



Full wwPDB EM Validation Report ⓘ

Mar 20, 2026 – 04:49 PM UTC

PDB ID : 8ZBM / pdb_00008zbm
EMDB ID : EMD-39905
Title : RAT skeletal muscle ATM complex
Authors : Li, D.N.; Zhao, Q.Y.; Liu, C.
Deposited on : 2024-04-26
Resolution : 3.32 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
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

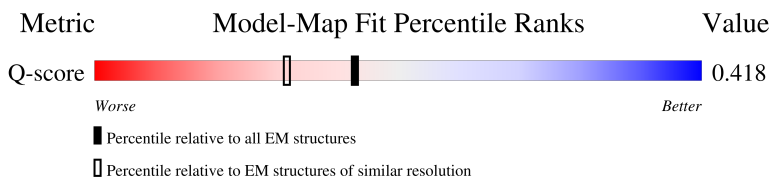
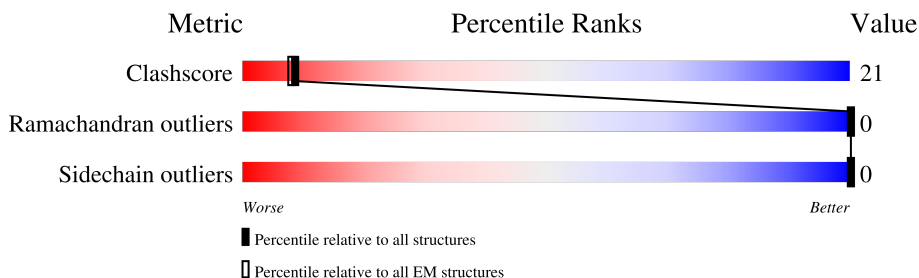
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.32 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.



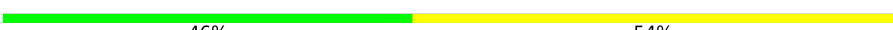
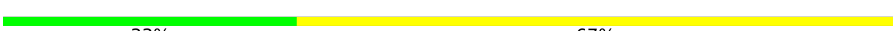
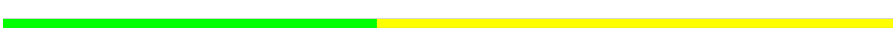
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	14518 (2.82 - 3.82)

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	E	371	 76%24%
1	H	371	 78%22%
1	O	371	 76%24%
1	P	371	 76%24%

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Mol	Chain	Length	Quality of chain
1	Q	371	 74%26%
1	R	371	 80%20%
2	B	166	 42%58%
2	C	166	 46%54%
2	F	166	 33%67%
2	G	166	 42%58%
3	A	780	 48%46%6%
3	D	780	 48%47%6%
3	J	780	 47%47%6%
3	K	780	 52%43%6%
3	L	780	 46%48%6%
3	N	780	 46%48%6%

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 58286 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 Actin, alpha skeletal muscle.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	E	371	Total	C	N	O	S	0	0
			2899	1836	489	553	21		
1	H	371	Total	C	N	O	S	0	0
			2899	1836	489	553	21		
1	O	371	Total	C	N	O	S	0	0
			2899	1836	489	553	21		
1	Q	371	Total	C	N	O	S	0	0
			2899	1836	489	553	21		
1	P	371	Total	C	N	O	S	0	0
			2899	1836	489	553	21		
1	R	371	Total	C	N	O	S	0	0
			2899	1836	489	553	21		

- Molecule 2 is a protein called Tropomyosin beta chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	C	166	Total	C	N	O	S	0	0
			1328	804	231	288	5		
2	B	166	Total	C	N	O	S	0	0
			1328	804	231	288	5		
2	G	166	Total	C	N	O	S	0	0
			1328	804	231	288	5		
2	F	166	Total	C	N	O	S	0	0
			1328	804	231	288	5		

- Molecule 3 is a protein called Myosin heavy chain 4.

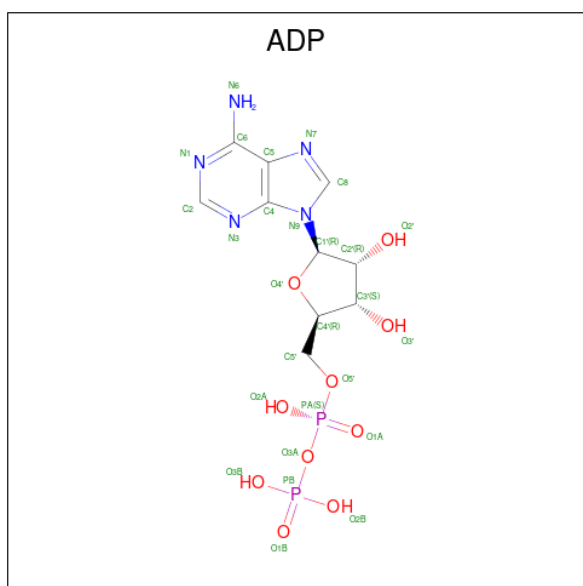
Mol	Chain	Residues	Atoms					AltConf	Trace
3	A	736	Total	C	N	O	S	0	0
			5903	3780	992	1101	30		
3	D	736	Total	C	N	O	S	0	0
			5903	3780	992	1101	30		
3	J	736	Total	C	N	O	S	0	0
			5903	3780	992	1101	30		

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Mol	Chain	Residues	Atoms					AltConf	Trace
3	L	736	Total	C	N	O	S	0	0
			5903	3780	992	1101	30		
3	K	736	Total	C	N	O	S	0	0
			5903	3780	992	1101	30		
3	N	736	Total	C	N	O	S	0	0
			5903	3780	992	1101	30		

- Molecule 4 is ADENOSINE-5'-DIPHOSPHATE (CCD ID: ADP) (formula: $C_{10}H_{15}N_5O_{10}P_2$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					AltConf
4	E	1	Total	C	N	O	P	0
			27	10	5	10	2	
4	H	1	Total	C	N	O	P	0
			27	10	5	10	2	
4	O	1	Total	C	N	O	P	0
			27	10	5	10	2	
4	Q	1	Total	C	N	O	P	0
			27	10	5	10	2	
4	P	1	Total	C	N	O	P	0
			27	10	5	10	2	
4	R	1	Total	C	N	O	P	0
			27	10	5	10	2	

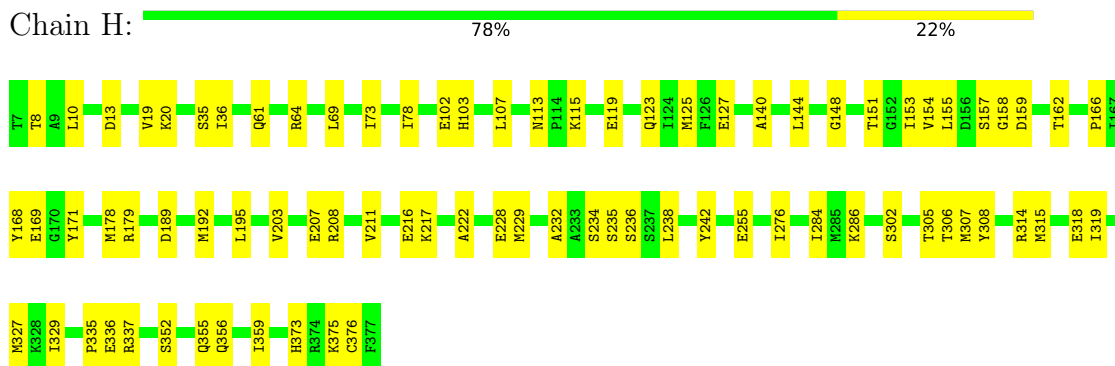
3 Residue-property plots

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.

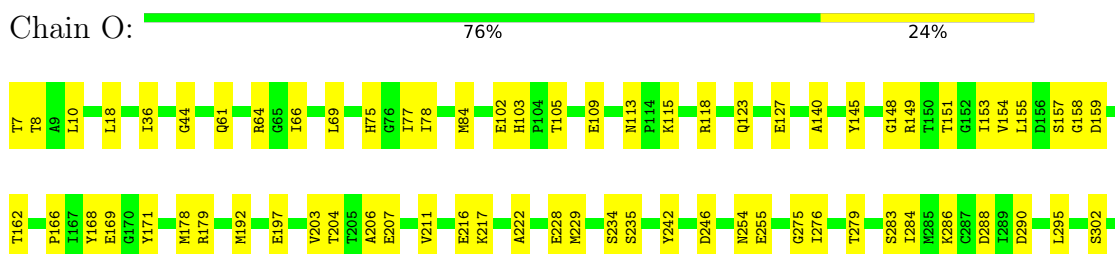
- Molecule 1: Actin, alpha skeletal muscle



- Molecule 1: Actin, alpha skeletal muscle



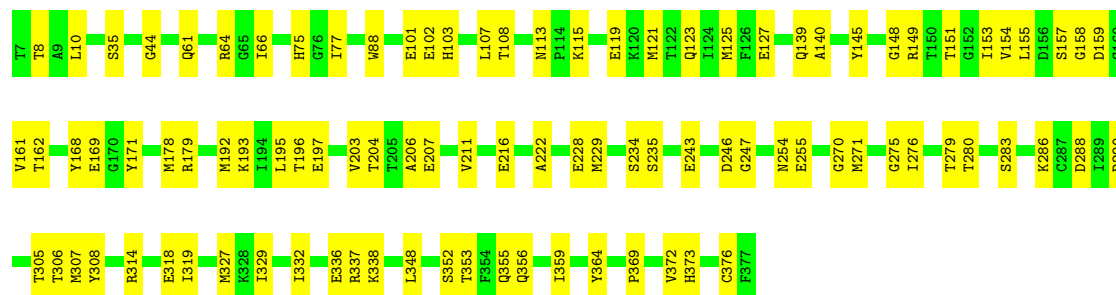
- Molecule 1: Actin, alpha skeletal muscle





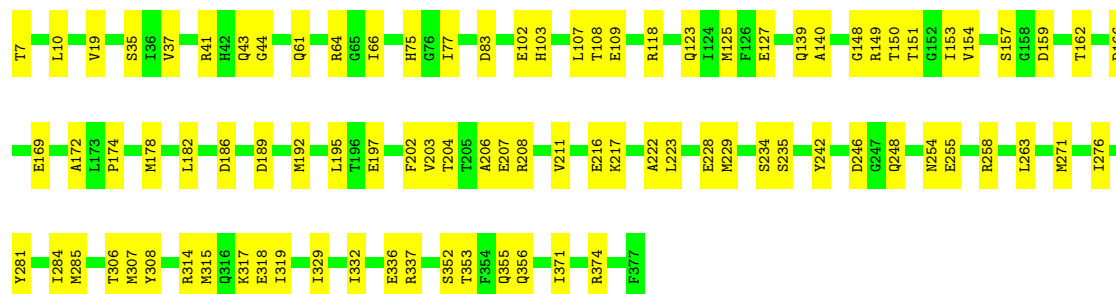
- Molecule 1: Actin, alpha skeletal muscle

Chain Q: 74% 26%



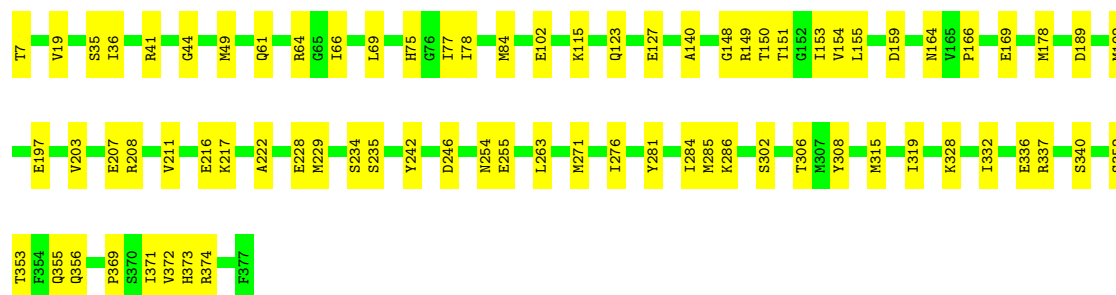
- Molecule 1: Actin, alpha skeletal muscle

