OE2	1:K:474:SER:OG	2.36	0.41
1:J:635:ASN:OD1	1:J:637:THR:HG22	2.21	0.41
1:L:200:GLN:O	1:L:201:PRO:C	2.54	0.41
6:Z:26:GLY:C	6:Z:27:THR:HG23	2.46	0.41
1:A:58:ASP:N	1:A:58:ASP:OD1	2.53	0.41
1:B:472:LEU:O	1:B:473:TYR:C	2.57	0.41
1:B:649:ALA:C	1:B:650:ASN:HD22	2.28	0.41
1:C:51:PRO:HD3	6:W:11:PRO:HA	2.01	0.41
1:C:133:GLU:HG2	1:C:167:VAL:HG13	2.02	0.41
1:C:325:TYR:CD2	1:C:543:ARG:HA	2.56	0.41
1:D:347:LEU:HA	1:D:579:THR:O	2.21	0.41
1:D:431:LYS:HB3	1:D:437:GLY:C	2.46	0.41
1:D:451:ILE:HA	1:F:169:GLY:O	2.20	0.41
1:E:275:ASN:O	1:E:275:ASN:ND2	2.54	0.41
1:E:432:THR:OG1	1:E:439:GLU:HB2	2.20	0.41
1:F:329:ARG:NH1	1:F:704:ILE:HG13	2.36	0.41
1:F:578:TYR:HE2	1:F:935:ILE:HG13	1.86	0.41
1:F:669:ARG:O	1:F:898:HIS:N	2.39	0.41
1:G:589:ASN:HD21	1:G:601:ARG:HB2	1.85	0.41
1:H:112:PHE:CE2	1:H:114:PRO:HD3	2.55	0.41
1:H:298:HIS:NE2	1:H:319:MET:HE2	2.35	0.41
1:H:335:LEU:HD23	1:H:335:LEU:HA	1.77	0.41
1:J:74:ASP:OD1	1:J:586:LYS:NZ	2.40	0.41
1:J:204:GLN:H	1:J:204:GLN:HG2	1.39	0.41
1:J:362:ASP:HB2	1:J:941:ARG:HH22	1.85	0.41
1:J:429:LYS:HE2	1:J:429:LYS:HB3	1.86	0.41
1:J:522:ARG:NH2	1:J:798:GLN:OE1	2.54	0.41
1:K:329:ARG:HB2	1:K:333:ILE:H	1.85	0.41
1:K:689:SER:O	1:K:691:GLY:N	2.52	0.41
1:L:400:ILE:HD13	1:L:525:LEU:HG	2.03	0.41
1:L:825:SER:O	1:L:827:PHE:HD2	2.02	0.41
2:N:154:THR:HB	2:N:156:ASP:OD1	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:M:259:THR:HA	3:M:262:ARG:NH1	2.36	0.41
5:V:147:ARG:O	5:V:148:PRO:C	2.62	0.41
6:W:30:MET:O	6:W:31:SER:C	2.61	0.41
6:Y:8:SER:C	6:Y:10:ALA:H	2.28	0.41
1:A:66:ARG:HH22	1:E:73:GLU:CD	2.27	0.41
1:A:379:ARG:HD2	1:A:379:ARG:HA	1.70	0.41
1:B:355:ASN:OD1	1:B:356:ALA:N	2.53	0.41
1:C:99:TYR:CD2	1:C:560:GLN:HB3	2.55	0.41
1:C:469:ARG:HE	1:C:514:ASP:CG	2.29	0.41
1:D:407:ASP:OD1	1:D:407:ASP:N	2.54	0.41
1:D:792:SER:O	1:D:796:ASN:ND2	2.54	0.41
1:E:212:GLU:H	1:E:212:GLU:HG2	1.60	0.41
1:E:651:MET:HE2	1:E:651:MET:HB3	1.93	0.41
1:F:328:PHE:CE1	1:F:549:LEU:HD11	2.55	0.41
1:F:374:ASP:OD1	1:F:789:ARG:HB3	2.20	0.41
1:F:864:LEU:HD23	1:F:864:LEU:HA	1.83	0.41
1:F:902:MET:HE3	1:F:904:PHE:CE1	2.54	0.41
1:G:754:ASN:HD22	1:G:759:ASN:HA	1.85	0.41
1:H:532:ASN:HA	1:H:533:PRO:HD3	1.94	0.41
1:H:624:ASN:OD1	1:H:624:ASN:N	2.53	0.41
1:H:673:ALA:HB2	1:I:9:TRP:CZ2	2.56	0.41
1:I:40:LEU:HA	1:I:40:LEU:HD23	1.88	0.41
1:J:93:LEU:HB2	1:J:618:PHE:CE2	2.55	0.41
1:J:823:ASN:O	1:J:824:ASN:C	2.60	0.41
1:K:125:PRO:HG2	1:K:128:ALA:HB2	2.01	0.41
1:K:275:ASN:O	1:K:279:LEU:N	2.54	0.41
1:K:302:MET:HE2	1:K:302:MET:HB2	1.94	0.41
1:K:889:GLN:NE2	1:L:52:THR:HG22	2.35	0.41
3:M:348:ALA:O	3:M:349:ARG:C	2.62	0.41
5:V:80:TYR:CE2	5:V:82:GLU:HA	2.56	0.41
6:Y:63:THR:HA	6:Y:66:MET:HG2	2.02	0.41
6:1:22:TRP:HE3	6:1:22:TRP:H	1.68	0.41
1:A:281:PRO:HD3	1:B:438:TRP:CE3	2.55	0.41
1:B:411:ASN:HD22	1:C:466:ASN:CG	2.27	0.41
1:B:810:TYR:HD2	1:B:813:TYR:N	2.18	0.41
1:B:829:GLY:HA2	1:B:837:GLU:HG2	2.03	0.41
1:C:224:LYS:HG3	1:C:288:GLU:C	2.46	0.41
1:C:737:LEU:HB2	1:C:763:ASP:OD2	2.20	0.41
1:D:45:ARG:HD2	6:Z:27:THR:HG22	2.03	0.41
1:D:572:LEU:HA	1:D:572:LEU:HD12	1.88	0.41
1:E:842:PRO:HB3	1:F:235:SER:HB2	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:482:ASP:OD2	1:F:502:TYR:OH	2.39	0.41
1:G:209:GLN:NE2	1:I:312:GLU:O	2.51	0.41
1:G:574:LEU:HD23	1:G:574:LEU:HA	1.86	0.41
1:G:841:TYR:O	1:G:842:PRO:C	2.54	0.41
1:I:744:ILE:HG12	1:I:764:TRP:CD2	2.56	0.41
1:J:369:TYR:HE1	1:J:569:LYS:HE3	1.85	0.41
1:J:472:LEU:O	1:J:473:TYR:C	2.60	0.41
1:J:779:GLY:N	1:K:97:SER:OG	2.53	0.41
1:J:921:VAL:HB	1:J:922:PHE:H	1.65	0.41
1:K:269:THR:OG1	1:L:424:THR:O	2.34	0.41
1:K:285:LEU:HD23	1:K:285:LEU:HA	1.83	0.41
1:L:55:VAL:O	1:L:622:ALA:N	2.43	0.41
1:L:372:LEU:O	1:L:375:SER:N	2.54	0.41
1:L:372:LEU:HD23	1:L:569:LYS:NZ	2.36	0.41
2:N:58:SER:OG	2:N:59:GLU:OE1	2.20	0.41
2:N:105:GLU:OE1	2:N:105:GLU:N	2.52	0.41
5:V:57:GLU:O	5:V:58:GLN:C	2.59	0.41
1:A:835:MET:HE2	1:B:416:LEU:HD23	2.03	0.41
1:A:910:ASP:OD1	1:A:910:ASP:N	2.39	0.41
1:A:921:VAL:HA	1:A:943:PRO:HG2	2.02	0.41
1:B:275:ASN:ND2	1:B:277:ASP:HB3	2.36	0.41
1:C:112:PHE:HD1	1:C:326:ILE:HB	1.85	0.41
1:C:135:ASP:HA	1:C:165:THR:HA	2.02	0.41
1:C:364:ASN:ND2	1:C:706:TYR:O	2.54	0.41
1:C:534:PHE:CZ	1:C:710:THR:HB	2.56	0.41
1:C:759:ASN:OD1	1:C:759:ASN:N	2.51	0.41
1:D:40:LEU:HD23	1:D:40:LEU:HA	1.82	0.41
1:D:90:ASN:OD1	1:D:90:ASN:N	2.52	0.41
1:D:236:TYR:CE2	1:F:848:PRO:HD3	2.56	0.41
1:D:374:ASP:OD1	1:D:789:ARG:HB3	2.21	0.41
1:D:468:TRP:O	1:D:469:ARG:C	2.60	0.41
1:D:745:LYS:NZ	4:P:48:THR:OG1	2.50	0.41
1:F:398:ARG:NH1	1:F:529:ASP:HA	2.35	0.41
1:F:463:LEU:HD23	1:F:463:LEU:HA	1.85	0.41
1:G:66:ARG:NH2	1:G:613:CYS:SG	2.93	0.41
1:G:366:GLU:HG3	1:G:707:LEU:HD22	2.02	0.41
1:G:538:ARG:HD3	6:1:67:LEU:HD11	2.03	0.41
1:H:112:PHE:HD1	1:H:326:ILE:HB	1.84	0.41
1:H:113:LYS:HE2	1:H:115:TYR:O	2.21	0.41
1:H:391:ASP:HB3	1:H:539:ASN:HD21	1.85	0.41
1:J:634:ARG:HD3	1:J:929:ARG:O	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:373:LEU:HD23	1:K:373:LEU:HA	1.82	0.41
1:K:426:THR:OG1	1:K:447:ASP:OD1	2.32	0.41
1:K:774:ASN:OD1	1:K:774:ASN:N	2.52	0.41
1:K:915:LEU:HG	1:K:917:VAL:HG22	2.03	0.41
3:M:146:PHE:HB2	3:M:187:TYR:CG	2.56	0.41
1:A:91:ARG:HD3	1:A:618:PHE:CD2	2.56	0.41
1:A:823:ASN:C	1:A:825:SER:N	2.74	0.41
1:A:845:PHE:O	1:A:846:PRO:C	2.60	0.41
1:B:35:GLU:OE2	1:B:41:ASN:ND2	2.54	0.41
1:B:318:SER:OG	1:B:319:MET:N	2.53	0.41
1:B:843:ALA:HB3	1:C:120:TYR:HD2	1.86	0.41
1:C:199:PHE:CD2	1:C:243:ASN:HB3	2.56	0.41
1:C:633:LEU:HD23	1:C:633:LEU:HA	1.88	0.41
1:C:713:LEU:HA	1:C:715:HIS:CE1	2.56	0.41
1:C:770:LEU:HD23	1:C:770:LEU:HA	1.89	0.41
1:C:845:PHE:O	1:C:846:PRO:C	2.58	0.41
1:D:806:ASP:OD1	1:D:809:LYS:N	2.37	0.41
1:E:112:PHE:CD1	1:E:326:ILE:HB	2.56	0.41
1:E:137:ALA:HA	1:E:163:GLN:HA	2.02	0.41
1:E:412:TYR:OH	1:F:835:MET:HA	2.21	0.41
1:E:528:MET:HE3	1:E:528:MET:HB3	1.88	0.41
1:E:539:ASN:O	1:E:543:ARG:HG3	2.21	0.41
1:E:646:LEU:O	1:E:647:SER:C	2.61	0.41
1:E:650:ASN:OD1	1:E:918:LEU:HD23	2.21	0.41
1:E:737:LEU:HA	1:F:62:ARG:HH21	1.85	0.41
1:E:939:TYR:N	1:E:939:TYR:CD1	2.89	0.41
1:F:392:SER:O	1:F:539:ASN:HA	2.21	0.41
1:F:724:PHE:CE1	1:F:900:LEU:HD13	2.56	0.41
1:F:866:ASP:OD1	1:F:866:ASP:N	2.54	0.41
1:F:910:ASP:OD1	1:F:910:ASP:N	2.52	0.41
1:G:82:ARG:HA	1:G:581:GLU:HA	2.03	0.41
1:G:93:LEU:HB2	1:G:618:PHE:CE1	2.55	0.41
1:G:565:PHE:O	1:G:569:LYS:HB3	2.20	0.41
1:H:202:GLU:O	1:H:203:PRO:C	2.60	0.41
1:H:328:PHE:HD1	1:H:549:LEU:HD11	1.86	0.41
1:H:371:LEU:HB3	1:H:645:TYR:HE2	1.85	0.41
1:H:373:LEU:HD13	1:H:379:ARG:HH12	1.85	0.41
1:H:521:ALA:HB2	1:I:551:ASN:CG	2.46	0.41
1:I:93:LEU:HB2	1:I:618:PHE:CE2	2.56	0.41
1:I:222:VAL:HG11	1:I:285:LEU:HD13	2.03	0.41
1:I:534:PHE:CZ	1:I:710:THR:HB	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:789:ARG:N	1:I:792:SER:OG	2.53	0.41
1:J:197:LYS:O	1:J:198:THR:C	2.61	0.41
1:J:199:PHE:CD2	1:J:243:ASN:HB3	2.55	0.41
1:J:251:LYS:HD2	1:J:256:LYS:HD2	2.03	0.41
1:J:373:LEU:HD23	1:J:373:LEU:HA	1.81	0.41
1:J:446:SER:O	1:J:449:ASN:ND2	2.52	0.41
1:K:95:MET:HE1	1:K:580:TYR:HE2	1.85	0.41
1:K:336:MET:HG3	1:K:561:VAL:HG11	2.03	0.41
1:L:210:TRP:CE3	1:L:417:GLY:HA3	2.56	0.41
1:L:321:ASN:CG	1:L:504:ASN:HD21	2.29	0.41
1:L:373:LEU:HD23	1:L:373:LEU:HA	1.84	0.41
1:L:753:TYR:O	1:L:762:LYS:HB2	2.21	0.41
2:N:168:PHE:HD2	2:N:187:ALA:HB1	1.86	0.41
2:N:170:LEU:HD22	2:N:183:LEU:HG	2.02	0.41
2:N:499:PHE:O	2:N:500:PRO:C	2.63	0.41
3:M:349:ARG:O	3:M:351:MET:N	2.51	0.41
4:Q:10:ILE:HG12	4:R:26:ARG:HA	2.03	0.41
5:U:57:GLU:O	5:U:58:GLN:C	2.61	0.41
5:U:128:ILE:H	5:U:128:ILE:HD12	1.86	0.41
5:V:205:PRO:HA	5:V:208:TYR:CE2	2.56	0.41
6:X:79:LYS:C	6:X:81:VAL:H	2.28	0.41
1:A:335:LEU:HD23	1:A:335:LEU:HA	1.87	0.41
1:A:456:ASN:OD1	1:A:456:ASN:N	2.54	0.41
1:A:542:LEU:HD23	1:A:542:LEU:HA	1.84	0.41
1:A:633:LEU:HD23	1:A:633:LEU:HA	1.87	0.41
1:B:500:TYR:HB2	1:B:598:ASN:ND2	2.36	0.41
1:B:820:HIS:HA	1:C:204:GLN:HE22	1.86	0.41
1:C:59:ARG:HD2	1:C:623:HIS:CE1	2.56	0.41
1:C:329:ARG:NH2	1:C:592:LEU:O	2.54	0.41
1:C:646:LEU:HD12	1:C:646:LEU:HA	1.84	0.41
1:D:380:THR:HG21	6:Y:71:LEU:HA	2.02	0.41
1:E:574:LEU:HD23	1:E:574:LEU:HA	1.84	0.41
1:F:104:GLY:HA3	1:F:557:PHE:CZ	2.56	0.41
1:F:302:MET:HE2	1:F:302:MET:HB2	1.99	0.41
1:G:85:LEU:HD21	1:G:95:MET:HE1	2.02	0.41
1:G:330:ASP:O	1:G:331:ASN:C	2.64	0.41
1:G:502:TYR:OH	1:G:506:ARG:NE	2.54	0.41
1:G:554:TYR:HB2	1:I:857:SER:HB3	2.03	0.41
1:H:338:TYR:CZ	1:H:564:LYS:HB2	2.56	0.41
1:I:573:LEU:HD11	1:I:578:TYR:CE2	2.56	0.41
1:I:776:GLY:HA2	1:I:780:PHE:HE1	1.86	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:832:ALA:O	1:I:834:THR:N	2.49	0.41
1:J:51:PRO:HD3	6:3:11:PRO:HA	2.03	0.41
1:J:664:ILE:HD11	1:J:902:MET:HG3	2.02	0.41
1:K:277:ASP:OD1	1:K:277:ASP:N	2.53	0.41
1:L:328:PHE:CD2	1:L:549:LEU:HD11	2.56	0.41
1:L:413:CYS:SG	1:L:459:MET:HB2	2.61	0.41
1:L:691:GLY:HA3	4:P:21:PRO:O	2.21	0.41
1:L:772:ASN:N	1:L:772:ASN:OD1	2.53	0.41
3:M:235:LEU:O	3:M:239:ILE:HG13	2.21	0.41
3:M:244:ASP:O	3:M:247:SER:OG	2.30	0.41
4:Q:104:LEU:HD23	4:Q:104:LEU:HA	1.91	0.41
5:U:13:TYR:HB2	5:U:188:PHE:CE2	2.56	0.41
5:V:211:GLN:H	5:V:211:GLN:HG2	1.60	0.41
6:O:32:GLY:O	6:O:33:GLY:C	2.64	0.41
1:A:680:THR:HG23	1:A:714:ASN:ND2	2.36	0.40
1:A:714:ASN:HD22	1:A:870:TRP:CD1	2.39	0.40
1:C:512:LEU:HD23	1:C:818:ILE:HG12	2.03	0.40
1:C:514:ASP:OD1	1:C:515:CYS:N	2.45	0.40
1:C:692:SER:OG	1:C:694:TYR:O	2.34	0.40
1:D:456:ASN:OD1	1:E:836:ARG:HD2	2.21	0.40
1:D:560:GLN:NE2	1:F:755:VAL:HG12	2.36	0.40
1:D:938:VAL:HB	1:E:12:MET:HE1	2.03	0.40
1:E:61:GLN:NE2	1:E:91:ARG:HG2	2.36	0.40
1:E:818:ILE:HA	1:E:821:GLN:HG2	2.03	0.40
1:F:201:PRO:CG	1:F:286:TYR:CE2	3.02	0.40
1:G:90:ASN:HD22	1:G:623:HIS:HB3	1.86	0.40
1:G:640:GLN:HG2	1:H:44:PHE:HE1	1.86	0.40
1:G:676:GLY:N	1:G:920:GLU:HB2	2.35	0.40
1:H:832:ALA:HA	1:H:833:PRO:HD3	1.93	0.40
1:I:178:ILE:HG13	1:I:217:HIS:HD2	1.86	0.40
1:I:373:LEU:HD23	1:I:373:LEU:HA	1.80	0.40
1:I:633:LEU:HD23	1:I:633:LEU:HA	1.86	0.40
1:J:65:LEU:HD23	1:J:65:LEU:HA	1.91	0.40
1:J:534:PHE:CE1	1:J:710:THR:HB	2.56	0.40
1:K:942:THR:O	5:U:29:THR:HG22	2.21	0.40
1:L:776:GLY:HA2	1:L:780:PHE:CE1	2.57	0.40
2:N:102:SER:HB2	2:N:105:GLU:OE1	2.20	0.40
3:M:179:GLU:OE2	5:U:207:HIS:NE2	2.38	0.40
6:X:62:SER:O	6:X:64:GLY:N	2.48	0.40
6:1:24:ASP:N	6:1:24:ASP:OD1	2.52	0.40
1:A:421:ASN:OD1	1:A:421:ASN:N	2.54	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:518:ASN:HB3	1:A:521:ALA:HB3	2.03	0.40
1:A:853:THR:OG1	1:B:293:GLU:OE2	2.33	0.40
1:B:680:THR:HG23	1:B:714:ASN:OD1	2.21	0.40
1:C:251:LYS:HB2	1:C:258:GLU:O	2.20	0.40
1:C:590:MET:HE2	1:C:590:MET:HB3	1.75	0.40
1:C:681:ARG:HH21	1:C:913:THR:HG21	1.85	0.40
1:C:774:ASN:OD1	1:C:774:ASN:N	2.55	0.40
1:E:294:THR:HB	1:E:297:THR:HG23	2.02	0.40
1:E:335:LEU:HA	1:E:335:LEU:HD23	1.87	0.40
1:E:757:GLN:HE21	1:E:757:GLN:HB2	1.73	0.40
1:F:759:ASN:ND2	1:F:861:LYS:O	2.43	0.40
1:G:758:CYS:SG	1:G:760:MET:HB3	2.61	0.40
1:G:876:SER:OG	1:G:886:ASP:OD2	2.30	0.40
1:H:871:ARG:NH1	6:1:31:SER:HB3	2.37	0.40
1:I:650:ASN:HB3	1:I:916:TYR:CE1	2.55	0.40
1:J:588:VAL:HA	1:J:591:VAL:HG22	2.03	0.40
1:K:864:LEU:HA	1:K:864:LEU:HD23	1.43	0.40
1:L:587:ASP:OD1	1:L:590:MET:N	2.54	0.40
1:L:789:ARG:HH22	6:3:80:VAL:HG11	1.86	0.40
1:B:221:ARG:HH21	1:B:288:GLU:CD	2.29	0.40
1:B:371:LEU:HD23	1:B:371:LEU:HA	1.83	0.40
1:B:530:ASN:HD22	1:B:909:MET:HE3	1.85	0.40
1:B:624:ASN:N	1:B:624:ASN:OD1	2.53	0.40
1:B:920:GLU:C	1:B:921:VAL:HG13	2.47	0.40
1:B:922:PHE:CE2	1:C:14:ILE:HG23	2.56	0.40
1:C:357:VAL:HA	1:C:939:TYR:OH	2.22	0.40
1:D:325:TYR:HD2	1:D:543:ARG:HA	1.86	0.40
1:F:918:LEU:O	1:F:919:PHE:C	2.63	0.40
1:G:573:LEU:HD11	1:G:578:TYR:CZ	2.56	0.40
1:G:818:ILE:H	1:G:818:ILE:HD12	1.86	0.40
1:H:17:GLN:HB3	1:H:21:GLU:HB2	2.03	0.40
1:H:788:ASP:OD2	1:H:795:ARG:HB2	2.21	0.40
1:J:40:LEU:HD23	1:J:40:LEU:HA	1.89	0.40
1:J:95:MET:HE2	1:J:95:MET:HB3	1.76	0.40
1:K:177:ASN:HA	1:K:217:HIS:CD2	2.57	0.40
1:K:807:ASP:N	1:K:807:ASP:OD1	2.54	0.40
1:L:18:ASP:OD1	1:L:18:ASP:N	2.54	0.40
1:L:136:GLU:HB3	1:L:166:HIS:CD2	2.56	0.40
1:L:266:PHE:O	1:L:282:LYS:N	2.46	0.40
1:L:800:MET:HE2	1:L:800:MET:HB3	1.99	0.40
1:L:811:LYS:HE3	1:L:811:LYS:HB2	1.76	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:N:226:VAL:O	2:N:287:LEU:HB3	2.21	0.40
3:M:99:LEU:HA	3:M:99:LEU:HD12	1.83	0.40
4:S:107:LEU:HD23	4:S:107:LEU:HA	1.89	0.40
5:U:58:GLN:O	5:U:59:ALA:C	2.61	0.40
5:V:210:ASP:HB3	5:V:216:PHE:CD2	2.56	0.40
1:A:36:THR:HG21	6:W:11:PRO:HG2	2.03	0.40
1:A:790:MET:SD	1:A:867:ARG:NH1	2.95	0.40
1:B:114:PRO:HA	1:B:325:TYR:CD1	2.57	0.40
1:B:177:ASN:OD1	1:B:178:ILE:N	2.53	0.40
1:B:522:ARG:NH2	1:B:798:GLN:OE1	2.52	0.40
1:B:685:LYS:HB3	1:B:685:LYS:HE2	1.87	0.40
1:B:941:ARG:HD2	1:B:944:PHE:O	2.21	0.40
1:D:75:THR:HG22	1:D:76:ALA:H	1.87	0.40
1:D:178:ILE:HD13	1:D:284:VAL:HG23	2.03	0.40
1:D:755:VAL:HG13	1:D:762:LYS:HG2	2.04	0.40
1:D:910:ASP:OD1	1:D:910:ASP:N	2.52	0.40
1:E:274:GLY:O	1:E:276:GLY:N	2.55	0.40
1:E:887:LEU:HD12	1:E:887:LEU:HA	1.89	0.40
1:F:134:TRP:HB2	1:F:309:ASN:HB3	2.03	0.40
1:F:405:THR:HG21	1:F:465:ALA:HA	2.03	0.40
1:H:213:THR:O	1:H:215:ILE:HG13	2.21	0.40
1:H:398:ARG:CZ	1:H:533:PRO:HG3	2.51	0.40
1:I:693:GLY:O	1:I:694:TYR:C	2.63	0.40
1:J:82:ARG:HD2	1:J:581:GLU:OE2	2.22	0.40
1:J:897:ALA:O	1:J:898:HIS:ND1	2.54	0.40
1:K:371:LEU:HD12	1:K:646:LEU:HD13	2.03	0.40
1:K:521:ALA:HB2	1:L:551:ASN:CG	2.47	0.40
1:K:938:VAL:HG13	5:U:33:TYR:HB3	2.03	0.40
1:L:85:LEU:HD13	1:L:614:LEU:HD21	2.01	0.40
4:P:58:GLU:O	4:P:62:SER:HB3	2.22	0.40
1:A:209:GLN:HB3	1:A:211:TYR:CE1	2.56	0.40
1:B:679:PHE:HA	1:B:916:TYR:O	2.21	0.40
1:C:177:ASN:OD1	1:C:178:ILE:N	2.52	0.40
1:D:178:ILE:HG12	1:D:183:ILE:HG22	2.03	0.40
1:D:249:LEU:HD23	1:D:249:LEU:HA	1.79	0.40
1:D:760:MET:HE2	1:D:760:MET:HB2	1.90	0.40
1:E:269:THR:OG1	1:F:424:THR:O	2.36	0.40
1:E:329:ARG:HG3	1:E:333:ILE:O	2.22	0.40
1:E:366:GLU:HG3	1:E:707:LEU:HD22	2.03	0.40
1:F:351:ALA:HB3	1:F:934:VAL:HG22	2.04	0.40
1:F:941:ARG:HD2	1:F:944:PHE:O	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:196:ASP:H	1:G:200:GLN:CB	2.35	0.40
1:G:248:ILE:HG21	1:G:289:ASP:HB2	2.03	0.40
1:G:619:PHE:O	1:G:621:MET:N	2.55	0.40
1:H:324:ASN:HA	1:H:595:SER:OG	2.21	0.40
1:H:471:PHE:O	1:H:475:ASN:HB2	2.22	0.40
1:H:528:MET:HE3	1:H:528:MET:HB3	1.87	0.40
1:H:595:SER:C	1:H:597:GLY:H	2.28	0.40
1:H:679:PHE:O	1:H:680:THR:OG1	2.33	0.40
1:I:178:ILE:HG13	1:I:217:HIS:CD2	2.55	0.40
1:I:312:GLU:H	1:I:312:GLU:HG3	1.60	0.40
1:I:518:ASN:OD1	1:I:802:ARG:NH1	2.48	0.40
1:I:936:GLU:HA	5:V:156:GLY:O	2.22	0.40
1:J:68:ILE:HD13	1:J:68:ILE:HA	1.81	0.40
1:J:370:GLN:HE21	1:J:708:ASP:HA	1.87	0.40
1:J:383:PHE:HD1	1:J:384:SER:N	2.20	0.40
1:J:572:LEU:HB3	1:J:640:GLN:HE22	1.86	0.40
1:K:317:GLN:HE22	1:K:835:MET:HB3	1.87	0.40
1:L:573:LEU:HA	1:L:929:ARG:NH1	2.31	0.40
2:N:445:MET:HB2	2:N:463:VAL:HG11	2.03	0.40
3:M:20:GLY:C	3:M:21:LEU:HD22	2.46	0.40
3:M:115:ASP:O	3:M:118:VAL:HG22	2.21	0.40
3:M:259:THR:HG22	3:M:262:ARG:HH12	1.86	0.40
6:Y:30:MET:HB3	6:Y:31:SER:H	1.26	0.40
6:1:71:LEU:O	6:1:73:GLU:N	2.54	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
1	A	925/952 (97%)	858 (93%)	65 (7%)	2 (0%)	43 71

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	925/952 (97%)	855 (92%)	69 (8%)	1 (0%)	48	78
1	C	929/952 (98%)	859 (92%)	69 (7%)	1 (0%)	48	78
1	D	925/952 (97%)	855 (92%)	69 (8%)	1 (0%)	48	78
1	E	922/952 (97%)	854 (93%)	63 (7%)	5 (0%)	24	56
1	F	925/952 (97%)	854 (92%)	66 (7%)	5 (0%)	24	56
1	G	927/952 (97%)	850 (92%)	76 (8%)	1 (0%)	48	78
1	H	929/952 (98%)	857 (92%)	71 (8%)	1 (0%)	48	78
1	I	923/952 (97%)	842 (91%)	78 (8%)	3 (0%)	36	65
1	J	924/952 (97%)	853 (92%)	66 (7%)	5 (0%)	24	56
1	K	927/952 (97%)	850 (92%)	75 (8%)	2 (0%)	43	71
1	L	925/952 (97%)	855 (92%)	67 (7%)	3 (0%)	36	65
2	N	462/571 (81%)	427 (92%)	31 (7%)	4 (1%)	14	45
3	M	355/585 (61%)	328 (92%)	26 (7%)	1 (0%)	36	65
4	P	132/140 (94%)	117 (89%)	14 (11%)	1 (1%)	16	47
4	Q	129/140 (92%)	112 (87%)	17 (13%)	0	100	100
4	R	97/140 (69%)	82 (84%)	15 (16%)	0	100	100
4	S	93/140 (66%)	87 (94%)	6 (6%)	0	100	100
5	U	161/227 (71%)	140 (87%)	21 (13%)	0	100	100
5	V	178/227 (78%)	148 (83%)	26 (15%)	4 (2%)	5	30
6	0	12/250 (5%)	11 (92%)	0	1 (8%)	0	9
6	1	53/250 (21%)	45 (85%)	8 (15%)	0	100	100
6	2	15/250 (6%)	10 (67%)	4 (27%)	1 (7%)	1	13
6	3	56/250 (22%)	52 (93%)	3 (5%)	1 (2%)	6	33
6	4	11/250 (4%)	6 (54%)	5 (46%)	0	100	100
6	W	33/250 (13%)	28 (85%)	4 (12%)	1 (3%)	3	26
6	X	74/250 (30%)	56 (76%)	15 (20%)	3 (4%)	2	20
6	Y	57/250 (23%)	46 (81%)	8 (14%)	3 (5%)	1	17
6	Z	21/250 (8%)	17 (81%)	1 (5%)	3 (14%)	0	3
All	All	13045/15844 (82%)	11954 (92%)	1038 (8%)	53 (0%)	31	60