Chain P: 76% 24%



- Molecule 1: Actin, alpha skeletal muscle

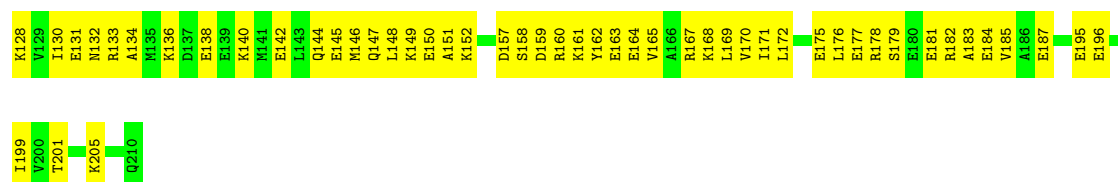
Chain R: 80% 20%



- Molecule 2: Tropomyosin beta chain

Chain C: 46% 54%

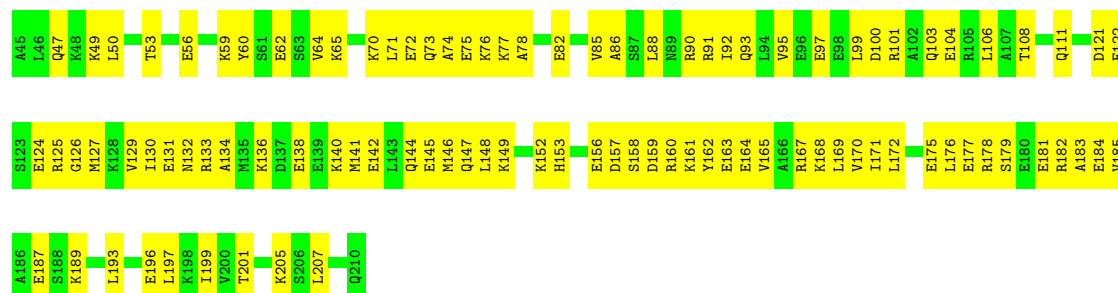




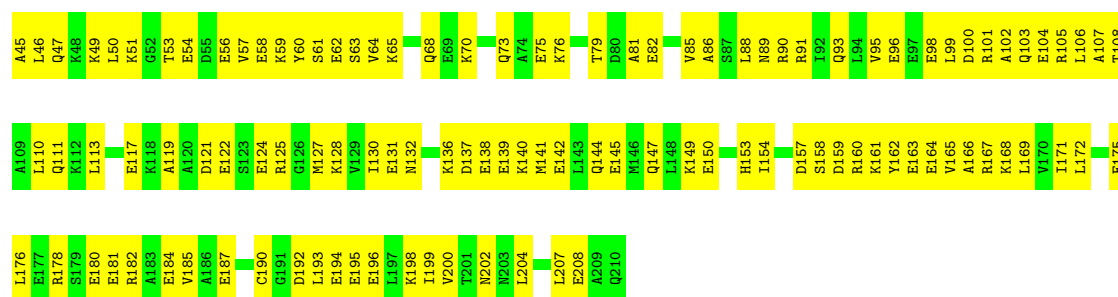
• Molecule 2: Tropomyosin beta chain



• Molecule 2: Tropomyosin beta chain

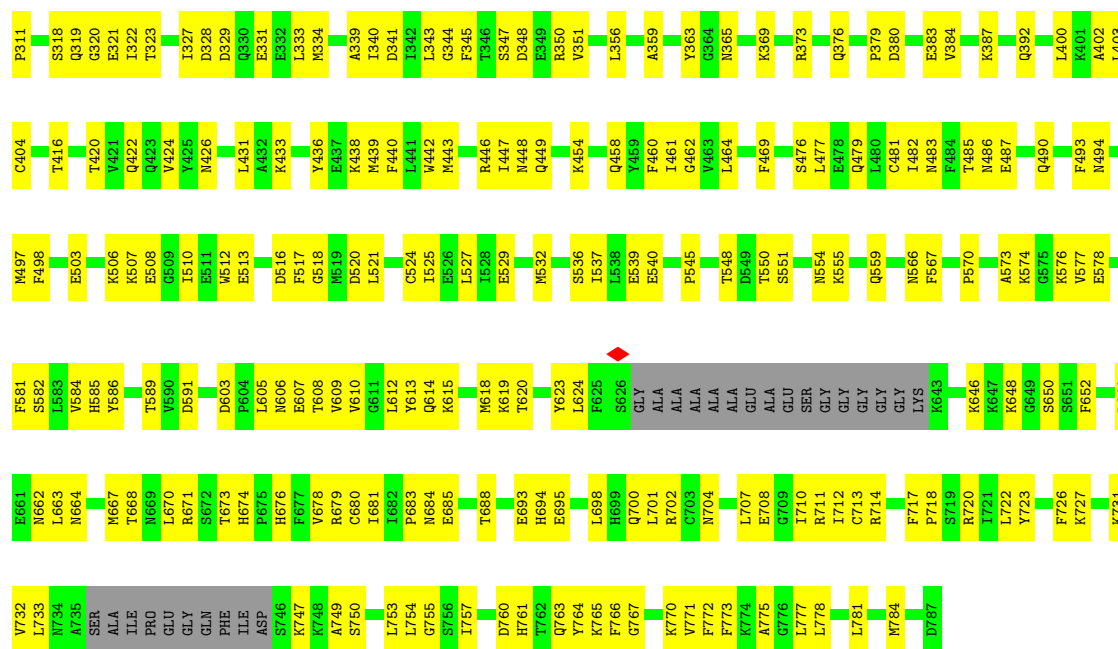


• Molecule 2: Tropomyosin beta chain



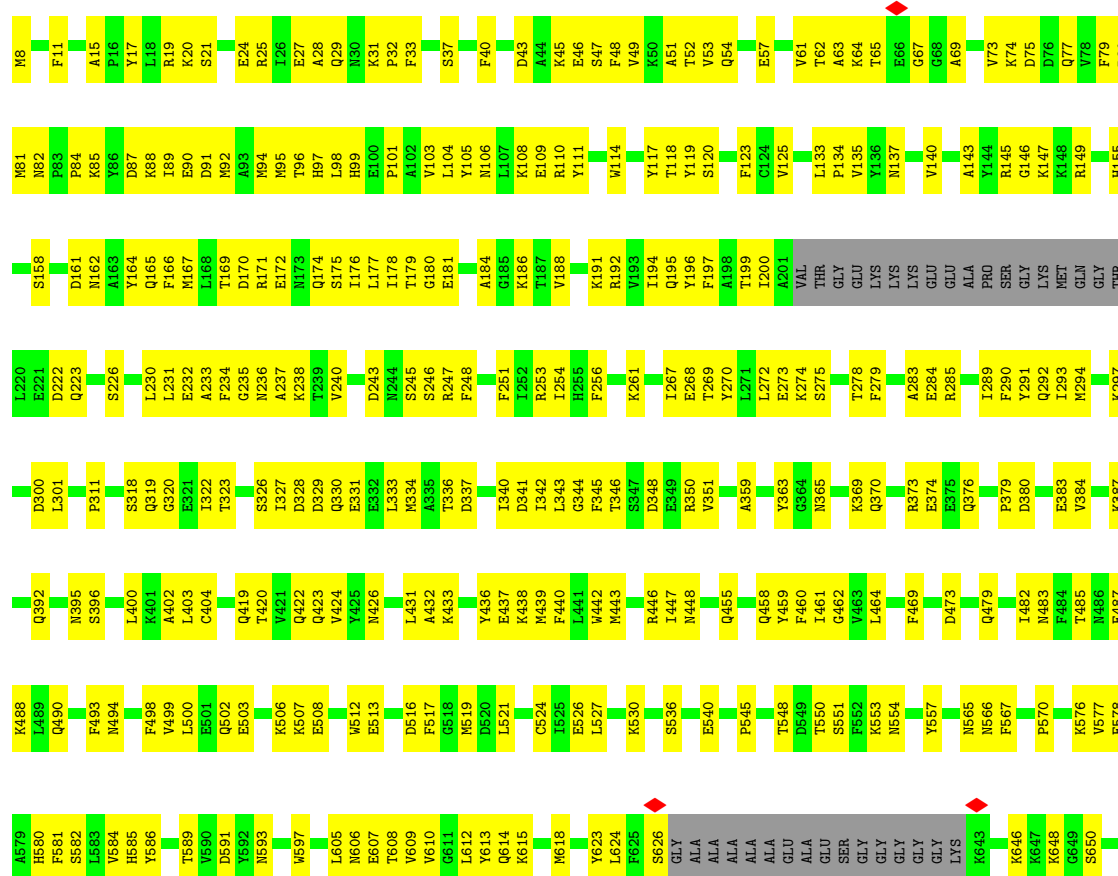
• Molecule 3: Myosin heavy chain 4

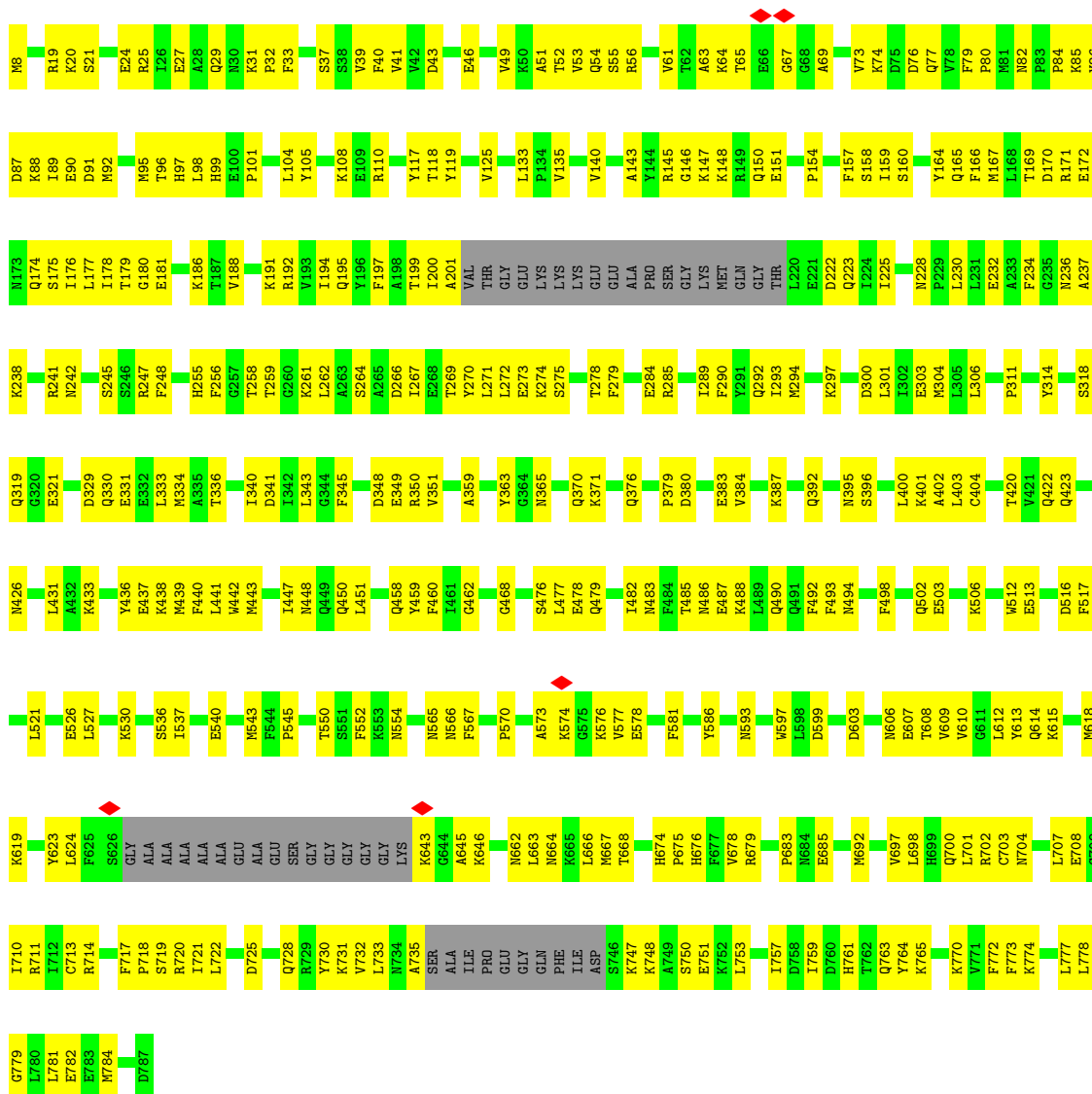




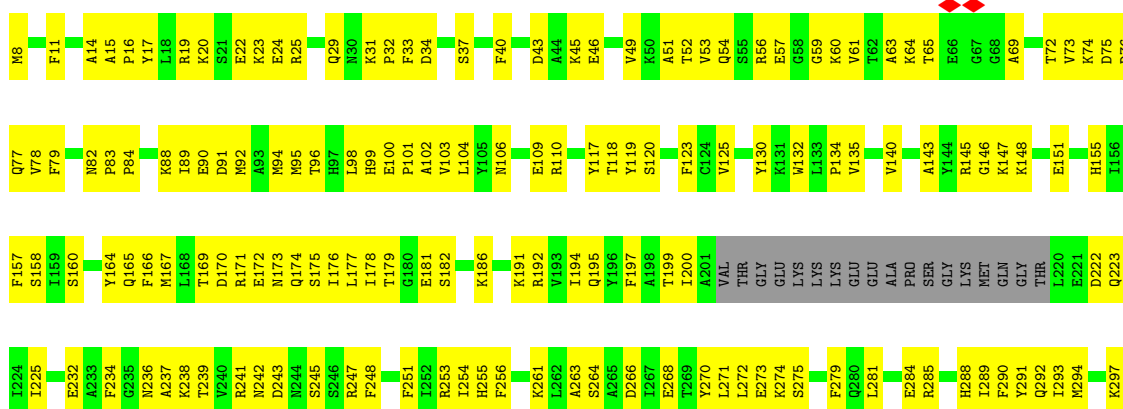
• Molecule 3: Myosin heavy chain 4

Chain J: 47% 47% 6%





• Molecule 3: Myosin heavy chain 4



K731	V732	L733	N734	A735	SER	ALA	ILE	PRO	GLU	GLY	GLN	PHE	ILE	ASP	S746	K747	K748	A749	S750	E751	K752	L753	L754	I757	D760	H761	T762	Q763	Y764	K765	F766	K770	V771	F772	F773	K774	A775	L778	L781	E782	E783	M784	R785	D786	D787									
M662	L663	L664	K665	L666	M667	T668	H674	P675	P676	H677	V678	R679	C680	I681	L682	P683	N684	E685	T686	K687	T688	P689	M692	E693	H694	V697	L698	H699	Q700	L701	R702	C703	N704	L707	E708	G709	I710	R711	R714	F717	P718	S719	R720	I721	L722	Y723	F726	K727	Q728	R729	Y730			
H580	F581	S582	L583	V584	H585	Y586	T589	V590	D591	Y592	N593	I594	W597	L605	N606	E607	T608	V609	V610	G611	L612	Y613	Q614	K615	S616	S617	Y623	L624	F625	S626	GLY	ALA	ALA	ALA	ALA	ALA	GLU	ALA	GLU	SER	GLY	GLY	GLY	GLY	GLY	LYS	K643	K646	K647	K648	G649	S650	S651	F652
Q490	F493	N494	F498	V499	Q502	E503	K506	W512	E513	D516	F517	C524	I525	E526	L527	I528	E529	K530	S536	I537	E540	P545	T548	D549	T550	S551	F552	K553	N554	Y557	E558	K563	S564	N565	N566	F567	P570	A573	K574	G575	K576	V577	E578	A579										
Q392	N395	S396	L400	K401	A402	C404	T420	V421	Q422	Q423	V424	Y425	N426	L431	A432	K433	Y436	E437	K438	M439	M443	I447	N448	R457	Q458	Y459	F460	I461	Q462	V463	L464	Q468	F469	E470	S476	L477	E478	Q479	L480	C481	I482	N483	F484	T485	N486	E487	K488	L489						
K298	L305	T308	T309	N310	P311	S318	Q319	G320	E321	I322	I327	D328	D329	Q330	E331	E332	L333	M334	D337	I340	D341	I342	L343	G344	F345	T346	S347	D348	E349	R350	V351	S352	I353	Y354	A359	Y363	G364	N365	Q372	R373	Q376	P379	E383	V384	K387									

4 Experimental information

Property	Value	Source
EM reconstruction method	HELICAL	Depositor
Imposed symmetry	HELICAL, twist=-166.69°, rise=27.4 Å, axial sym=C1	Depositor
Number of segments used	62956	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{Å}^2$)	55	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	0.028	Depositor
Minimum map value	-0.006	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.001	Depositor
Recommended contour level	0.003	Depositor
Map size (Å)	424.96, 424.96, 424.96	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.83, 0.83, 0.83	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: ADP

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	E	0.37	0/2962	0.40	0/4012
1	H	0.35	0/2962	0.40	0/4012
1	O	0.39	0/2962	0.42	0/4012
1	P	0.34	0/2962	0.38	0/4012
1	Q	0.38	0/2962	0.41	0/4012
1	R	0.37	0/2962	0.40	0/4012
2	B	0.19	0/1330	0.43	0/1769
2	C	0.19	0/1330	0.43	0/1769
2	F	0.20	0/1330	0.45	0/1769
2	G	0.18	0/1330	0.44	0/1769
3	A	0.17	0/6028	0.38	2/8123 (0.0%)
3	D	0.17	0/6028	0.38	0/8123
3	J	0.17	0/6028	0.38	0/8123
3	K	0.16	0/6028	0.37	0/8123
3	L	0.17	0/6028	0.38	0/8123
3	N	0.16	0/6028	0.37	0/8123
All	All	0.25	0/59260	0.39	2/79886 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	127	VAL	CA-C-N	-5.64	110.56	123.15
3	A	127	VAL	C-N-CA	-5.64	110.56	123.15

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	E	2899	0	2871	63	0
1	H	2899	0	2871	58	0
1	O	2899	0	2871	63	0
1	P	2899	0	2871	67	0
1	Q	2899	0	2871	74	0
1	R	2899	0	2871	60	0
2	B	1328	0	1327	111	0
2	C	1328	0	1327	99	0
2	F	1328	0	1327	135	0
2	G	1328	0	1327	115	0
3	A	5903	0	5883	303	0
3	D	5903	0	5883	300	0
3	J	5903	0	5883	294	0
3	K	5903	0	5883	267	0
3	L	5903	0	5883	308	0
3	N	5903	0	5883	289	0
4	E	27	0	12	3	0
4	H	27	0	12	3	0
4	O	27	0	12	3	0
4	P	27	0	12	3	0
4	Q	27	0	12	3	0
4	R	27	0	12	3	0
All	All	58286	0	57904	2462	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 21.

All (2462) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:64:VAL:HG12	2:B:68:GLN:HE22	1.35	0.92
3:A:297:LYS:HZ1	3:A:334:MET:HB2	1.34	0.92
3:D:710:ILE:O	3:D:714:ARG:HB2	1.72	0.89
1:P:151:THR:HG22	1:P:169:GLU:H	1.36	0.88
1:O:151:THR:HG22	1:O:169:GLU:H	1.39	0.88