All (53) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	733	ASN
1	D	733	ASN
1	F	197	LYS
1	F	203	PRO
2	N	495	VAL
5	V	85	ALA
6	W	31	SER
1	A	734	ASP
1	E	562	PRO
1	E	566	PHE
1	E	754	ASN
1	F	204	GLN
1	J	647	SER
1	L	826	GLY
6	Z	25	ILE
6	Z	27	THR
1	C	717	PHE
1	E	752	GLY
1	F	410	PRO
1	I	845	PHE
1	I	919	PHE
1	J	566	PHE
1	J	845	PHE
1	L	647	SER
2	N	480	ALA
6	Y	9	LEU
6	Y	59	TRP
6	Y	62	SER
1	F	845	PHE
1	G	845	PHE
2	N	266	PRO
4	P	62	SER
5	V	80	TYR
5	V	83	SER
6	X	75	ASN
6	X	88	ILE
1	I	47	PRO
1	L	845	PHE
2	N	380	LYS
3	M	350	ASN
6	X	81	VAL
6	Z	32	GLY
1	H	845	PHE

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Mol	Chain	Res	Type
1	J	826	GLY
1	K	47	PRO
1	K	845	PHE
6	0	32	GLY
1	A	828	VAL
6	3	25	ILE
1	E	748	VAL
1	J	921	VAL
5	V	148	PRO
6	2	33	GLY

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	806/829 (97%)	743 (92%)	63 (8%)	11	37
1	B	807/829 (97%)	748 (93%)	59 (7%)	13	39
1	C	809/829 (98%)	746 (92%)	63 (8%)	11	37
1	D	806/829 (97%)	760 (94%)	46 (6%)	18	45
1	E	804/829 (97%)	744 (92%)	60 (8%)	12	39
1	F	807/829 (97%)	745 (92%)	62 (8%)	12	37
1	G	808/829 (98%)	760 (94%)	48 (6%)	18	44
1	H	809/829 (98%)	760 (94%)	49 (6%)	17	44
1	I	805/829 (97%)	746 (93%)	59 (7%)	13	39
1	J	804/829 (97%)	755 (94%)	49 (6%)	17	44
1	K	808/829 (98%)	753 (93%)	55 (7%)	14	41
1	L	806/829 (97%)	748 (93%)	58 (7%)	13	40
2	N	423/489 (86%)	370 (88%)	53 (12%)	4	21
3	M	304/500 (61%)	276 (91%)	28 (9%)	8	32
4	P	107/112 (96%)	92 (86%)	15 (14%)	3	18
4	Q	104/112 (93%)	93 (89%)	11 (11%)	6	27

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
4	R	86/112 (77%)	78 (91%)	8 (9%)	8	32
4	S	85/112 (76%)	77 (91%)	8 (9%)	8	31
5	U	136/186 (73%)	121 (89%)	15 (11%)	6	26
5	V	152/186 (82%)	134 (88%)	18 (12%)	5	23
6	0	12/210 (6%)	10 (83%)	2 (17%)	2	14
6	1	47/210 (22%)	40 (85%)	7 (15%)	3	16
6	2	13/210 (6%)	12 (92%)	1 (8%)	12	37
6	3	50/210 (24%)	43 (86%)	7 (14%)	3	18
6	4	11/210 (5%)	11 (100%)	0	100	100
6	W	26/210 (12%)	20 (77%)	6 (23%)	1	6
6	X	54/210 (26%)	49 (91%)	5 (9%)	8	32
6	Y	50/210 (24%)	38 (76%)	12 (24%)	1	5
6	Z	18/210 (9%)	15 (83%)	3 (17%)	2	14
All	All	11357/13647 (83%)	10487 (92%)	870 (8%)	14	37

All (870) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	14	ILE
1	A	18	ASP
1	A	25	PRO
1	A	40	LEU
1	A	48	THR
1	A	57	THR
1	A	68	ILE
1	A	75	THR
1	A	79	TYR
1	A	90	ASN
1	A	92	VAL
1	A	188	GLU
1	A	198	THR
1	A	202	GLU
1	A	207	GLU
1	A	213	THR
1	A	241	ASN
1	A	249	LEU
1	A	254	ASN

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Mol	Chain	Res	Type
1	A	279	LEU
1	A	343	ASN
1	A	353	GLN
1	A	391	ASP
1	A	461	ILE
1	A	490	ASN
1	A	493	ILE
1	A	495	ASP
1	A	499	THR
1	A	507	VAL
1	A	513	VAL
1	A	542	LEU
1	A	549	LEU
1	A	589	ASN
1	A	596	LEU
1	A	607	ILE
1	A	612	ILE
1	A	637	THR
1	A	639	ASP
1	A	651	MET
1	A	664	ILE
1	A	682	LEU
1	A	718	LYS
1	A	727	SER
1	A	728	VAL
1	A	733	ASN
1	A	741	GLU
1	A	749	ASP
1	A	754	ASN
1	A	755	VAL
1	A	758	CYS
1	A	761	THR
1	A	796	ASN
1	A	828	VAL
1	A	836	ARG
1	A	837	GLU
1	A	841	TYR
1	A	856	ASP
1	A	858	ILE
1	A	866	ASP
1	A	892	LEU
1	A	918	LEU