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:J:710:ILE:O	3:J:714:ARG:HB2	1.73	0.87
3:L:297:LYS:HZ1	3:L:334:MET:HB2	1.39	0.87
3:D:297:LYS:HZ1	3:D:334:MET:HB2	1.39	0.86
1:E:151:THR:HG22	1:E:169:GLU:H	1.40	0.85
1:R:151:THR:HG22	1:R:169:GLU:H	1.41	0.85
2:G:127:MET:HA	2:G:130:ILE:HG12	1.61	0.82
2:F:64:VAL:HG12	2:F:68:GLN:HE22	1.43	0.82
3:K:610:VAL:HG13	3:K:624:LEU:HD23	1.61	0.82
2:G:187:GLU:HB2	2:F:182:ARG:HH22	1.46	0.81
3:K:610:VAL:HG12	3:K:614:GLN:HE21	1.45	0.81
3:A:292:GLN:HA	3:A:329:ASP:HB3	1.63	0.80
1:E:178:MET:SD	1:E:286:LYS:NZ	2.55	0.80
3:N:719:SER:HB2	3:N:773:PHE:HB2	1.62	0.79
3:L:610:VAL:HG12	3:L:614:GLN:HE21	1.48	0.78
1:R:222:ALA:HB1	1:R:228:GLU:HG3	1.66	0.78
1:Q:151:THR:HG22	1:Q:169:GLU:H	1.48	0.78
1:Q:222:ALA:HB1	1:Q:228:GLU:HG3	1.64	0.77
3:J:178:ILE:HG22	3:J:678:VAL:HB	1.66	0.77
3:L:369:LYS:HD2	3:L:380:ASP:HB3	1.65	0.77
3:L:176:ILE:HD11	3:L:678:VAL:HG23	1.66	0.77
3:J:292:GLN:HA	3:J:329:ASP:HB3	1.65	0.77
3:K:710:ILE:O	3:K:714:ARG:HB2	1.86	0.76
3:D:610:VAL:HG12	3:D:614:GLN:HE21	1.51	0.76
3:A:711:ARG:HA	3:A:714:ARG:HG2	1.66	0.75
3:D:51:ALA:HB1	3:D:63:ALA:HB1	1.68	0.75
1:P:352:SER:HA	1:P:355:GLN:HG2	1.65	0.75
1:R:155:LEU:HD12	1:R:164:ASN:HD21	1.50	0.75
3:D:521:LEU:HD11	3:D:586:TYR:HB3	1.66	0.75
3:J:61:VAL:HG22	3:J:73:VAL:H	1.51	0.75
1:H:178:MET:SD	1:H:286:LYS:NZ	2.60	0.74
3:L:717:PHE:O	3:L:720:ARG:NH1	2.19	0.74
3:A:50:LYS:NZ	3:A:51:ALA:O	2.21	0.74
3:J:65:THR:H	3:J:69:ALA:H	1.35	0.74
3:A:241:ARG:HE	3:A:242:ASN:HB3	1.53	0.74
3:D:610:VAL:HG13	3:D:624:LEU:HD23	1.70	0.74
3:K:292:GLN:HA	3:K:329:ASP:HB3	1.69	0.74
3:A:234:PHE:HD1	3:A:289:ILE:HG13	1.53	0.73
3:A:527:LEU:HD21	3:A:567:PHE:HB2	1.71	0.73
3:N:92:MET:HG2	3:N:103:VAL:HG23	1.70	0.73
1:R:178:MET:SD	1:R:286:LYS:NZ	2.61	0.73
3:N:610:VAL:HG13	3:N:624:LEU:HD23	1.71	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:O:178:MET:SD	1:O:286:LYS:NZ	2.61	0.73
3:N:90:GLU:OE1	3:N:110:ARG:NH2	2.21	0.73
3:L:172:GLU:O	3:L:174:GLN:NE2	2.22	0.73
1:Q:178:MET:SD	1:Q:286:LYS:NZ	2.62	0.73
3:N:238:LYS:HD2	3:N:243:ASP:HA	1.71	0.72
3:D:174:GLN:HG3	3:D:674:HIS:HB3	1.72	0.72
3:D:623:TYR:HB2	3:D:624:LEU:HD12	1.71	0.72
3:K:719:SER:HB2	3:K:773:PHE:HB2	1.71	0.72
2:C:164:GLU:HG3	2:C:167:ARG:HH21	1.55	0.72
3:D:684:ASN:ND2	3:D:688:THR:O	2.23	0.72
1:H:222:ALA:HB1	1:H:228:GLU:HG3	1.72	0.72
3:J:95:MET:SD	3:J:106:ASN:ND2	2.63	0.72
3:L:182:SER:OG	3:L:242:ASN:ND2	2.22	0.72
3:A:172:GLU:O	3:A:174:GLN:NE2	2.23	0.72
3:A:610:VAL:HG12	3:A:614:GLN:HE21	1.55	0.71
3:J:498:PHE:HB2	3:J:517:PHE:HB2	1.71	0.71
3:D:234:PHE:HD1	3:D:289:ILE:HG13	1.55	0.71
2:C:60:TYR:HE2	2:B:57:VAL:HG13	1.55	0.71
3:D:379:PRO:HG3	3:D:400:LEU:HD13	1.72	0.71
1:E:222:ALA:HB1	1:E:228:GLU:HG3	1.71	0.71
2:C:127:MET:HA	2:C:130:ILE:HG12	1.70	0.71
2:C:88:LEU:HD21	2:B:85:VAL:HG23	1.72	0.70
3:A:40:PHE:N	3:A:79:PHE:O	2.24	0.70
3:N:178:ILE:HG22	3:N:678:VAL:HB	1.72	0.70
3:N:182:SER:OG	3:N:242:ASN:ND2	2.24	0.70
1:O:171:TYR:HA	1:P:44:GLY:HA2	1.73	0.70
1:O:204:THR:HG22	1:O:206:ALA:H	1.57	0.70
3:A:701:LEU:HG	3:A:707:LEU:HD23	1.74	0.70
3:N:711:ARG:HA	3:N:714:ARG:HB3	1.73	0.70
1:E:7:THR:OG1	3:A:646:LYS:NZ	2.25	0.70
3:D:270:TYR:HB3	3:D:271:LEU:HD12	1.74	0.70
3:D:479:GLN:O	3:D:483:ASN:ND2	2.19	0.70
1:Q:171:TYR:HA	1:R:44:GLY:HA2	1.74	0.70
3:J:782:GLU:HA	3:J:785:ARG:HE	1.57	0.69
3:J:234:PHE:HD1	3:J:289:ILE:HG13	1.56	0.69
1:H:151:THR:HG22	1:H:169:GLU:H	1.56	0.69
3:J:172:GLU:O	3:J:174:GLN:NE2	2.25	0.69
3:K:148:LYS:HD2	3:K:150:GLN:H	1.56	0.69
3:D:201:ALA:HB2	3:D:262:LEU:HD23	1.73	0.69
3:A:684:ASN:ND2	3:A:688:THR:O	2.26	0.69
3:J:331:GLU:OE1	3:J:331:GLU:N	2.26	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:J:708:GLU:OE1	3:J:711:ARG:NH1	2.26	0.69
3:D:550:THR:O	3:D:554:ASN:ND2	2.26	0.69
3:K:178:ILE:HG22	3:K:678:VAL:HB	1.74	0.69
3:K:238:LYS:HG2	3:K:285:ARG:HG2	1.75	0.69
3:N:98:LEU:O	3:N:714:ARG:NH1	2.25	0.69
1:R:352:SER:HA	1:R:355:GLN:HG2	1.73	0.69
3:A:781:LEU:HA	3:A:784:MET:HG2	1.73	0.69
2:C:130:ILE:HB	2:B:130:ILE:HG21	1.75	0.69
2:C:175:GLU:HG3	2:B:176:LEU:HD11	1.73	0.69
3:A:331:GLU:OE1	3:A:331:GLU:N	2.24	0.69
3:K:550:THR:O	3:K:554:ASN:ND2	2.26	0.68
3:N:172:GLU:O	3:N:174:GLN:NE2	2.27	0.68
3:J:51:ALA:HB1	3:J:63:ALA:HB1	1.74	0.68
3:N:101:PRO:HA	3:N:104:LEU:HB3	1.75	0.68
3:D:172:GLU:O	3:D:174:GLN:NE2	2.27	0.68
3:J:521:LEU:HD11	3:J:586:TYR:HB3	1.74	0.68
3:L:238:LYS:HD2	3:L:243:ASP:HA	1.75	0.68
3:L:623:TYR:HB2	3:L:624:LEU:HD12	1.76	0.68
3:K:241:ARG:HE	3:K:242:ASN:HB3	1.57	0.68
3:N:40:PHE:HB2	3:N:79:PHE:HB2	1.74	0.68
2:C:122:GLU:O	2:C:125:ARG:NH1	2.26	0.68
3:A:311:PRO:O	3:A:318:SER:OG	2.12	0.68
3:D:422:GLN:O	3:D:426:ASN:ND2	2.25	0.68
1:H:255:GLU:OE1	1:H:255:GLU:N	2.26	0.68
2:G:179:SER:O	2:G:182:ARG:NH1	2.26	0.68
3:A:502:GLN:NE2	3:A:512:TRP:O	2.22	0.68
3:A:521:LEU:HD11	3:A:586:TYR:HB3	1.76	0.68
2:F:47:GLN:O	2:F:51:LYS:NZ	2.26	0.68
3:A:95:MET:SD	3:A:106:ASN:ND2	2.66	0.68
3:K:331:GLU:OE1	3:K:331:GLU:N	2.27	0.68
3:N:177:LEU:O	3:N:679:ARG:NH2	2.27	0.68
3:N:717:PHE:O	3:N:720:ARG:NH1	2.23	0.68
2:C:50:LEU:HG	2:B:46:LEU:HD12	1.73	0.68
3:K:431:LEU:HD11	3:K:609:VAL:HG21	1.75	0.68
3:A:422:GLN:O	3:A:426:ASN:ND2	2.26	0.67
3:A:717:PHE:O	3:A:720:ARG:NH1	2.27	0.67
3:D:82:ASN:ND2	3:D:95:MET:SD	2.67	0.67
2:F:98:GLU:O	2:F:101:ARG:NH1	2.27	0.67
3:J:698:LEU:O	3:J:702:ARG:NE	2.26	0.67
3:J:722:LEU:HG	3:J:770:LYS:HE2	1.74	0.67
1:O:255:GLU:N	1:O:255:GLU:OE2	2.28	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:D:74:LYS:HB2	3:D:77:GLN:HE22	1.58	0.67
2:G:71:LEU:HD11	2:F:70:LYS:HB2	1.76	0.67
3:K:341:ASP:OD1	3:K:350:ARG:NH2	2.28	0.67
3:A:270:TYR:HB3	3:A:271:LEU:HD12	1.77	0.67
3:D:331:GLU:OE1	3:D:331:GLU:N	2.25	0.67
3:J:40:PHE:N	3:J:79:PHE:O	2.28	0.67
3:L:781:LEU:HA	3:L:784:MET:HG2	1.76	0.67
3:K:51:ALA:HB1	3:K:63:ALA:HB1	1.76	0.67
3:K:90:GLU:OE1	3:K:110:ARG:NH2	2.27	0.67
3:D:177:LEU:O	3:D:679:ARG:NH2	2.27	0.67
3:A:698:LEU:O	3:A:702:ARG:NE	2.27	0.67
2:F:144:GLN:O	2:F:147:GLN:NE2	2.25	0.67
3:J:89:ILE:HG22	3:J:91:ASP:H	1.58	0.67
3:J:177:LEU:O	3:J:679:ARG:NH2	2.28	0.67
3:N:331:GLU:OE1	3:N:331:GLU:N	2.27	0.67
3:N:731:LYS:HD2	3:N:753:LEU:HD21	1.77	0.67
1:P:222:ALA:HB1	1:P:228:GLU:HG3	1.77	0.67
2:B:127:MET:HA	2:B:130:ILE:HG22	1.77	0.67
3:D:61:VAL:HG22	3:D:73:VAL:H	1.60	0.67
3:D:65:THR:H	3:D:69:ALA:H	1.42	0.67
3:D:292:GLN:HA	3:D:329:ASP:HB3	1.77	0.67
3:A:550:THR:O	3:A:554:ASN:ND2	2.28	0.67
2:F:145:GLU:O	2:F:149:LYS:HG2	1.95	0.67
3:A:178:ILE:HB	3:A:186:LYS:HE3	1.77	0.66
3:D:40:PHE:N	3:D:79:PHE:O	2.24	0.66
3:J:311:PRO:O	3:J:318:SER:OG	2.12	0.66
3:L:234:PHE:HD1	3:L:289:ILE:HG13	1.60	0.66
3:A:94:MET:HE1	3:A:720:ARG:HB2	1.77	0.66
2:G:182:ARG:HA	2:G:185:VAL:HG22	1.77	0.66
3:L:270:TYR:HB3	3:L:271:LEU:HD12	1.77	0.66
3:L:331:GLU:OE1	3:L:331:GLU:N	2.25	0.66
3:L:422:GLN:O	3:L:426:ASN:ND2	2.28	0.66
3:K:376:GLN:NE2	3:K:404:CYS:O	2.28	0.66
3:N:82:ASN:ND2	3:N:95:MET:SD	2.68	0.66
1:H:171:TYR:HA	1:Q:44:GLY:HA2	1.78	0.66
3:A:369:LYS:HD2	3:A:380:ASP:HB3	1.76	0.66
3:D:176:ILE:HD11	3:D:678:VAL:HG23	1.77	0.66
3:K:731:LYS:HD2	3:K:753:LEU:HD21	1.77	0.66
3:L:65:THR:H	3:L:69:ALA:H	1.42	0.66
3:L:292:GLN:HA	3:L:329:ASP:HB3	1.76	0.66
1:E:171:TYR:HA	1:O:44:GLY:HA2	1.77	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:J:710:ILE:O	3:J:714:ARG:CB	2.44	0.66
1:P:352:SER:H	3:K:540:GLU:CD	2.04	0.66
3:K:256:PHE:HB3	3:K:261:LYS:H	1.61	0.66
1:O:197:GLU:HB2	1:Q:115:LYS:HG3	1.77	0.66
1:O:222:ALA:HB1	1:O:228:GLU:HG3	1.77	0.66
2:C:126:GLY:O	2:C:130:ILE:HG23	1.94	0.66
3:A:149:ARG:NH1	3:A:150:GLN:OE1	2.29	0.66
3:A:681:ILE:HG21	3:A:697:VAL:HG23	1.77	0.66
3:D:255:HIS:N	3:D:264:SER:OG	2.28	0.66
2:F:204:LEU:O	2:F:208:GLU:HB2	1.96	0.66
1:Q:8:THR:HG23	3:L:646:LYS:HD3	1.78	0.66
2:B:149:LYS:O	2:B:153:HIS:ND1	2.24	0.66
3:K:101:PRO:HA	3:K:104:LEU:HB3	1.77	0.66
3:K:730:TYR:HE2	3:K:781:LEU:HD13	1.60	0.66
3:N:292:GLN:HA	3:N:329:ASP:HB3	1.77	0.66
2:B:124:GLU:O	2:B:127:MET:HG3	1.95	0.66
3:J:90:GLU:OE1	3:J:110:ARG:NH2	2.29	0.66
3:J:105:TYR:HA	3:J:108:LYS:HB3	1.77	0.66
3:L:345:PHE:O	3:L:350:ARG:NH1	2.27	0.66
3:N:256:PHE:HB3	3:N:261:LYS:H	1.60	0.66
3:D:54:GLN:HE22	3:D:57:GLU:HB2	1.60	0.66
3:L:570:PRO:HD3	3:L:581:PHE:HA	1.77	0.66
1:E:255:GLU:OE1	1:E:255:GLU:N	2.26	0.65
3:D:89:ILE:HG22	3:D:91:ASP:H	1.59	0.65
1:Q:352:SER:HA	1:Q:355:GLN:HG2	1.77	0.65
2:C:179:SER:O	2:C:182:ARG:NH1	2.29	0.65
3:D:341:ASP:OD1	3:D:350:ARG:NH2	2.29	0.65
3:K:61:VAL:HG22	3:K:73:VAL:H	1.62	0.65
3:K:177:LEU:O	3:K:679:ARG:NH2	2.29	0.65
3:N:191:LYS:HA	3:N:194:ILE:HG12	1.76	0.65
3:D:490:GLN:HA	3:D:493:PHE:CE1	2.30	0.65
2:G:106:LEU:HD22	2:F:105:ARG:NH2	2.11	0.65
3:J:684:ASN:ND2	3:J:688:THR:O	2.29	0.65
3:D:761:HIS:HA	3:D:764:TYR:HE1	1.61	0.65
2:G:130:ILE:HB	2:F:130:ILE:HG21	1.79	0.65
3:L:99:HIS:HB2	3:L:101:PRO:HD2	1.79	0.65
3:L:191:LYS:HA	3:L:194:ILE:HG12	1.78	0.65
3:L:684:ASN:ND2	3:L:688:THR:O	2.29	0.65
3:K:176:ILE:HD11	3:K:678:VAL:HG23	1.79	0.65
1:E:352:SER:HA	1:E:355:GLN:HG2	1.78	0.65
1:H:352:SER:HA	1:H:355:GLN:HG2	1.78	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:92:MET:HB3	3:A:95:MET:HE2	1.78	0.65
2:B:145:GLU:O	2:B:149:LYS:HG2	1.96	0.65
3:D:182:SER:OG	3:D:242:ASN:ND2	2.30	0.65
3:K:40:PHE:N	3:K:79:PHE:O	2.29	0.65
3:N:95:MET:SD	3:N:106:ASN:ND2	2.70	0.65
3:A:345:PHE:O	3:A:350:ARG:NH1	2.29	0.65
3:D:178:ILE:HB	3:D:186:LYS:HE3	1.79	0.65
3:D:311:PRO:O	3:D:318:SER:OG	2.15	0.65
3:L:52:THR:HB	3:L:64:LYS:HB2	1.78	0.65
3:K:365:ASN:HB2	3:K:384:VAL:HG21	1.78	0.65
3:D:181:GLU:OE2	3:D:700:GLN:NE2	2.29	0.65
2:C:169:LEU:HD13	2:B:168:LYS:HB3	1.79	0.65
3:D:698:LEU:O	3:D:702:ARG:NE	2.29	0.64
3:J:345:PHE:O	3:J:350:ARG:NH1	2.30	0.64
3:J:379:PRO:HG3	3:J:400:LEU:HD13	1.76	0.64
3:K:172:GLU:O	3:K:174:GLN:NE2	2.24	0.64
3:N:274:LYS:HD2	3:N:433:LYS:HB3	1.78	0.64
3:L:61:VAL:HG22	3:L:73:VAL:H	1.63	0.64
3:K:698:LEU:O	3:K:702:ARG:NE	2.29	0.64
3:L:340:ILE:HG21	3:L:350:ARG:HG2	1.79	0.64
3:N:379:PRO:HG3	3:N:400:LEU:HD13	1.80	0.64
1:P:189:ASP:OD1	1:P:208:ARG:NH1	2.31	0.64
3:A:233:ALA:HB2	3:A:336:THR:HG21	1.79	0.64
1:P:153:ILE:HD13	1:P:284:ILE:HD11	1.79	0.64
3:D:52:THR:HB	3:D:64:LYS:HB2	1.78	0.64
3:D:570:PRO:HD3	3:D:581:PHE:HA	1.80	0.64
3:L:733:LEU:HG	3:L:757:ILE:HG23	1.79	0.64
3:K:438:LYS:HB3	3:K:623:TYR:HB3	1.80	0.64
3:K:606:ASN:OD1	3:K:607:GLU:N	2.31	0.64
3:J:29:GLN:HE21	3:J:85:LYS:HE2	1.62	0.64
3:N:550:THR:O	3:N:554:ASN:ND2	2.30	0.64
3:N:781:LEU:HA	3:N:784:MET:HG2	1.78	0.64
1:O:102:GLU:OE1	1:O:102:GLU:N	2.30	0.64
1:Q:352:SER:H	3:L:540:GLU:CD	2.05	0.64
3:D:527:LEU:HD21	3:D:567:PHE:HB2	1.80	0.64
2:F:49:LYS:O	2:F:53:THR:OG1	2.15	0.64
3:J:52:THR:HB	3:J:64:LYS:HB2	1.79	0.64
3:J:88:LYS:O	3:J:110:ARG:NH1	2.31	0.64
3:J:490:GLN:HA	3:J:493:PHE:CE1	2.32	0.64
3:J:781:LEU:HA	3:J:784:MET:HG2	1.80	0.64
3:L:50:LYS:NZ	3:L:51:ALA:O	2.31	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:K:31:LYS:HE2	3:K:32:PRO:HD2	1.80	0.64
3:K:340:ILE:HG21	3:K:350:ARG:HG2	1.80	0.64
1:Q:356:GLN:OE1	1:Q:356:GLN:N	2.31	0.64
3:K:502:GLN:NE2	3:K:513:GLU:O	2.31	0.64
3:A:516:ASP:HB3	3:A:519:MET:HG2	1.79	0.64
2:G:108:THR:HA	2:G:111:GLN:HE21	1.62	0.64
3:J:422:GLN:O	3:J:426:ASN:ND2	2.31	0.64
3:A:761:HIS:HA	3:A:764:TYR:HE1	1.64	0.63
3:D:85:LYS:HG3	3:D:86:TYR:HD1	1.62	0.63
2:G:86:ALA:O	2:G:90:ARG:HG2	1.97	0.63
2:G:97:GLU:O	2:G:101:ARG:NE	2.28	0.63
2:G:178:ARG:HA	2:G:181:GLU:HG2	1.80	0.63
3:J:256:PHE:HB3	3:J:261:LYS:H	1.63	0.63
3:D:345:PHE:O	3:D:350:ARG:NH1	2.31	0.63
3:D:673:THR:HG22	3:D:674:HIS:H	1.61	0.63
2:C:187:GLU:HB2	2:B:182:ARG:HH22	1.63	0.63
3:D:90:GLU:OE1	3:D:110:ARG:NH2	2.32	0.63
3:J:717:PHE:O	3:J:720:ARG:NH1	2.27	0.63
1:P:356:GLN:OE1	1:P:356:GLN:N	2.32	0.63
3:D:403:LEU:HD22	3:D:609:VAL:HG11	1.81	0.63
3:L:458:GLN:HG2	3:L:459:TYR:H	1.62	0.63
3:K:274:LYS:HD2	3:K:433:LYS:HB3	1.79	0.63
3:A:431:LEU:HD11	3:A:609:VAL:HG21	1.80	0.63
3:D:766:PHE:HA	3:D:771:VAL:HA	1.81	0.63
2:G:189:LYS:HZ3	2:F:190:CYS:HB2	1.63	0.63
3:L:51:ALA:HB1	3:L:63:ALA:HB1	1.80	0.63
3:L:679:ARG:HD2	3:L:704:ASN:HB3	1.80	0.63
3:K:52:THR:HB	3:K:64:LYS:HB2	1.79	0.63
3:K:294:MET:HG3	3:K:311:PRO:HB3	1.79	0.63
3:D:527:LEU:HD22	3:D:566:ASN:HB2	1.81	0.63
2:G:130:ILE:HA	2:G:133:ARG:HE	1.63	0.63
3:L:550:THR:O	3:L:554:ASN:ND2	2.32	0.63
3:K:725:ASP:OD1	3:K:728:GLN:NE2	2.32	0.63
3:N:422:GLN:O	3:N:426:ASN:ND2	2.32	0.63
3:A:85:LYS:HG3	3:A:86:TYR:HD1	1.64	0.63
3:D:95:MET:SD	3:D:106:ASN:ND2	2.72	0.63
3:J:270:TYR:CG	3:J:666:LEU:HD11	2.34	0.63
3:L:606:ASN:OD1	3:L:607:GLU:N	2.32	0.63