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Mol	Chain	Res	Type
1	A	937	THR
1	A	941	ARG
1	B	5	MET
1	B	18	ASP
1	B	41	ASN
1	B	48	THR
1	B	57	THR
1	B	89	ASP
1	B	188	GLU
1	B	249	LEU
1	B	254	ASN
1	B	313	LEU
1	B	314	MET
1	B	347	LEU
1	B	350	GLN
1	B	373	LEU
1	B	386	TRP
1	B	391	ASP
1	B	400	ILE
1	B	419	VAL
1	B	436	ASN
1	B	445	PHE
1	B	461	ILE
1	B	466	ASN
1	B	472	LEU
1	B	490	ASN
1	B	495	ASP
1	B	499	THR
1	B	507	VAL
1	B	508	VAL
1	B	513	VAL
1	B	526	ASP
1	B	542	LEU
1	B	560	GLN
1	B	588	VAL
1	B	602	VAL
1	B	607	ILE
1	B	612	ILE
1	B	625	THR
1	B	627	SER
1	B	635	ASN
1	B	644	ASP

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Mol	Chain	Res	Type
1	B	690	LEU
1	B	701	SER
1	B	725	ASP
1	B	728	VAL
1	B	733	ASN
1	B	741	GLU
1	B	751	GLU
1	B	774	ASN
1	B	796	ASN
1	B	800	MET
1	B	836	ARG
1	B	856	ASP
1	B	858	ILE
1	B	869	LEU
1	B	892	LEU
1	B	901	ASP
1	B	915	LEU
1	B	928	HIS
1	B	948	ASN
1	C	18	ASP
1	C	37	TYR
1	C	42	ASN
1	C	48	THR
1	C	54	ASP
1	C	57	THR
1	C	58	ASP
1	C	64	THR
1	C	75	THR
1	C	130	ASN
1	C	163	GLN
1	C	183	ILE
1	C	190	GLN
1	C	198	THR
1	C	202	GLU
1	C	227	THR
1	C	249	LEU
1	C	252	GLN
1	C	260	GLN
1	C	262	GLU
1	C	275	ASN
1	C	278	ASN
1	C	330	ASP

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Mol	Chain	Res	Type
1	C	343	ASN
1	C	373	LEU
1	C	374	ASP
1	C	376	ILE
1	C	380	THR
1	C	391	ASP
1	C	420	ILE
1	C	443	THR
1	C	461	ILE
1	C	476	ILE
1	C	493	ILE
1	C	495	ASP
1	C	508	VAL
1	C	560	GLN
1	C	588	VAL
1	C	596	LEU
1	C	608	LYS
1	C	610	ASP
1	C	612	ILE
1	C	636	ASP
1	C	639	ASP
1	C	651	MET
1	C	670	ASN
1	C	680	THR
1	C	682	LEU
1	C	716	THR
1	C	718	LYS
1	C	749	ASP
1	C	754	ASN
1	C	811	LYS
1	C	836	ARG
1	C	850	ILE
1	C	858	ILE
1	C	868	THR
1	C	869	LEU
1	C	915	LEU
1	C	925	VAL
1	C	929	ARG
1	C	938	VAL
1	C	942	THR
1	D	8	GLN
1	D	18	ASP

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Mol	Chain	Res	Type
1	D	68	ILE
1	D	75	THR
1	D	90	ASN
1	D	185	ILE
1	D	198	THR
1	D	202	GLU
1	D	204	GLN
1	D	205	ILE
1	D	222	VAL
1	D	297	THR
1	D	312	GLU
1	D	326	ILE
1	D	335	LEU
1	D	343	ASN
1	D	347	LEU
1	D	352	SER
1	D	353	GLN
1	D	374	ASP
1	D	443	THR
1	D	461	ILE
1	D	469	ARG
1	D	476	ILE
1	D	490	ASN
1	D	508	VAL
1	D	563	GLN
1	D	579	THR
1	D	582	TRP
1	D	607	ILE
1	D	628	THR
1	D	639	ASP
1	D	650	ASN
1	D	682	LEU
1	D	683	LYS
1	D	699	THR
1	D	741	GLU
1	D	754	ASN
1	D	759	ASN
1	D	760	MET
1	D	761	THR
1	D	812	ASP
1	D	836	ARG
1	D	866	ASP

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Mol	Chain	Res	Type
1	D	911	GLU
1	D	925	VAL
1	E	46	ASN
1	E	48	THR
1	E	53	HIS
1	E	57	THR
1	E	68	ILE
1	E	70	VAL
1	E	75	THR
1	E	90	ASN
1	E	101	ASP
1	E	106	LEU
1	E	178	ILE
1	E	198	THR
1	E	202	GLU
1	E	222	VAL
1	E	235	SER
1	E	253	GLN
1	E	335	LEU
1	E	337	TYR
1	E	343	ASN
1	E	347	LEU
1	E	358	VAL
1	E	359	ASP
1	E	374	ASP
1	E	386	TRP
1	E	391	ASP
1	E	405	THR
1	E	408	GLU
1	E	428	VAL
1	E	461	ILE
1	E	466	ASN
1	E	467	LEU
1	E	490	ASN
1	E	506	ARG
1	E	507	VAL
1	E	508	VAL
1	E	513	VAL
1	E	545	ARG
1	E	560	GLN
1	E	561	VAL
1	E	588	VAL

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Mol	Chain	Res	Type
1	E	607	ILE
1	E	612	ILE
1	E	637	THR
1	E	639	ASP
1	E	647	SER
1	E	651	MET
1	E	682	LEU
1	E	741	GLU
1	E	751	GLU
1	E	757	GLN
1	E	805	VAL
1	E	828	VAL
1	E	836	ARG
1	E	850	ILE
1	E	858	ILE
1	E	866	ASP
1	E	906	VAL
1	E	918	LEU
1	E	935	ILE
1	E	938	VAL
1	F	18	ASP
1	F	34	THR
1	F	42	ASN
1	F	52	THR
1	F	58	ASP
1	F	68	ILE
1	F	70	VAL
1	F	91	ARG
1	F	141	LEU
1	F	165	THR
1	F	198	THR
1	F	200	GLN
1	F	201	PRO
1	F	214	GLU
1	F	216	ASN
1	F	235	SER
1	F	246	GLN
1	F	248	ILE
1	F	260	GLN
1	F	278	ASN
1	F	316	GLN
1	F	319	MET

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Mol	Chain	Res	Type
1	F	333	ILE
1	F	335	LEU
1	F	341	THR
1	F	343	ASN
1	F	374	ASP
1	F	391	ASP
1	F	403	HIS
1	F	419	VAL
1	F	441	ASP
1	F	443	THR
1	F	461	ILE
1	F	466	ASN
1	F	490	ASN
1	F	508	VAL
1	F	526	ASP
1	F	579	THR
1	F	588	VAL
1	F	589	ASN
1	F	607	ILE
1	F	612	ILE
1	F	636	ASP
1	F	639	ASP
1	F	651	MET
1	F	658	ASN
1	F	682	LEU
1	F	738	THR
1	F	741	GLU
1	F	754	ASN
1	F	755	VAL
1	F	759	ASN
1	F	805	VAL
1	F	836	ARG
1	F	849	LEU
1	F	850	ILE
1	F	853	THR
1	F	858	ILE
1	F	885	THR
1	F	918	LEU
1	F	942	THR
1	F	948	ASN
1	G	18	ASP
1	G	48	THR

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Mol	Chain	Res	Type
1	G	68	ILE
1	G	90	ASN
1	G	130	ASN
1	G	179	THR
1	G	203	PRO
1	G	246	GLN
1	G	270	GLU
1	G	284	VAL
1	G	288	GLU
1	G	313	LEU
1	G	326	ILE
1	G	333	ILE
1	G	335	LEU
1	G	343	ASN
1	G	394	ASP
1	G	411	ASN
1	G	441	ASP
1	G	445	PHE
1	G	461	ILE
1	G	466	ASN
1	G	476	ILE
1	G	490	ASN
1	G	507	VAL
1	G	508	VAL
1	G	581	GLU
1	G	588	VAL
1	G	612	ILE
1	G	647	SER
1	G	682	LEU
1	G	710	THR
1	G	734	ASP
1	G	738	THR
1	G	754	ASN
1	G	760	MET
1	G	788	ASP
1	G	789	ARG
1	G	819	LEU
1	G	836	ARG
1	G	841	TYR
1	G	842	PRO
1	G	858	ILE
1	G	901	ASP

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Mol	Chain	Res	Type
1	G	918	LEU
1	G	925	VAL
1	G	929	ARG
1	G	945	SER
1	H	46	ASN
1	H	53	HIS
1	H	68	ILE
1	H	70	VAL
1	H	71	ASP
1	H	75	THR
1	H	106	LEU
1	H	183	ILE
1	H	187	VAL
1	H	205	ILE
1	H	253	GLN
1	H	278	ASN
1	H	313	LEU
1	H	317	GLN
1	H	335	LEU
1	H	343	ASN
1	H	374	ASP
1	H	387	ASN
1	H	406	GLU
1	H	409	LEU
1	H	416	LEU
1	H	420	ILE
1	H	421	ASN
1	H	461	ILE
1	H	463	LEU
1	H	467	LEU
1	H	469	ARG
1	H	472	LEU
1	H	490	ASN
1	H	508	VAL
1	H	560	GLN
1	H	582	TRP
1	H	588	VAL
1	H	596	LEU
1	H	607	ILE
1	H	612	ILE
1	H	640	GLN
1	H	660	THR

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Mol	Chain	Res	Type
1	H	666	ILE
1	H	700	TYR
1	H	758	CYS
1	H	775	ILE
1	H	856	ASP
1	H	866	ASP
1	H	902	MET
1	H	905	GLU
1	H	906	VAL
1	H	911	GLU
1	H	925	VAL
1	I	34	THR
1	I	48	THR
1	I	53	HIS
1	I	70	VAL
1	I	91	ARG
1	I	102	ILE
1	I	141	LEU
1	I	185	ILE
1	I	222	VAL
1	I	253	GLN
1	I	277	ASP
1	I	278	ASN
1	I	284	VAL
1	I	297	THR
1	I	312	GLU
1	I	322	ARG
1	I	326	ILE
1	I	330	ASP
1	I	333	ILE
1	I	341	THR
1	I	370	GLN
1	I	374	ASP
1	I	378	ASP
1	I	403	HIS
1	I	419	VAL
1	I	436	ASN
1	I	441	ASP
1	I	443	THR
1	I	461	ILE
1	I	469	ARG
1	I	470	ASN

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Mol	Chain	Res	Type
1	I	508	VAL
1	I	526	ASP
1	I	574	LEU
1	I	596	LEU
1	I	612	ILE
1	I	637	THR
1	I	639	ASP
1	I	651	MET
1	I	652	LEU
1	I	664	ILE
1	I	666	ILE
1	I	680	THR
1	I	689	SER
1	I	696	PRO
1	I	728	VAL
1	I	754	ASN
1	I	755	VAL
1	I	758	CYS
1	I	786	TYR
1	I	811	LYS
1	I	812	ASP
1	I	818	ILE
1	I	834	THR
1	I	866	ASP
1	I	892	LEU
1	I	918	LEU
1	I	925	VAL
1	I	935	ILE
1	J	18	ASP
1	J	58	ASP
1	J	68	ILE
1	J	74	ASP
1	J	75	THR
1	J	106	LEU
1	J	179	THR
1	J	204	GLN
1	J	213	THR
1	J	215	ILE
1	J	235	SER
1	J	284	VAL
1	J	376	ILE
1	J	380	THR

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Mol	Chain	Res	Type
1	J	390	VAL
1	J	438	TRP
1	J	443	THR
1	J	461	ILE
1	J	466	ASN
1	J	467	LEU
1	J	469	ARG
1	J	476	ILE
1	J	490	ASN
1	J	499	THR
1	J	508	VAL
1	J	519	LEU
1	J	561	VAL
1	J	563	GLN
1	J	579	THR
1	J	612	ILE
1	J	621	MET
1	J	647	SER
1	J	651	MET
1	J	680	THR
1	J	682	LEU
1	J	714	ASN
1	J	734	ASP
1	J	754	ASN
1	J	755	VAL
1	J	759	ASN
1	J	760	MET
1	J	865	CYS
1	J	892	LEU
1	J	910	ASP
1	J	915	LEU
1	J	922	PHE
1	J	924	VAL
1	J	929	ARG
1	J	948	ASN
1	K	48	THR
1	K	53	HIS
1	K	57	THR
1	K	64	THR
1	K	68	ILE
1	K	73	GLU
1	K	90	ASN

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Mol	Chain	Res	Type
1	K	92	VAL
1	K	185	ILE
1	K	198	THR
1	K	202	GLU
1	K	204	GLN
1	K	205	ILE
1	K	275	ASN
1	K	278	ASN
1	K	339	ASN
1	K	343	ASN
1	K	370	GLN
1	K	374	ASP
1	K	390	VAL
1	K	391	ASP
1	K	405	THR
1	K	408	GLU
1	K	420	ILE
1	K	428	VAL
1	K	461	ILE
1	K	490	ASN
1	K	506	ARG
1	K	508	VAL
1	K	560	GLN
1	K	582	TRP
1	K	588	VAL
1	K	610	ASP
1	K	612	ILE
1	K	625	THR
1	K	647	SER
1	K	651	MET
1	K	682	LEU
1	K	686	GLU
1	K	714	ASN
1	K	738	THR
1	K	749	ASP
1	K	773	TYR
1	K	775	ILE
1	K	804	VAL
1	K	805	VAL
1	K	828	VAL
1	K	836	ARG
1	K	850	ILE

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Mol	Chain	Res	Type
1	K	891	LEU
1	K	910	ASP
1	K	915	LEU
1	K	917	VAL
1	K	918	LEU
1	K	941	ARG
1	L	15	SER
1	L	42	ASN
1	L	48	THR
1	L	53	HIS
1	L	57	THR
1	L	61	GLN
1	L	74	ASP
1	L	75	THR
1	L	185	ILE
1	L	214	GLU
1	L	235	SER
1	L	241	ASN
1	L	279	LEU
1	L	297	THR
1	L	326	ILE
1	L	341	THR
1	L	353	GLN
1	L	373	LEU
1	L	390	VAL
1	L	408	GLU
1	L	421	ASN
1	L	428	VAL
1	L	443	THR
1	L	445	PHE
1	L	451	ILE
1	L	461	ILE
1	L	466	ASN
1	L	469	ARG
1	L	490	ASN
1	L	507	VAL
1	L	508	VAL
1	L	529	ASP
1	L	596	LEU
1	L	607	ILE
1	L	610	ASP
1	L	612	ILE

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Mol	Chain	Res	Type
1	L	625	THR
1	L	632	MET
1	L	634	ARG
1	L	637	THR
1	L	675	ARG
1	L	682	LEU
1	L	689	SER
1	L	734	ASP
1	L	748	VAL
1	L	754	ASN
1	L	758	CYS
1	L	763	ASP
1	L	804	VAL
1	L	842	PRO
1	L	849	LEU
1	L	850	ILE
1	L	858	ILE
1	L	866	ASP
1	L	885	THR
1	L	892	LEU
1	L	916	TYR
1	L	918	LEU
2	N	37	ASP
2	N	41	VAL
2	N	46	LEU
2	N	47	ARG
2	N	48	PRO
2	N	49	THR
2	N	55	ILE
2	N	59	GLU
2	N	65	ASP
2	N	79	VAL
2	N	85	GLN
2	N	96	ILE
2	N	97	GLN
2	N	99	ASN
2	N	115	ASP
2	N	154	THR
2	N	155	LYS
2	N	157	ASN
2	N	171	PRO
2	N	174	ASN

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Mol	Chain	Res	Type
2	N	176	SER
2	N	195	VAL
2	N	205	ASP
2	N	232	THR
2	N	239	ASP
2	N	240	ILE
2	N	256	SER
2	N	274	THR
2	N	277	ASP
2	N	289	VAL
2	N	293	GLN
2	N	374	GLN
2	N	376	LYS
2	N	387	LYS
2	N	405	SER
2	N	430	VAL
2	N	437	VAL
2	N	450	THR
2	N	454	THR
2	N	457	ILE
2	N	479	GLN
2	N	489	PHE
2	N	492	LEU
2	N	493	THR
2	N	531	LEU
2	N	535	ILE
2	N	538	VAL
2	N	548	ARG
2	N	549	ARG
2	N	555	TYR
2	N	567	SER
2	N	570	THR
2	N	571	PHE
3	M	7	ASP
3	M	14	LEU
3	M	21	LEU
3	M	24	THR
3	M	49	PRO
3	M	58	LEU
3	M	62	VAL
3	M	74	LEU
3	M	76	ILE

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Mol	Chain	Res	Type
3	M	86	ILE
3	M	89	ASP
3	M	117	LEU
3	M	169	ARG
3	M	206	LYS
3	M	208	LEU
3	M	215	ARG
3	M	231	ASN
3	M	235	LEU
3	M	243	THR
3	M	276	GLN
3	M	331	LEU
3	M	338	VAL
3	M	339	THR
3	M	364	ASN
3	M	370	LEU
3	M	371	HIS
3	M	390	TRP
3	M	396	PHE
4	P	10	ILE
4	P	28	ASN
4	P	55	THR
4	P	57	LEU
4	P	58	GLU
4	P	75	ILE
4	P	76	VAL
4	P	81	PHE
4	P	98	ASP
4	P	103	LEU
4	P	110	LEU
4	P	113	GLU
4	P	121	LEU
4	P	124	LEU
4	P	128	VAL
4	Q	6	PHE
4	Q	28	ASN
4	Q	55	THR
4	Q	57	LEU
4	Q	71	THR
4	Q	73	ARG
4	Q	75	ILE
4	Q	99	LYS

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Mol	Chain	Res	Type
4	Q	100	LEU
4	Q	121	LEU
4	Q	125	ARG
4	R	10	ILE
4	R	17	THR
4	R	26	ARG
4	R	47	LEU
4	R	97	ASP
4	R	107	LEU
4	R	110	LEU
4	R	121	LEU
4	S	7	ASP
4	S	17	THR
4	S	22	TRP
4	S	29	VAL
4	S	121	LEU
4	S	127	GLN
4	S	128	VAL
4	S	132	LYS
5	U	5	ILE
5	U	7	THR
5	U	26	ASP
5	U	39	HIS
5	U	41	ILE
5	U	55	LEU
5	U	129	ARG
5	U	134	GLN
5	U	146	LEU
5	U	173	THR
5	U	196	VAL
5	U	198	PHE
5	U	215	ASN
5	U	219	VAL
5	U	221	ASP
5	V	25	GLN
5	V	44	VAL
5	V	47	ILE
5	V	64	THR
5	V	79	VAL
5	V	135	LEU
5	V	140	VAL
5	V	144	LEU

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Mol	Chain	Res	Type
5	V	151	THR
5	V	159	ARG
5	V	169	LEU
5	V	170	THR
5	V	179	ARG
5	V	193	VAL
5	V	207	HIS
5	V	211	GLN
5	V	213	ILE
5	V	215	ASN
6	W	6	PHE
6	W	9	LEU
6	W	22	TRP
6	W	23	GLN
6	W	25	ILE
6	W	30	MET
6	X	4	ILE
6	X	29	ASN
6	X	59	TRP
6	X	71	LEU
6	X	80	VAL
6	Y	4	ILE
6	Y	23	GLN
6	Y	25	ILE
6	Y	27	THR
6	Y	41	TRP
6	Y	57	LYS
6	Y	60	ASN
6	Y	63	THR
6	Y	67	LEU
6	Y	70	LYS
6	Y	77	GLN
6	Y	78	GLN
6	Z	24	ASP
6	Z	25	ILE
6	Z	30	MET
6	0	27	THR
6	0	30	MET
6	1	25	ILE
6	1	40	LEU
6	1	60	ASN
6	1	63	THR

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Mol	Chain	Res	Type
6	1	70	LYS
6	1	71	LEU
6	1	74	GLN
6	2	30	MET
6	3	30	MET
6	3	69	ASP
6	3	71	LEU
6	3	72	LYS
6	3	77	GLN
6	3	80	VAL
6	3	81	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (116) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	246	GLN
1	A	264	GLN
1	A	343	ASN
1	A	436	ASN
1	A	504	ASN
1	A	658	ASN
1	A	714	ASN
1	A	822	HIS
1	A	889	GLN
1	B	216	ASN
1	B	350	GLN
1	B	455	ASN
1	B	464	ASN
1	B	558	HIS
1	B	560	GLN
1	B	623	HIS
1	C	8	GLN
1	C	17	GLN
1	C	264	GLN
1	C	670	ASN
1	C	821	GLN
1	C	822	HIS
1	C	824	ASN
1	C	839	GLN
1	D	13	HIS
1	D	217	HIS
1	D	246	GLN

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Mol	Chain	Res	Type
1	D	331	ASN
1	D	411	ASN
1	D	551	ASN
1	D	650	ASN
1	D	658	ASN
1	D	948	ASN
1	E	264	GLN
1	E	316	GLN
1	E	350	GLN
1	E	470	ASN
1	E	814	GLN
1	E	822	HIS
1	F	42	ASN
1	F	162	GLN
1	F	177	ASN
1	F	246	GLN
1	F	317	GLN
1	F	350	GLN
1	F	411	ASN
1	F	466	ASN
1	F	772	ASN
1	F	796	ASN
1	F	822	HIS
1	F	824	ASN
1	G	13	HIS
1	G	41	ASN
1	G	200	GLN
1	G	204	GLN
1	G	217	HIS
1	G	252	GLN
1	G	260	GLN
1	G	331	ASN
1	G	434	GLN
1	G	455	ASN
1	G	658	ASN
1	G	714	ASN
1	G	733	ASN
1	G	740	ASN
1	G	822	HIS
1	H	41	ASN
1	H	204	GLN
1	H	217	HIS

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Mol	Chain	Res	Type
1	H	814	GLN
1	H	928	HIS
1	I	246	GLN
1	I	309	ASN
1	I	370	GLN
1	I	421	ASN
1	I	456	ASN
1	I	895	ASN
1	J	200	GLN
1	J	204	GLN
1	J	246	GLN
1	J	456	ASN
1	J	466	ASN
1	J	558	HIS
1	J	583	ASN
1	K	170	GLN
1	K	184	GLN
1	K	370	GLN
1	K	455	ASN
1	K	658	ASN
1	K	803	GLN
1	K	814	GLN
1	K	822	HIS
1	K	889	GLN
1	L	177	ASN
1	L	456	ASN
1	L	624	ASN
2	N	83	ASN
2	N	99	ASN
2	N	174	ASN
2	N	199	ASN
2	N	214	ASN
2	N	252	HIS
3	M	50	GLN
3	M	83	ASN
3	M	207	ASN
3	M	273	HIS
3	M	276	GLN
4	Q	127	GLN
5	V	81	GLN
6	X	74	GLN
6	Y	13	HIS

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Mol	Chain	Res	Type
6	Y	23	GLN
6	Y	77	GLN
6	Z	23	GLN
6	1	74	GLN
6	4	29	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

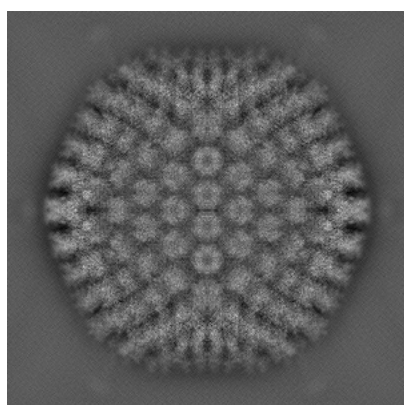
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-24881. These allow visual inspection of the internal detail of the map and identification of artifacts.