1:Q:102:GLU:N	1:Q:102:GLU:OE1	2.32	0.63
3:A:65:THR:H	3:A:69:ALA:H	1.47	0.63
3:J:274:LYS:HD2	3:J:433:LYS:HB3	1.79	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:88:LEU:HD22	2:B:89:ASN:HB3	1.81	0.63
3:L:311:PRO:O	3:L:318:SER:OG	2.14	0.63
1:E:356:GLN:N	1:E:356:GLN:OE1	2.32	0.62
2:C:99:LEU:HD22	2:B:95:VAL:HG13	1.80	0.62
1:R:102:GLU:OE1	1:R:102:GLU:N	2.32	0.62
3:A:733:LEU:HG	3:A:757:ILE:HG23	1.81	0.62
3:D:373:ARG:NH1	2:G:159:ASP:OD2	2.32	0.62
3:N:376:GLN:NE2	3:N:404:CYS:O	2.32	0.62
3:N:431:LEU:HD11	3:N:609:VAL:HG21	1.79	0.62
3:N:760:ASP:OD1	3:N:763:GLN:NE2	2.32	0.62
1:O:356:GLN:OE1	1:O:356:GLN:N	2.31	0.62
1:Q:255:GLU:OE1	1:Q:255:GLU:N	2.26	0.62
3:D:53:VAL:HG23	3:D:62:THR:H	1.64	0.62
3:L:291:TYR:HE1	3:L:322:ILE:HG22	1.64	0.62
3:A:510:ILE:HG12	3:A:765:LYS:HG2	1.81	0.62
3:L:291:TYR:OH	3:L:317:VAL:O	2.18	0.62
3:N:345:PHE:O	3:N:350:ARG:NH1	2.31	0.62
3:N:698:LEU:O	3:N:702:ARG:NE	2.26	0.62
1:O:352:SER:H	3:J:540:GLU:CD	2.07	0.62
1:R:356:GLN:N	1:R:356:GLN:OE1	2.32	0.62
3:J:576:LYS:NZ	3:J:578:GLU:O	2.31	0.62
3:N:96:THR:OG1	3:N:775:ALA:O	2.16	0.62
3:N:683:PRO:HB2	3:N:692:MET:HB3	1.79	0.62
3:A:718:PRO:HD2	3:A:774:LYS:HA	1.81	0.62
2:F:56:GLU:HA	2:F:59:LYS:HG2	1.81	0.62
2:B:49:LYS:O	2:B:53:THR:OG1	2.15	0.62
3:J:536:SER:O	3:J:540:GLU:HG2	1.99	0.62
3:J:733:LEU:HG	3:J:757:ILE:HG23	1.82	0.62
3:K:192:ARG:HH11	3:K:195:GLN:HE22	1.48	0.62
1:E:115:LYS:HG3	1:Q:197:GLU:HB2	1.81	0.62
3:A:379:PRO:HG3	3:A:400:LEU:HD13	1.81	0.62
3:A:479:GLN:OE1	3:A:479:GLN:N	2.32	0.62
3:J:488:LYS:HG3	3:J:663:LEU:HD21	1.80	0.62
3:L:490:GLN:HA	3:L:493:PHE:CE1	2.34	0.62
3:N:490:GLN:HA	3:N:493:PHE:CE1	2.34	0.62
1:O:78:ILE:HD13	1:O:84:MET:HG2	1.82	0.62
2:B:73:GLN:HA	2:B:76:LYS:HD2	1.81	0.62
2:B:86:ALA:HB1	2:B:90:ARG:HH12	1.65	0.62
3:D:42:VAL:HG13	3:D:77:GLN:HB2	1.82	0.62
3:K:37:SER:HA	3:K:53:VAL:HG12	1.80	0.62
3:K:140:VAL:HA	3:K:143:ALA:HB3	1.81	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:274:LYS:HD2	3:A:433:LYS:HB3	1.82	0.62
3:A:707:LEU:HA	3:A:710:ILE:HG12	1.82	0.62
3:K:8:MET:SD	3:K:25:ARG:NH2	2.68	0.62
1:E:119:GLU:OE2	1:E:373:HIS:NE2	2.30	0.62
2:G:122:GLU:O	2:G:125:ARG:NH1	2.33	0.62
3:J:230:LEU:HD22	3:J:340:ILE:HG12	1.81	0.62
3:N:270:TYR:CG	3:N:666:LEU:HD11	2.34	0.62
1:E:189:ASP:OD1	1:E:208:ARG:NH1	2.33	0.61
2:C:140:LYS:O	2:C:144:GLN:NE2	2.32	0.61
3:D:698:LEU:HD23	3:D:701:LEU:HD23	1.82	0.61
3:K:108:LYS:HZ3	3:K:692:MET:HB2	1.65	0.61
3:N:74:LYS:HB2	3:N:77:GLN:HE22	1.65	0.61
1:Q:159:ASP:OD1	4:Q:401:ADP:O3'	2.18	0.61
2:B:117:GLU:OE1	3:J:373:ARG:NH2	2.32	0.61
3:L:20:LYS:HG2	3:L:115:MET:HE2	1.80	0.61
3:L:698:LEU:O	3:L:702:ARG:NE	2.30	0.61
3:A:606:ASN:OD1	3:A:607:GLU:N	2.33	0.61
2:B:144:GLN:O	2:B:147:GLN:NE2	2.33	0.61
3:D:431:LEU:HD11	3:D:609:VAL:HG21	1.81	0.61
2:G:74:ALA:HA	2:G:77:LYS:HD2	1.81	0.61
3:J:550:THR:O	3:J:554:ASN:ND2	2.32	0.61
3:L:40:PHE:HB2	3:L:79:PHE:HB2	1.81	0.61
3:K:422:GLN:O	3:K:426:ASN:ND2	2.34	0.61
3:N:311:PRO:O	3:N:318:SER:OG	2.16	0.61
2:F:73:GLN:HA	2:F:76:LYS:HG2	1.83	0.61
2:F:158:SER:HA	2:F:161:LYS:HG2	1.81	0.61
3:N:140:VAL:HA	3:N:143:ALA:HB3	1.83	0.61
1:E:158:GLY:O	1:E:305:THR:OG1	2.18	0.61
2:C:97:GLU:O	2:C:101:ARG:NE	2.29	0.61
2:F:124:GLU:O	2:F:127:MET:HG3	2.01	0.61
2:F:157:ASP:OD1	2:F:160:ARG:NH2	2.32	0.61
3:J:256:PHE:O	3:J:458:GLN:N	2.34	0.61
3:L:192:ARG:HH11	3:L:195:GLN:HE22	1.47	0.61
3:K:479:GLN:OE1	3:K:479:GLN:N	2.34	0.61
3:N:89:ILE:HG22	3:N:91:ASP:H	1.66	0.61
3:N:238:LYS:NZ	3:N:239:THR:O	2.28	0.61
3:A:238:LYS:HE2	3:A:285:ARG:HE	1.66	0.61
3:A:291:TYR:OH	3:A:317:VAL:O	2.18	0.61
3:A:747:LYS:HG3	3:A:766:PHE:HE2	1.64	0.61
3:D:238:LYS:HD2	3:D:243:ASP:HA	1.82	0.61
3:J:251:PHE:HD1	3:J:464:LEU:HB2	1.64	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:K:279:PHE:HA	3:K:319:GLN:HE21	1.64	0.61
3:K:494:ASN:ND2	3:K:517:PHE:O	2.34	0.61
3:N:570:PRO:HD3	3:N:581:PHE:HA	1.81	0.61
1:H:36:ILE:HD12	1:H:69:LEU:HD13	1.82	0.61
1:O:159:ASP:OD1	4:O:401:ADP:O3'	2.18	0.61
2:B:47:GLN:OE1	2:B:48:LYS:NZ	2.31	0.61
3:J:431:LEU:HD11	3:J:609:VAL:HG21	1.81	0.61
3:L:40:PHE:N	3:L:79:PHE:O	2.30	0.61
3:K:336:THR:O	3:K:340:ILE:HG12	2.00	0.61
3:N:251:PHE:HD1	3:N:464:LEU:HB2	1.66	0.61
3:N:341:ASP:OD1	3:N:350:ARG:NH2	2.33	0.61
1:H:356:GLN:OE1	1:H:356:GLN:N	2.33	0.61
3:D:178:ILE:HG22	3:D:678:VAL:HB	1.82	0.61
3:D:238:LYS:NZ	3:D:239:THR:O	2.30	0.61
3:J:606:ASN:OD1	3:J:607:GLU:N	2.33	0.61
3:K:498:PHE:HB2	3:K:517:PHE:HB2	1.82	0.61
1:O:158:GLY:O	1:O:305:THR:OG1	2.18	0.61
3:A:340:ILE:HG21	3:A:350:ARG:HG2	1.83	0.61
3:J:54:GLN:HG2	3:J:62:THR:HG22	1.83	0.61
3:K:490:GLN:HA	3:K:493:PHE:CE1	2.35	0.61
3:K:570:PRO:HD3	3:K:581:PHE:HA	1.83	0.61
2:B:98:GLU:O	2:B:101:ARG:NH1	2.34	0.61
3:J:346:THR:OG1	3:J:348:ASP:OD1	2.17	0.61
3:J:718:PRO:HD2	3:J:774:LYS:HA	1.83	0.61
3:D:155:HIS:O	3:D:158:SER:OG	2.15	0.60
3:D:566:ASN:HA	3:D:584:VAL:HG22	1.83	0.60
2:G:50:LEU:HG	2:F:46:LEU:HD12	1.81	0.60
2:F:117:GLU:OE1	3:L:373:ARG:NH1	2.34	0.60
2:C:183:ALA:O	2:B:182:ARG:NH1	2.30	0.60
3:A:90:GLU:OE1	3:A:110:ARG:NH2	2.34	0.60
3:D:606:ASN:OD1	3:D:607:GLU:N	2.34	0.60
3:L:270:TYR:CG	3:L:666:LEU:HD11	2.36	0.60
3:K:345:PHE:O	3:K:350:ARG:NH1	2.32	0.60
3:K:363:TYR:OH	3:K:613:TYR:OH	2.18	0.60
3:N:494:ASN:ND2	3:N:517:PHE:O	2.35	0.60
2:C:175:GLU:O	2:C:178:ARG:NH1	2.34	0.60
3:A:479:GLN:O	3:A:483:ASN:ND2	2.34	0.60
3:D:438:LYS:HB3	3:D:623:TYR:HB3	1.83	0.60
2:F:144:GLN:HA	2:F:147:GLN:HG3	1.84	0.60
3:L:178:ILE:HG22	3:L:678:VAL:HB	1.84	0.60
3:N:234:PHE:HD1	3:N:289:ILE:HG13	1.67	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:336:GLU:OE1	1:E:336:GLU:N	2.34	0.60
2:B:60:TYR:O	2:B:64:VAL:HG23	2.01	0.60
2:B:106:LEU:O	2:B:110:LEU:HG	2.01	0.60
3:J:570:PRO:HD3	3:J:581:PHE:HA	1.83	0.60
3:L:431:LEU:HD11	3:L:609:VAL:HG21	1.81	0.60
3:N:468:GLY:O	3:N:486:ASN:ND2	2.34	0.60
1:H:102:GLU:OE1	1:H:102:GLU:N	2.34	0.60
2:G:88:LEU:HA	2:G:91:ARG:HD3	1.81	0.60
2:G:144:GLN:HB3	2:F:144:GLN:CD	2.27	0.60
2:F:98:GLU:HG3	2:F:101:ARG:CZ	2.32	0.60
3:J:238:LYS:HG2	3:J:285:ARG:HG2	1.84	0.60
3:K:674:HIS:HD2	3:K:675:PRO:HD2	1.65	0.60
1:R:189:ASP:OD1	1:R:208:ARG:NH1	2.34	0.60
3:L:98:LEU:O	3:L:714:ARG:NH2	2.35	0.60
3:K:443:MET:O	3:K:447:ILE:HG12	2.02	0.60
3:N:176:ILE:HD11	3:N:678:VAL:HG23	1.84	0.60
3:A:494:ASN:ND2	3:A:517:PHE:O	2.35	0.60
2:B:144:GLN:HA	2:B:147:GLN:HG3	1.84	0.60
3:N:340:ILE:HG21	3:N:350:ARG:HG2	1.82	0.60
2:C:73:GLN:HA	2:C:76:LYS:HD2	1.84	0.60
3:A:77:GLN:N	3:A:77:GLN:OE1	2.34	0.60
3:D:191:LYS:HA	3:D:194:ILE:HG12	1.82	0.60
3:J:101:PRO:HA	3:J:104:LEU:HB3	1.83	0.60
3:K:256:PHE:O	3:K:458:GLN:N	2.32	0.60
3:D:20:LYS:HG2	3:D:115:MET:HE2	1.84	0.60
3:D:550:THR:HG22	3:D:554:ASN:HD21	1.67	0.60
3:L:479:GLN:O	3:L:483:ASN:ND2	2.34	0.60
3:K:311:PRO:O	3:K:318:SER:OG	2.19	0.60
3:N:499:VAL:O	3:N:503:GLU:HB2	2.01	0.60
3:N:503:GLU:HA	3:N:506:LYS:HG2	1.82	0.60
3:A:197:PHE:HA	3:A:200:ILE:HG22	1.84	0.60
3:J:21:SER:N	3:J:24:GLU:OE2	2.34	0.60
3:N:256:PHE:O	3:N:458:GLN:N	2.33	0.60
1:H:189:ASP:OD1	1:H:208:ARG:NH1	2.35	0.59
1:R:159:ASP:OD1	4:R:401:ADP:O3'	2.19	0.59
3:J:24:GLU:HA	3:J:27:GLU:HG2	1.83	0.59
3:J:273:GLU:OE2	3:J:275:SER:OG	2.19	0.59
3:N:274:LYS:HE2	3:N:437:GLU:HB2	1.83	0.59
1:E:197:GLU:HB2	1:H:115:LYS:HG3	1.83	0.59
2:B:127:MET:O	2:B:131:GLU:HG2	2.02	0.59
3:J:176:ILE:HD11	3:J:678:VAL:HG23	1.84	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:J:701:LEU:HG	3:J:707:LEU:HD22	1.84	0.59
1:E:102:GLU:OE1	1:E:102:GLU:N	2.35	0.59
1:H:159:ASP:OD1	4:H:401:ADP:O3'	2.20	0.59
3:J:237:ALA:O	3:J:245:SER:OG	2.20	0.59
3:K:718:PRO:HD2	3:K:774:LYS:HA	1.83	0.59
1:P:102:GLU:OE1	1:P:102:GLU:N	2.36	0.59
3:A:570:PRO:HD3	3:A:581:PHE:HA	1.84	0.59
2:G:175:GLU:O	2:G:178:ARG:NH1	2.35	0.59
3:J:164:TYR:HA	3:J:167:MET:HE3	1.85	0.59
2:C:71:LEU:HD11	2:B:70:LYS:HB2	1.84	0.59
2:C:102:ALA:O	2:C:105:ARG:NH1	2.36	0.59
2:C:152:LYS:NZ	2:B:147:GLN:OE1	2.35	0.59
3:A:341:ASP:OD1	3:A:350:ARG:NH2	2.34	0.59
3:D:710:ILE:O	3:D:714:ARG:CB	2.47	0.59
2:G:99:LEU:HD22	2:F:95:VAL:HG22	1.83	0.59
3:J:731:LYS:HD2	3:J:753:LEU:HD21	1.85	0.59
3:K:98:LEU:O	3:K:714:ARG:NE	2.31	0.59
3:J:341:ASP:OD1	3:J:350:ARG:NH2	2.36	0.59
3:L:291:TYR:HA	3:L:294:MET:HB2	1.84	0.59
3:L:379:PRO:HG3	3:L:400:LEU:HD13	1.82	0.59
3:D:134:PRO:O	3:D:137:ASN:ND2	2.35	0.59
3:D:731:LYS:HD2	3:D:753:LEU:HD21	1.83	0.59
3:L:479:GLN:OE1	3:L:479:GLN:N	2.29	0.59
3:N:40:PHE:N	3:N:79:PHE:O	2.35	0.59
1:H:235:SER:OG	1:H:236:SER:N	2.34	0.59
3:A:166:PHE:O	3:A:169:THR:OG1	2.19	0.59
3:J:469:PHE:HB3	3:J:703:CYS:HA	1.84	0.59
3:L:241:ARG:HE	3:L:242:ASN:HB3	1.67	0.59
3:A:173:ASN:OD1	3:A:460:PHE:N	2.33	0.59
2:B:47:GLN:O	2:B:51:LYS:NZ	2.26	0.59
2:B:157:ASP:OD1	2:B:160:ARG:NH2	2.35	0.59
3:J:502:GLN:NE2	3:J:513:GLU:O	2.35	0.59
3:L:766:PHE:HA	3:L:771:VAL:HA	1.84	0.59
3:J:766:PHE:HA	3:J:771:VAL:HA	1.83	0.59
3:L:20:LYS:O	3:L:25:ARG:NE	2.30	0.59
3:L:527:LEU:HD22	3:L:566:ASN:HB2	1.85	0.59
2:G:121:ASP:HA	2:G:124:GLU:HG2	1.84	0.58
3:J:279:PHE:HA	3:J:319:GLN:HE21	1.68	0.58
3:L:255:HIS:N	3:L:264:SER:OG	2.35	0.58
3:N:760:ASP:OD2	3:N:762:THR:OG1	2.19	0.58
1:O:229:MET:SD	1:O:254:ASN:ND2	2.76	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:84:PRO:HA	3:A:87:ASP:HB2	1.86	0.58
3:A:270:TYR:CG	3:A:666:LEU:HD11	2.38	0.58
3:D:197:PHE:HA	3:D:200:ILE:HG22	1.84	0.58
2:G:62:GLU:HA	2:G:65:LYS:HE2	1.84	0.58
3:J:118:THR:HB	3:J:125:VAL:HG13	1.86	0.58
3:J:234:PHE:O	3:J:436:TYR:OH	2.21	0.58
3:K:698:LEU:HD13	3:K:701:LEU:HD23	1.83	0.58
3:N:606:ASN:OD1	3:N:607:GLU:N	2.35	0.58
2:C:144:GLN:HA	2:C:147:GLN:HG3	1.84	0.58
2:C:160:ARG:NH1	2:C:161:LYS:HB2	2.18	0.58
3:J:274:LYS:HE2	3:J:437:GLU:HB2	1.83	0.58
3:L:140:VAL:HA	3:L:143:ALA:HB3	1.85	0.58
3:L:164:TYR:HA	3:L:167:MET:HE3	1.84	0.58
1:E:159:ASP:OD1	4:E:401:ADP:O3'	2.19	0.58
1:P:306:THR:O	1:P:337:ARG:NH1	2.35	0.58
3:D:192:ARG:HH11	3:D:195:GLN:HE22	1.49	0.58
3:J:140:VAL:HA	3:J:143:ALA:HB3	1.85	0.58
3:L:238:LYS:NZ	3:L:239:THR:O	2.28	0.58
3:L:341:ASP:OD1	3:L:350:ARG:NH2	2.35	0.58
3:L:701:LEU:HD11	3:L:707:LEU:HB3	1.85	0.58
3:D:173:ASN:HB3	3:D:673:THR:HG23	1.85	0.58
3:D:494:ASN:ND2	3:D:520:ASP:OD2	2.36	0.58
2:F:127:MET:HA	2:F:130:ILE:HG22	1.83	0.58
3:L:731:LYS:HD2	3:L:753:LEU:HD21	1.84	0.58
3:K:180:GLY:HA3	3:K:186:LYS:HB2	1.86	0.58
1:R:352:SER:H	3:N:540:GLU:CD	2.10	0.58
3:D:369:LYS:HD2	3:D:380:ASP:HB3	1.86	0.58
3:J:236:ASN:ND2	3:J:246:SER:HA	2.19	0.58
3:K:29:GLN:HA	3:K:85:LYS:HA	1.86	0.58
3:K:576:LYS:HD3	3:K:577:VAL:N	2.19	0.58
1:O:352:SER:HA	1:O:355:GLN:HG2	1.85	0.58
1:P:204:THR:HG22	1:P:206:ALA:H	1.69	0.58
2:F:149:LYS:O	2:F:153:HIS:ND1	2.30	0.58
3:L:85:LYS:HG3	3:L:86:TYR:HD1	1.69	0.58
3:K:503:GLU:O	3:K:506:LYS:NZ	2.31	0.58
3:K:708:GLU:OE1	3:K:711:ARG:NH1	2.37	0.58
3:N:164:TYR:HA	3:N:167:MET:HE3	1.84	0.58
3:A:612:LEU:HD23	3:A:615:LYS:HZ3	1.67	0.58
3:L:256:PHE:HB3	3:L:261:LYS:H	1.68	0.58
1:P:159:ASP:OD1	4:P:401:ADP:O3'	2.21	0.58
3:A:502:GLN:NE2	3:A:513:GLU:O	2.37	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:731:LYS:HD2	3:A:753:LEU:HD21	1.86	0.58
2:F:149:LYS:C	2:F:153:HIS:HD1	2.11	0.58
3:J:177:LEU:HD21	3:J:670:LEU:HD21	1.85	0.58
3:L:476:SER:OG	3:L:477:LEU:N	2.37	0.58
1:H:119:GLU:OE2	1:H:373:HIS:NE2	2.37	0.58
3:A:191:LYS:HA	3:A:194:ILE:HG12	1.86	0.58
3:D:516:ASP:OD1	3:D:518:GLY:N	2.36	0.58
3:D:577:VAL:HG13	3:D:578:GLU:H	1.69	0.58
3:J:482:ILE:O	3:J:485:THR:OG1	2.21	0.58
2:C:99:LEU:HB2	2:B:95:VAL:HG13	1.84	0.57
2:G:124:GLU:O	2:G:127:MET:HG2	2.05	0.57
3:N:536:SER:O	3:N:540:GLU:HG2	2.04	0.57
3:D:443:MET:O	3:D:447:ILE:HG12	2.04	0.57
3:J:29:GLN:HA	3:J:85:LYS:HA	1.85	0.57
3:K:274:LYS:HE2	3:K:437:GLU:HB2	1.86	0.57
3:A:201:ALA:HB2	3:A:262:LEU:HD13	1.86	0.57
3:D:25:ARG:O	3:D:29:GLN:HB2	2.04	0.57
3:D:248:PHE:HB3	3:D:272:LEU:HD13	1.86	0.57
3:J:719:SER:HB2	3:J:773:PHE:HB2	1.86	0.57
3:L:234:PHE:O	3:L:436:TYR:OH	2.22	0.57
3:N:117:TYR:CE1	3:N:135:VAL:HG21	2.39	0.57
3:N:527:LEU:HD21	3:N:567:PHE:HB2	1.86	0.57
3:A:269:THR:HG21	3:A:440:PHE:HE2	1.69	0.57
1:Q:158:GLY:O	1:Q:305:THR:OG1	2.23	0.57
2:B:45:ALA:N	2:B:47:GLN:OE1	2.37	0.57
3:J:348:ASP:HA	3:J:351:VAL:HG12	1.86	0.57
3:L:403:LEU:HD22	3:L:609:VAL:HG11	1.87	0.57
3:L:498:PHE:HB2	3:L:517:PHE:HB2	1.87	0.57
3:N:612:LEU:HD23	3:N:615:LYS:HZ3	1.68	0.57
1:Q:119:GLU:OE2	1:Q:373:HIS:NE2	2.33	0.57
3:J:479:GLN:OE1	3:J:479:GLN:N	2.33	0.57
3:J:610:VAL:HG12	3:J:614:GLN:HE21	1.69	0.57
3:K:683:PRO:HB2	3:K:692:MET:HG3	1.85	0.57
2:C:106:LEU:HD22	2:B:105:ARG:HH21	1.69	0.57
2:F:60:TYR:O	2:F:64:VAL:HG23	2.05	0.57