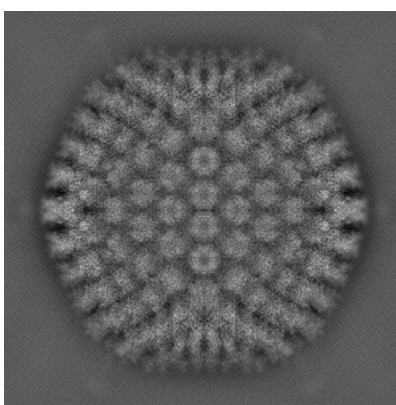
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

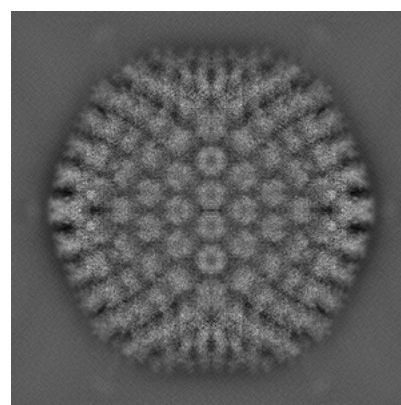
6.1.1 Primary map



X



Y

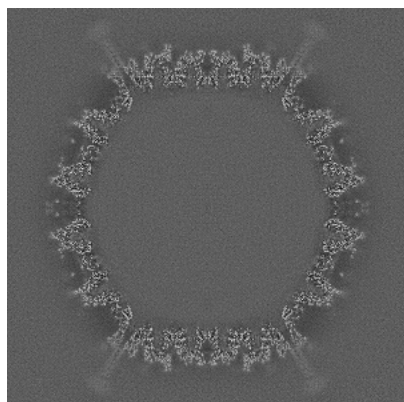


Z

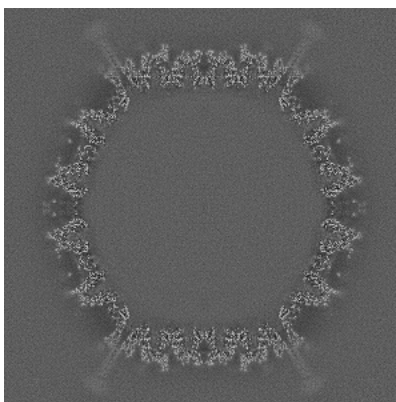
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

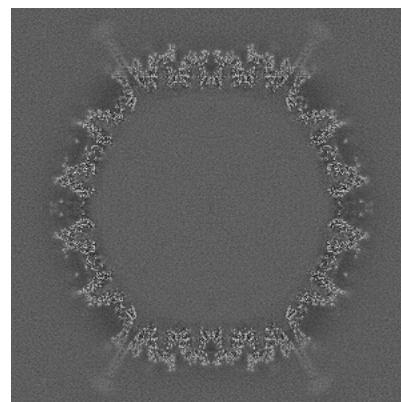
6.2.1 Primary map



X Index: 416



Y Index: 416

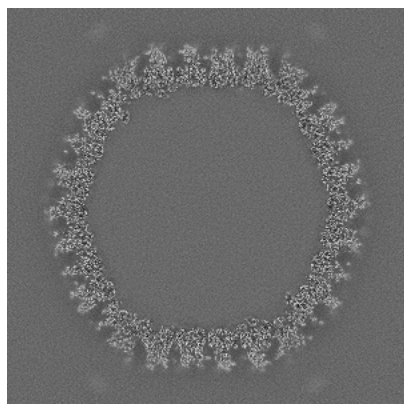


Z Index: 416

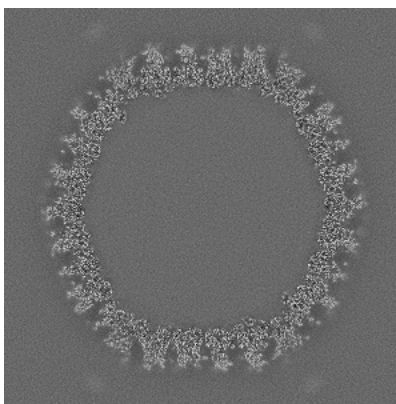
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

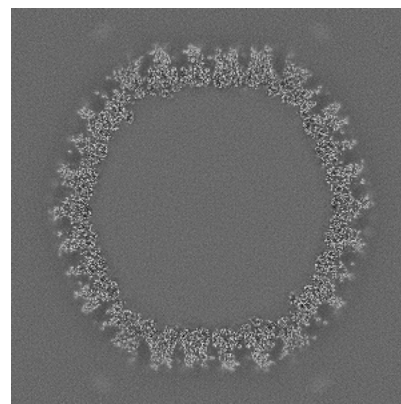
6.3.1 Primary map



X Index: 431



Y Index: 431

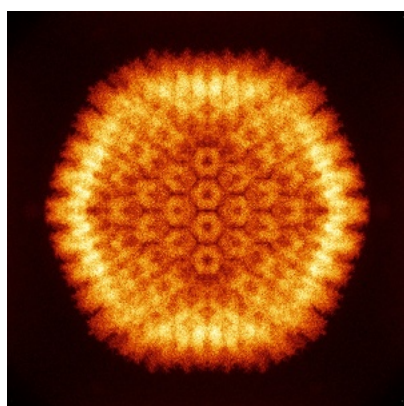


Z Index: 431

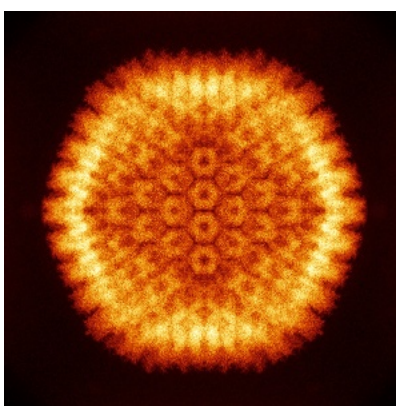
The images above show the largest variance slices of the map in three orthogonal directions.

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

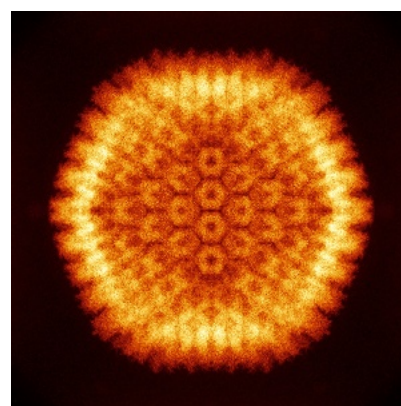
6.4.1 Primary map



X



Y

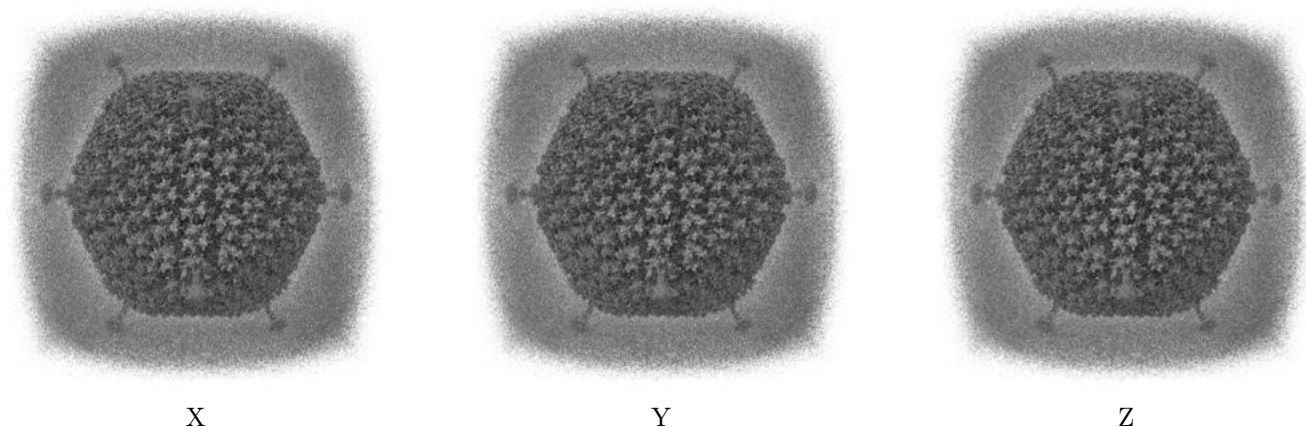


Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 3.15. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

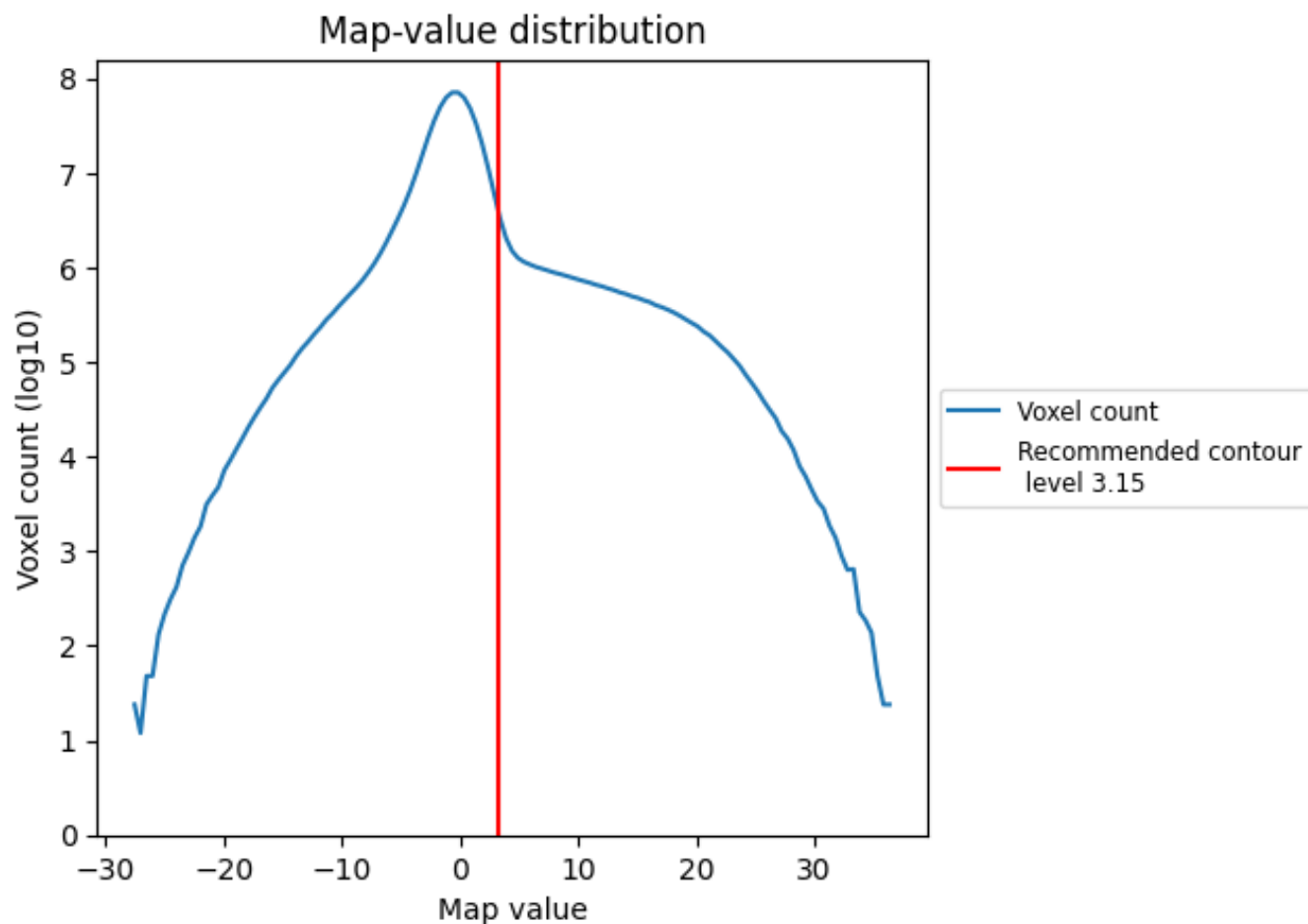
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