3:A:234:PHE:CD1	3:A:289:ILE:HG13	2.38	0.57
3:A:548:THR:HG23	3:A:551:SER:H	1.70	0.57
3:D:276:ARG:NH1	3:D:284:GLU:OE2	2.38	0.57
3:D:532:MET:HE2	3:D:559:GLN:HE21	1.70	0.57
3:J:503:GLU:O	3:J:506:LYS:NZ	2.36	0.57
3:N:345:PHE:HE2	3:N:353:ILE:HD11	1.70	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:N:584:VAL:HA	3:N:589:THR:HA	1.87	0.57
3:J:166:PHE:O	3:J:169:THR:OG1	2.23	0.57
3:L:251:PHE:HD1	3:L:464:LEU:HB2	1.68	0.57
2:C:133:ARG:NH2	2:B:131:GLU:OE2	2.38	0.57
3:A:134:PRO:O	3:A:137:ASN:ND2	2.38	0.57
3:A:186:LYS:HD3	3:A:189:ASN:HD22	1.69	0.57
3:A:720:ARG:HG3	3:A:772:PHE:CD1	2.40	0.57
3:D:476:SER:OG	3:D:477:LEU:N	2.38	0.57
3:J:376:GLN:NE2	3:J:404:CYS:O	2.38	0.57
1:E:203:VAL:N	1:E:207:GLU:OE2	2.30	0.56
3:A:761:HIS:HA	3:A:764:TYR:CE1	2.39	0.56
2:G:99:LEU:HD11	2:F:98:GLU:HG2	1.86	0.56
3:J:8:MET:O	3:J:19:ARG:NH2	2.38	0.56
3:L:178:ILE:HB	3:L:186:LYS:HE3	1.87	0.56
3:L:346:THR:OG1	3:L:348:ASP:OD1	2.18	0.56
3:L:494:ASN:ND2	3:L:517:PHE:O	2.38	0.56
3:A:174:GLN:HG3	3:A:674:HIS:HB3	1.86	0.56
3:K:74:LYS:HB2	3:K:77:GLN:HE22	1.68	0.56
3:K:297:LYS:HZ1	3:K:334:MET:HB2	1.69	0.56
3:N:438:LYS:HB3	3:N:623:TYR:HB3	1.87	0.56
1:O:36:ILE:HD12	1:O:69:LEU:HD13	1.87	0.56
1:R:336:GLU:OE1	1:R:336:GLU:N	2.38	0.56
3:A:237:ALA:O	3:A:245:SER:OG	2.21	0.56
3:A:492:PHE:HB2	3:A:667:MET:HE1	1.87	0.56
3:D:77:GLN:OE1	3:D:77:GLN:N	2.39	0.56
3:J:181:GLU:OE1	3:J:181:GLU:N	2.38	0.56
3:L:92:MET:HE1	3:L:103:VAL:HG23	1.87	0.56
3:N:285:ARG:HH12	3:N:288:HIS:HA	1.69	0.56
2:F:100:ASP:O	2:F:103:GLN:NE2	2.38	0.56
3:N:498:PHE:HB2	3:N:517:PHE:HB2	1.87	0.56
2:C:88:LEU:HA	2:C:91:ARG:HD3	1.88	0.56
3:A:698:LEU:HD13	3:A:701:LEU:HD23	1.88	0.56
2:B:124:GLU:HG3	2:B:128:LYS:HZ2	1.69	0.56
3:D:99:HIS:HB2	3:D:101:PRO:HD2	1.88	0.56
3:D:165:GLN:O	3:D:169:THR:HG23	2.05	0.56
2:G:152:LYS:NZ	2:F:147:GLN:OE1	2.39	0.56
3:L:197:PHE:HA	3:L:200:ILE:HG22	1.86	0.56
3:N:343:LEU:HD13	3:N:447:ILE:HD12	1.87	0.56
3:D:181:GLU:N	3:D:181:GLU:OE1	2.38	0.56
3:D:340:ILE:HG21	3:D:350:ARG:HG2	1.86	0.56
3:D:498:PHE:HB2	3:D:517:PHE:CG	2.41	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:90:ARG:O	2:F:93:GLN:NE2	2.39	0.56
3:L:181:GLU:N	3:L:181:GLU:OE1	2.39	0.56
3:L:612:LEU:HD23	3:L:615:LYS:HZ3	1.71	0.56
3:K:53:VAL:HG23	3:K:61:VAL:HB	1.88	0.56
3:K:181:GLU:OE1	3:K:181:GLU:N	2.38	0.56
3:K:273:GLU:OE2	3:K:275:SER:OG	2.21	0.56
1:P:192:MET:HG2	1:P:211:VAL:HG21	1.88	0.56
3:D:81:MET:HE3	3:D:82:ASN:HB2	1.86	0.56
3:D:707:LEU:HA	3:D:710:ILE:HG12	1.87	0.56
3:J:269:THR:HG21	3:J:440:PHE:HE2	1.70	0.56
3:K:476:SER:OG	3:K:477:LEU:N	2.39	0.56
3:N:279:PHE:HA	3:N:319:GLN:HE21	1.70	0.56
3:A:45:LYS:HD2	3:A:46:GLU:HG2	1.85	0.56
2:G:175:GLU:O	2:G:178:ARG:HD3	2.06	0.56
2:F:192:ASP:O	2:F:195:GLU:HG3	2.05	0.56
3:K:289:ILE:O	3:K:293:ILE:HG12	2.06	0.56
3:N:56:ARG:NH2	3:N:60:LYS:O	2.39	0.56
3:A:8:MET:O	3:A:19:ARG:NH2	2.39	0.56
3:A:266:ASP:HB3	3:A:448:ASN:HD21	1.71	0.56
3:A:319:GLN:N	3:A:319:GLN:OE1	2.39	0.56
2:B:56:GLU:HA	2:B:59:LYS:HG2	1.87	0.56
3:D:695:GLU:HA	3:D:698:LEU:HD12	1.88	0.56
3:L:77:GLN:OE1	3:L:77:GLN:N	2.38	0.56
3:L:376:GLN:NE2	3:L:404:CYS:O	2.39	0.56
1:P:197:GLU:HB2	1:R:115:LYS:HG3	1.87	0.56
3:D:733:LEU:HG	3:D:757:ILE:HG23	1.88	0.56
3:L:179:THR:OG1	3:L:704:ASN:ND2	2.39	0.56
3:N:88:LYS:O	3:N:110:ARG:NH1	2.39	0.56
3:N:181:GLU:OE1	3:N:181:GLU:N	2.39	0.56
3:N:684:ASN:ND2	3:N:688:THR:O	2.39	0.56
3:D:134:PRO:HB2	3:D:137:ASN:HD21	1.71	0.55
3:D:234:PHE:CD1	3:D:289:ILE:HG13	2.40	0.55
2:G:148:LEU:HA	2:F:147:GLN:HE22	1.71	0.55
3:J:369:LYS:HD2	3:J:380:ASP:HB3	1.88	0.55
3:K:359:ALA:HB2	3:K:392:GLN:HE22	1.71	0.55
3:D:536:SER:O	3:D:540:GLU:HG2	2.06	0.55
3:L:90:GLU:OE1	3:L:110:ARG:NH2	2.39	0.55
1:H:107:LEU:HD11	1:H:125:MET:HE3	1.87	0.55
1:Q:192:MET:HG3	1:Q:211:VAL:HG11	1.88	0.55
1:Q:216:GLU:HG2	4:Q:401:ADP:C5	2.41	0.55
1:R:255:GLU:OE1	1:R:255:GLU:N	2.32	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:D:781:LEU:HA	3:D:784:MET:HG2	1.87	0.55
2:G:99:LEU:HG	2:G:103:GLN:HE22	1.71	0.55
2:G:140:LYS:O	2:G:144:GLN:NE2	2.40	0.55
2:F:104:GLU:O	2:F:108:THR:HG23	2.06	0.55
3:J:234:PHE:CD1	3:J:289:ILE:HG13	2.39	0.55
3:J:291:TYR:HE1	3:J:322:ILE:HG22	1.72	0.55
3:L:681:ILE:HG21	3:L:697:VAL:HG23	1.88	0.55
1:E:352:SER:H	3:A:540:GLU:CD	2.15	0.55
1:O:153:ILE:HG22	1:O:166:PRO:HB3	1.87	0.55
1:Q:10:LEU:HD13	1:Q:103:HIS:HB3	1.89	0.55
3:A:550:THR:HG22	3:A:554:ASN:HD21	1.72	0.55
2:B:86:ALA:HB1	2:B:90:ARG:NH1	2.20	0.55
2:F:168:LYS:O	2:F:172:LEU:HG	2.05	0.55
3:J:681:ILE:HG21	3:J:697:VAL:HG13	1.87	0.55
1:H:306:THR:O	1:H:337:ARG:NH1	2.39	0.55
2:G:103:GLN:NE2	2:F:98:GLU:OE2	2.39	0.55
2:G:134:ALA:O	2:G:138:GLU:HG2	2.07	0.55
3:J:188:VAL:O	3:J:191:LYS:HG2	2.07	0.55
3:J:479:GLN:O	3:J:483:ASN:ND2	2.39	0.55
3:K:248:PHE:HB3	3:K:272:LEU:HD13	1.89	0.55
3:K:380:ASP:OD1	3:K:380:ASP:N	2.39	0.55
3:A:123:PHE:HE1	3:A:679:ARG:HH21	1.54	0.55
3:A:289:ILE:O	3:A:293:ILE:HG12	2.07	0.55
3:A:498:PHE:HB2	3:A:517:PHE:HB2	1.89	0.55
3:J:343:LEU:HD13	3:J:447:ILE:HD12	1.89	0.55
3:L:761:HIS:HA	3:L:764:TYR:CE1	2.42	0.55
3:K:164:TYR:O	3:K:167:MET:HG2	2.06	0.55
3:N:476:SER:OG	3:N:477:LEU:N	2.39	0.55
3:N:524:CYS:SG	3:N:585:HIS:ND1	2.75	0.55
3:N:582:SER:HA	3:N:591:ASP:HA	1.89	0.55
1:R:78:ILE:HD13	1:R:84:MET:HG2	1.88	0.55
3:A:719:SER:HB2	3:A:773:PHE:HB2	1.88	0.55
3:J:720:ARG:HG3	3:J:772:PHE:CD1	2.41	0.55
3:A:184:ALA:HB1	3:A:682:ILE:HD11	1.89	0.55
3:A:279:PHE:HA	3:A:319:GLN:HE21	1.71	0.55
3:A:778:LEU:O	3:A:782:GLU:N	2.35	0.55
3:L:155:HIS:O	3:L:158:SER:OG	2.18	0.55
3:N:104:LEU:HD11	3:N:694:HIS:HD2	1.70	0.55
3:N:346:THR:OG1	3:N:348:ASP:OD1	2.18	0.55
3:A:322:ILE:HG13	3:A:323:THR:H	1.72	0.55
3:K:232:GLU:O	3:K:236:ASN:HB2	2.06	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:403:LEU:HD22	3:A:609:VAL:HG11	1.89	0.55
3:D:173:ASN:OD1	3:D:460:PHE:N	2.34	0.55
3:D:503:GLU:OE1	3:D:503:GLU:N	2.40	0.55
3:L:536:SER:O	3:L:540:GLU:HG2	2.06	0.55
3:K:319:GLN:OE1	3:K:319:GLN:N	2.40	0.55
3:N:263:ALA:O	3:N:457:ARG:NH2	2.40	0.55
3:N:469:PHE:HB3	3:N:703:CYS:HA	1.89	0.55
3:A:254:ILE:HB	3:A:461:ILE:HG22	1.89	0.54
3:D:119:TYR:OH	3:D:158:SER:OG	2.25	0.54
3:D:254:ILE:HB	3:D:461:ILE:HG22	1.88	0.54
3:D:586:TYR:HD2	3:D:708:GLU:HG3	1.72	0.54