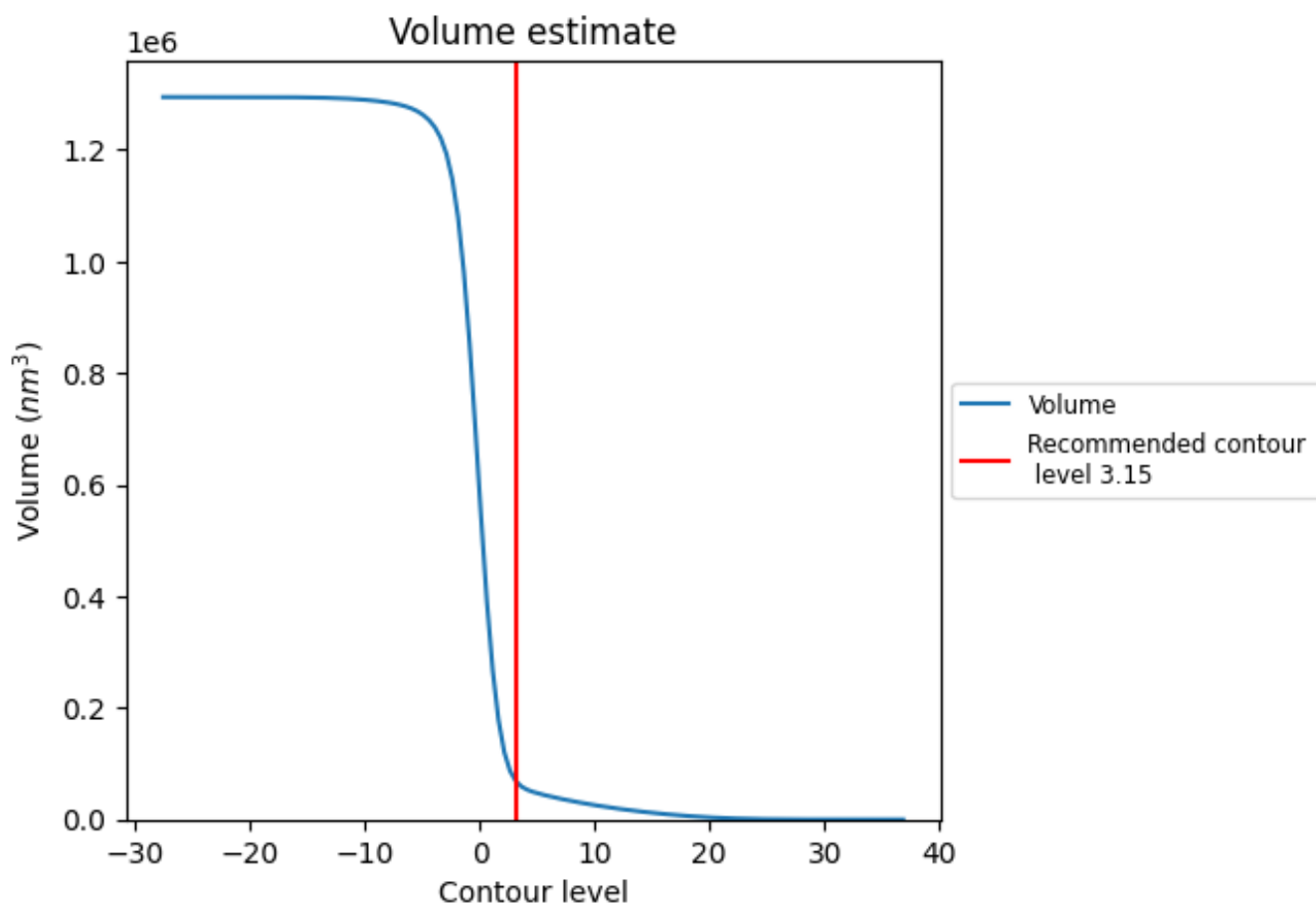
This section contains the results of statistical analysis of the map.

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.

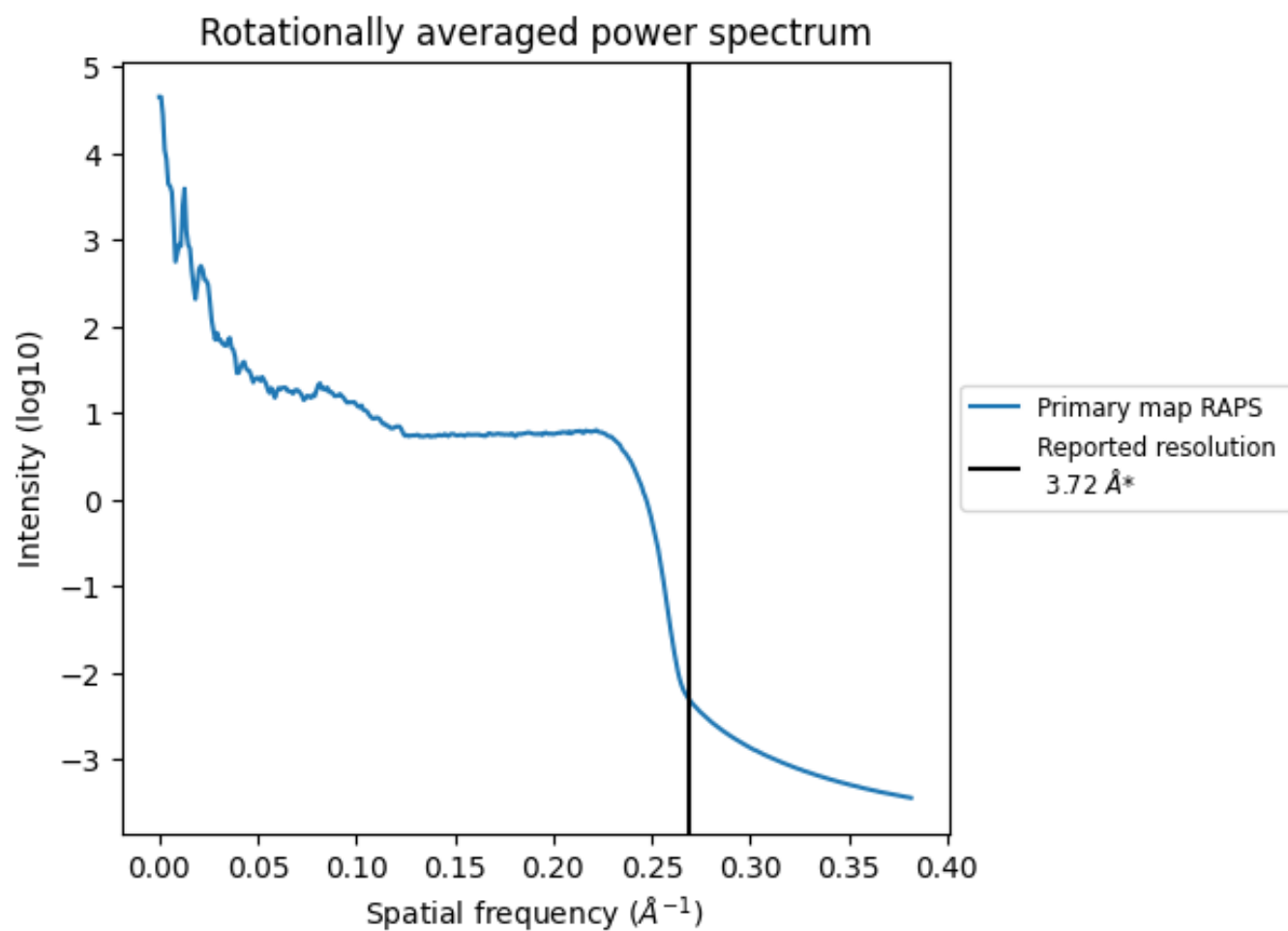
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 68380 nm³; this corresponds to an approximate mass of 61769 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 ⓘ

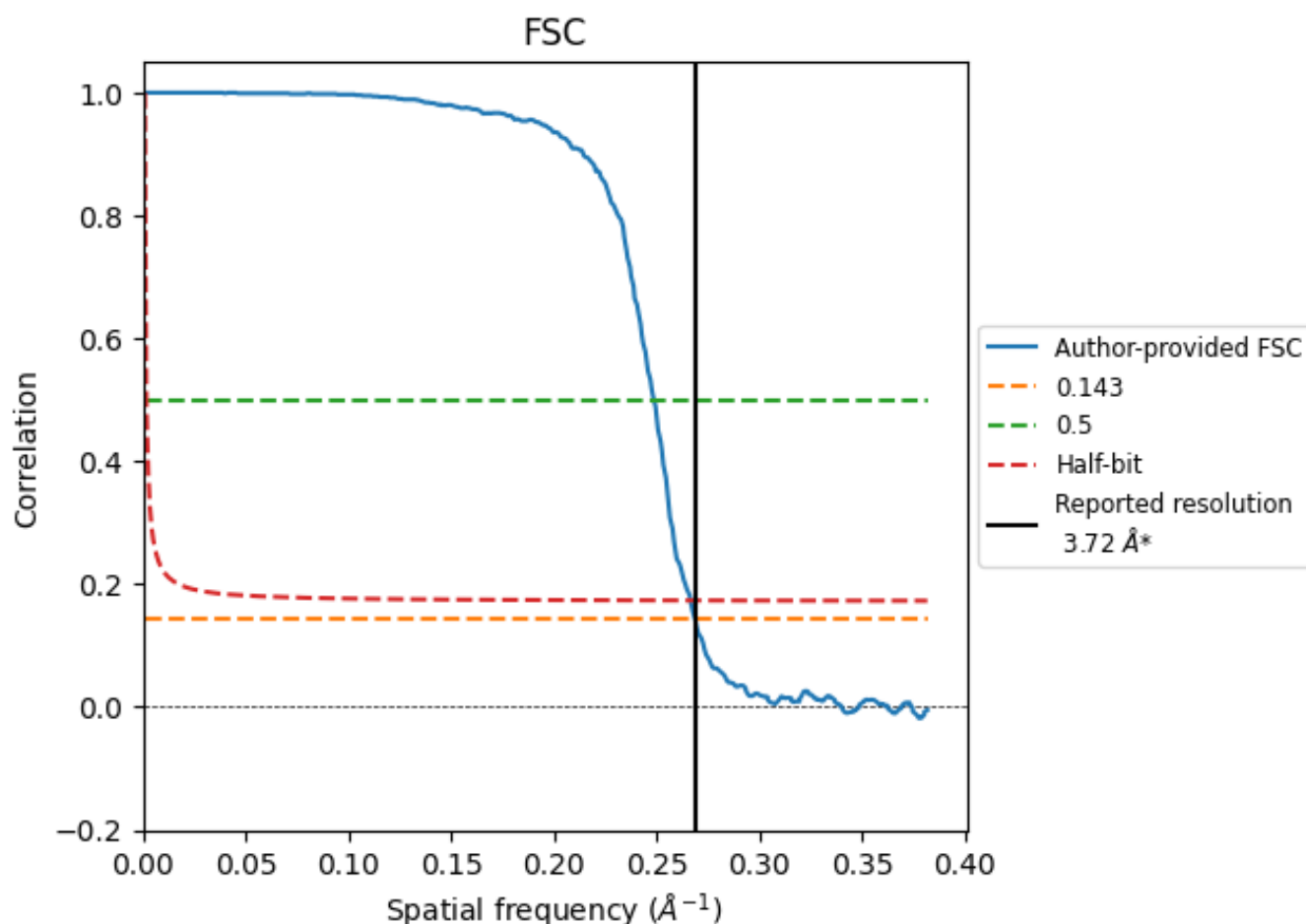


*Reported resolution corresponds to spatial frequency of 0.269 $\text{\AA}^{-1}$

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 0.269 Å⁻¹

8.2 Resolution estimates [i](#)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.72	-	-
Author-provided FSC curve	3.72	4.02	3.75
Unmasked-calculated*	-	-	-

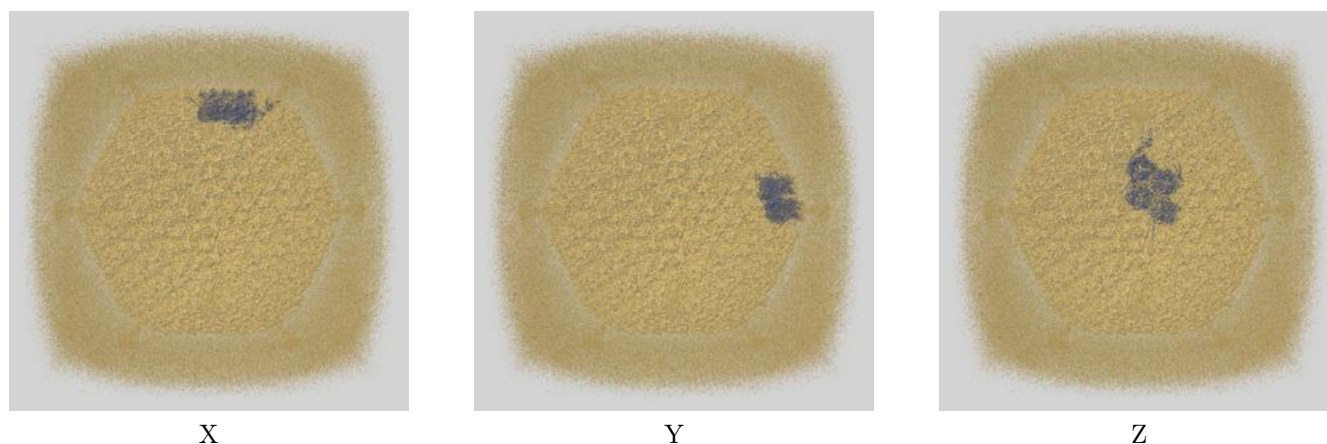
*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

9 Map-model fit [i](#)

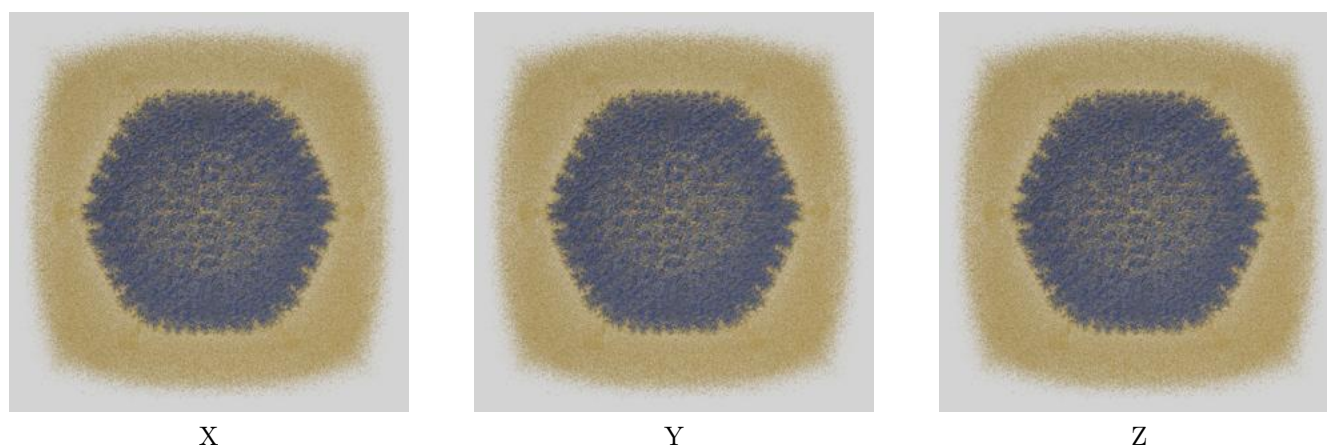
This section contains information regarding the fit between EMDB map EMD-24881 and PDB model 7S78. Per-residue inclusion information can be found in section 3 on page 8.

9.1 Map-model overlays

9.1.1 Map-model overlay [i](#)

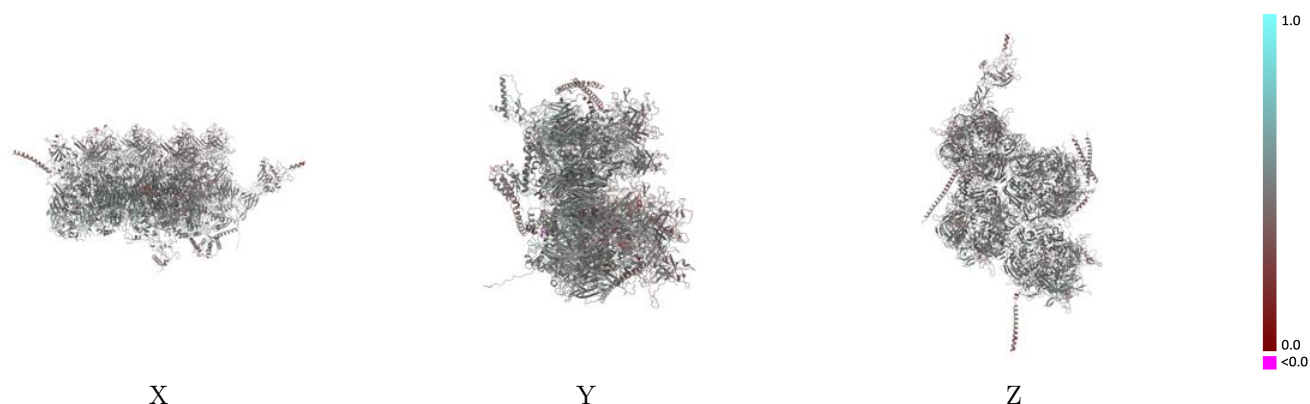


9.1.2 Map-model assembly overlay [i](#)



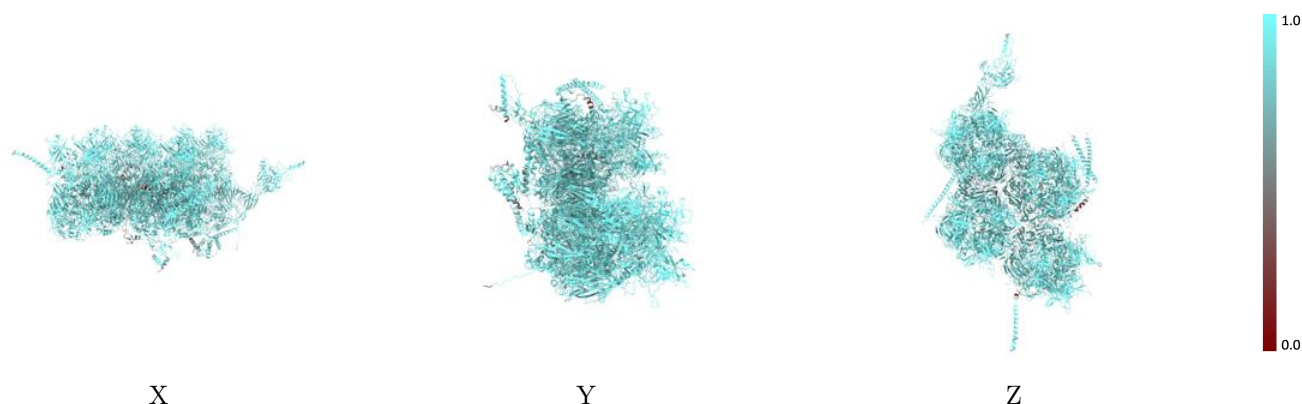
The images above show the 3D surface view of the map at the recommended contour level 3.15 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



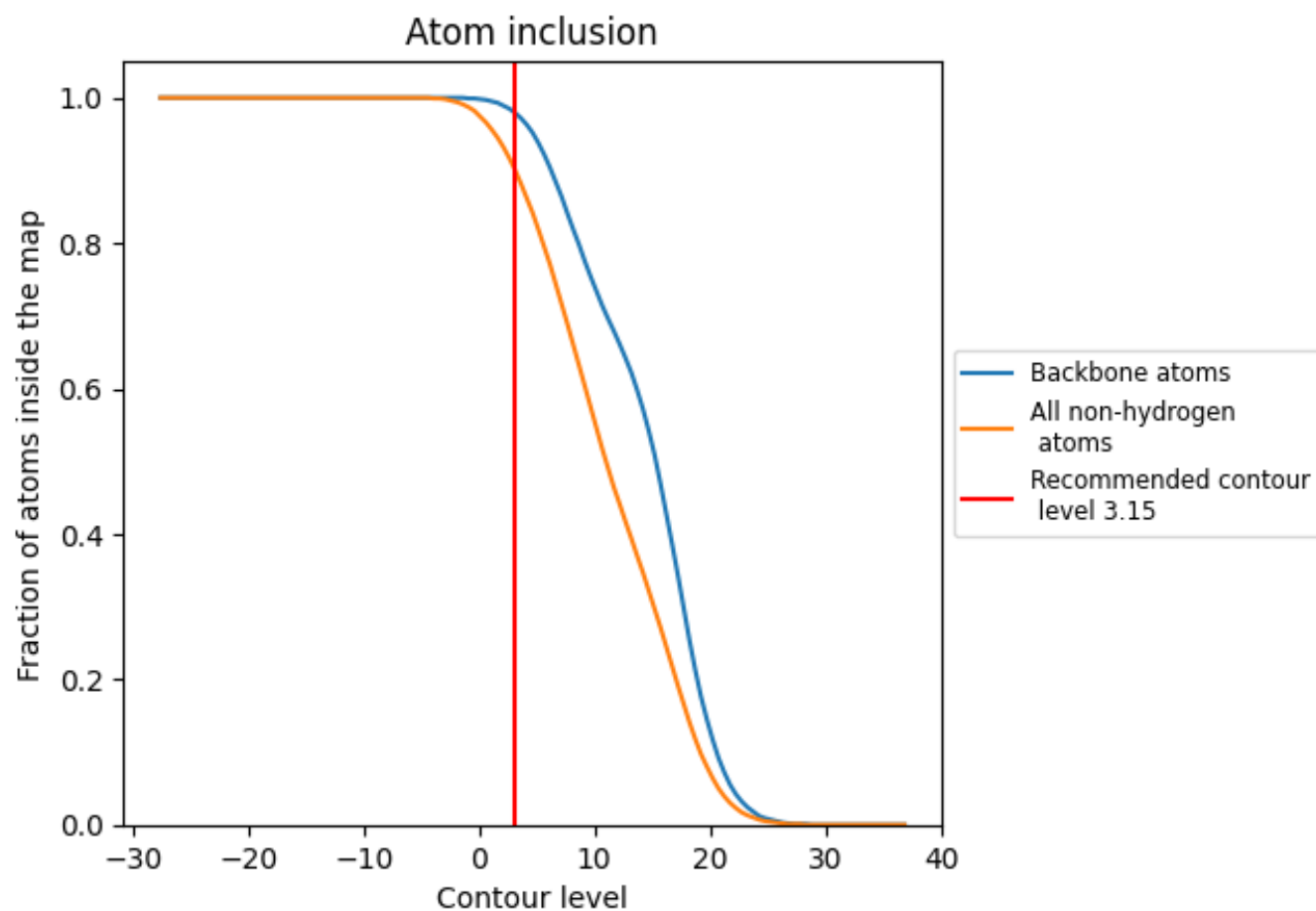
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (3.15).

9.4 Atom inclusion [i](#)



At the recommended contour level, 98% of all backbone atoms, 90% 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 (3.15) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9000	 0.4710
0	 0.7140	 0.4920
1	 0.7680	 0.4890
2	 0.6560	 0.5190
3	 0.7170	 0.4610
4	 0.6440	 0.4730
5	 0.5120	 0.4670
6	 0.6800	 0.4480
A	 0.9180	 0.4710
B	 0.9160	 0.4650
C	 0.9160	 0.4680
D	 0.9140	 0.4770
E	 0.9140	 0.4770
F	 0.9180	 0.4790
G	 0.9140	 0.4810
H	 0.9140	 0.4810
I	 0.9160	 0.4790
J	 0.9160	 0.4770
K	 0.9190	 0.4740
L	 0.9130	 0.4770
M	 0.8070	 0.4370
N	 0.8880	 0.4510
P	 0.7860	 0.4080
Q	 0.7960	 0.4230
R	 0.8270	 0.4160
S	 0.8740	 0.4330
U	 0.8340	 0.4650
V	 0.7900	 0.4650
W	 0.5590	 0.4460
X	 0.7530	 0.4480
Y	 0.6800	 0.4580
Z	 0.6860	 0.4860