3:J:712:ILE:HD12	3:J:715:LYS:HE3	1.88	0.54
3:K:191:LYS:HA	3:K:194:ILE:HG22	1.88	0.54
1:O:157:SER:HB2	1:O:162:THR:HG23	1.87	0.54
1:Q:107:LEU:HD11	1:Q:125:MET:HE3	1.89	0.54
3:J:502:GLN:NE2	3:J:512:TRP:O	2.33	0.54
3:N:348:ASP:HA	3:N:351:VAL:HG12	1.89	0.54
1:O:113:ASN:OD1	1:O:179:ARG:NH1	2.31	0.54
3:A:234:PHE:O	3:A:436:TYR:OH	2.24	0.54
3:A:536:SER:O	3:A:540:GLU:HG2	2.07	0.54
3:J:81:MET:HE3	3:J:82:ASN:HB2	1.88	0.54
3:L:548:THR:HG23	3:L:551:SER:H	1.72	0.54
3:L:576:LYS:HZ2	3:L:578:GLU:H	1.56	0.54
3:N:248:PHE:HB3	3:N:272:LEU:HD13	1.89	0.54
3:N:614:GLN:NE2	3:N:626:SER:O	2.40	0.54
2:G:181:GLU:O	2:G:184:GLU:HG2	2.07	0.54
3:L:37:SER:HA	3:L:53:VAL:HG12	1.88	0.54
3:L:120:SER:HB2	3:L:123:PHE:HB2	1.89	0.54
3:L:165:GLN:O	3:L:169:THR:HG23	2.07	0.54
3:K:89:ILE:HG22	3:K:91:ASP:H	1.72	0.54
3:N:681:ILE:HG21	3:N:697:VAL:HG13	1.90	0.54
1:O:359:ILE:HG12	1:O:376:CYS:HB3	1.88	0.54
1:P:10:LEU:HD13	1:P:103:HIS:HB3	1.88	0.54
3:J:33:PHE:CD1	3:J:84:PRO:HD3	2.42	0.54
3:J:92:MET:HG2	3:J:103:VAL:HG23	1.89	0.54
3:J:359:ALA:HB2	3:J:392:GLN:HE22	1.72	0.54
3:L:576:LYS:NZ	3:L:578:GLU:O	2.41	0.54
3:N:722:LEU:HG	3:N:770:LYS:HE2	1.90	0.54
1:Q:8:THR:H	3:L:646:LYS:NZ	2.04	0.54
3:A:701:LEU:HD11	3:A:707:LEU:HB3	1.89	0.54
2:F:45:ALA:N	2:F:47:GLN:OE1	2.41	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:J:494:ASN:ND2	3:J:517:PHE:O	2.41	0.54
3:J:610:VAL:HG13	3:J:624:LEU:HD23	1.90	0.54
3:J:707:LEU:HA	3:J:710:ILE:HG12	1.88	0.54
3:A:232:GLU:O	3:A:236:ASN:HB2	2.08	0.54
3:J:134:PRO:O	3:J:137:ASN:ND2	2.40	0.54
3:L:503:GLU:OE1	3:L:503:GLU:N	2.40	0.54
3:N:479:GLN:O	3:N:483:ASN:ND2	2.41	0.54
1:Q:204:THR:HG22	1:Q:206:ALA:H	1.73	0.54
1:P:107:LEU:HD11	1:P:125:MET:HE3	1.90	0.54
3:A:195:GLN:O	3:A:199:THR:HG23	2.08	0.54
3:A:376:GLN:NE2	3:A:404:CYS:O	2.41	0.54
2:B:104:GLU:O	2:B:108:THR:HG23	2.08	0.54
3:D:140:VAL:HA	3:D:143:ALA:HB3	1.89	0.54
3:D:195:GLN:O	3:D:199:THR:HG23	2.08	0.54
3:D:494:ASN:ND2	3:D:517:PHE:O	2.41	0.54
2:G:172:LEU:HD22	2:F:169:LEU:HD23	1.90	0.54
3:K:234:PHE:HD1	3:K:289:ILE:HG13	1.73	0.54
2:C:104:GLU:O	2:C:108:THR:HG23	2.08	0.54
3:J:290:PHE:O	3:J:294:MET:HG2	2.08	0.54
3:L:60:LYS:HA	3:L:72:THR:HG23	1.90	0.54
3:L:175:SER:N	3:L:674:HIS:O	2.41	0.54
3:K:21:SER:HA	3:K:25:ARG:HH21	1.73	0.54
3:N:576:LYS:NZ	3:N:578:GLU:O	2.40	0.54
1:O:148:GLY:C	3:J:545:PRO:HB3	2.33	0.54
3:A:179:THR:OG1	3:A:679:ARG:NH1	2.41	0.54
3:D:273:GLU:OE1	3:D:276:ARG:HG2	2.08	0.54
2:F:147:GLN:HA	2:F:150:GLU:HG3	1.88	0.54
3:K:238:LYS:NZ	3:K:321:GLU:HB2	2.23	0.54
3:K:618:MET:HG2	3:K:619:LYS:H	1.73	0.54
1:H:123:GLN:O	1:H:127:GLU:HG2	2.07	0.53
1:R:203:VAL:N	1:R:207:GLU:OE2	2.32	0.53
3:A:251:PHE:HB2	3:A:464:LEU:HD12	1.89	0.53
2:F:47:GLN:H	2:F:47:GLN:CD	2.15	0.53
2:F:196:GLU:HA	2:F:199:ILE:HD12	1.89	0.53
3:J:114:TRP:HZ3	3:J:689:PRO:HB2	1.72	0.53
3:K:39:VAL:HA	3:K:80:PRO:HA	1.90	0.53
3:K:175:SER:O	3:K:676:HIS:N	2.40	0.53
3:N:479:GLN:OE1	3:N:479:GLN:N	2.36	0.53
3:N:761:HIS:HA	3:N:764:TYR:CE1	2.43	0.53
1:E:204:THR:HG22	1:E:206:ALA:H	1.72	0.53
3:J:240:VAL:HG12	3:J:283:ALA:HB3	1.89	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:J:363:TYR:HH	3:J:613:TYR:HH	1.52	0.53
3:J:403:LEU:HD22	3:J:609:VAL:HG11	1.90	0.53
3:N:294:MET:HG3	3:N:311:PRO:HB3	1.90	0.53
3:N:334:MET:HE3	3:N:337:ASP:HB3	1.90	0.53
1:Q:123:GLN:O	1:Q:127:GLU:HG2	2.09	0.53
2:C:148:LEU:HA	2:B:147:GLN:HE22	1.73	0.53
3:A:251:PHE:HD1	3:A:464:LEU:HB2	1.73	0.53
3:D:701:LEU:HD11	3:D:707:LEU:HB3	1.90	0.53
2:F:102:ALA:HA	2:F:105:ARG:NE	2.23	0.53
3:L:145:ARG:NH1	3:L:161:ASP:OD1	2.38	0.53
3:K:278:THR:O	3:K:319:GLN:NE2	2.42	0.53
3:N:297:LYS:HZ1	3:N:334:MET:HB3	1.74	0.53
1:E:192:MET:HG3	1:E:211:VAL:HG11	1.90	0.53
3:A:393:ASN:ND2	3:A:618:MET:SD	2.82	0.53
3:D:612:LEU:HD23	3:D:615:LYS:HZ3	1.74	0.53
2:G:175:GLU:HG3	2:F:176:LEU:HD11	1.90	0.53
3:L:164:TYR:O	3:L:167:MET:HG2	2.08	0.53
3:K:188:VAL:O	3:K:191:LYS:HG2	2.08	0.53
3:N:290:PHE:O	3:N:294:MET:HG2	2.08	0.53
2:C:107:ALA:HA	2:C:110:LEU:HD12	1.89	0.53
3:A:623:TYR:HB2	3:A:624:LEU:HD12	1.91	0.53
3:A:685:GLU:H	3:A:685:GLU:CD	2.17	0.53
3:N:241:ARG:HH21	3:N:242:ASN:ND2	2.05	0.53
1:H:8:THR:H	3:D:646:LYS:NZ	2.07	0.53
1:O:178:MET:HG3	1:O:283:SER:HB2	1.91	0.53
2:B:75:GLU:O	2:B:79:THR:HG23	2.09	0.53
3:J:269:THR:HG21	3:J:440:PHE:CE2	2.43	0.53
3:N:297:LYS:HZ1	3:N:334:MET:CB	2.22	0.53
3:N:700:GLN:HA	3:N:703:CYS:SG	2.49	0.53
1:E:314:ARG:NE	1:E:318:GLU:OE2	2.31	0.53
1:H:336:GLU:OE1	1:H:336:GLU:N	2.32	0.53
2:C:93:GLN:O	2:C:97:GLU:HG2	2.08	0.53
2:C:111:GLN:HA	2:C:114:GLU:HG2	1.90	0.53
3:A:88:LYS:O	3:A:110:ARG:NH1	2.41	0.53
2:B:129:VAL:HA	2:B:132:ASN:HD22	1.73	0.53
3:D:162:ASN:HA	3:D:165:GLN:HE21	1.72	0.53
3:D:757:ILE:HG22	3:D:784:MET:HE2	1.90	0.53
3:J:37:SER:HA	3:J:53:VAL:HG12	1.89	0.53
1:O:192:MET:HG3	1:O:211:VAL:HG11	1.90	0.53
3:A:148:LYS:HD2	3:A:150:GLN:H	1.72	0.53
2:F:121:ASP:O	2:F:125:ARG:HG3	2.08	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:J:195:GLN:O	3:J:199:THR:HG23	2.09	0.53
3:L:442:TRP:HB3	3:L:623:TYR:HE1	1.73	0.53
1:H:192:MET:HG3	1:H:211:VAL:HG11	1.90	0.53
1:Q:101:GLU:N	1:Q:101:GLU:OE2	2.40	0.53
1:Q:336:GLU:OE1	1:Q:336:GLU:N	2.38	0.53
3:A:610:VAL:HG13	3:A:624:LEU:HD23	1.90	0.53
3:A:766:PHE:HA	3:A:771:VAL:HA	1.90	0.53
2:B:171:ILE:HG13	2:B:172:LEU:HD23	1.91	0.53
3:D:164:TYR:O	3:D:167:MET:HG2	2.09	0.53
3:D:186:LYS:HD3	3:D:189:ASN:HD22	1.74	0.53
2:G:136:LYS:HB3	2:G:140:LYS:HE2	1.91	0.53
3:L:85:LYS:HG3	3:L:86:TYR:CD1	2.44	0.53
3:L:88:LYS:O	3:L:110:ARG:NH1	2.41	0.53
3:L:101:PRO:HA	3:L:104:LEU:HB3	1.89	0.53
3:L:134:PRO:O	3:L:137:ASN:ND2	2.42	0.53
3:L:266:ASP:HB3	3:L:448:ASN:HD21	1.72	0.53
3:K:502:GLN:NE2	3:K:512:TRP:O	2.31	0.53
3:K:599:ASP:N	3:K:599:ASP:OD1	2.39	0.53
1:O:216:GLU:HG2	4:O:401:ADP:C5	2.44	0.53
2:C:121:ASP:HA	2:C:124:GLU:HG2	1.91	0.53
2:C:144:GLN:HB3	2:B:144:GLN:CD	2.33	0.53
1:R:192:MET:HG3	1:R:211:VAL:HG11	1.91	0.53
1:R:229:MET:SD	1:R:254:ASN:ND2	2.82	0.53
3:A:256:PHE:O	3:A:458:GLN:N	2.38	0.53
2:B:61:SER:O	2:B:65:LYS:HG2	2.09	0.53
3:D:256:PHE:O	3:D:458:GLN:N	2.42	0.53
3:D:701:LEU:HG	3:D:707:LEU:HD23	1.90	0.53
3:J:40:PHE:HB2	3:J:79:PHE:HB2	1.90	0.53
3:J:179:THR:OG1	3:J:704:ASN:ND2	2.41	0.53
3:J:222:ASP:OD1	3:J:223:GLN:N	2.42	0.53
3:L:582:SER:HB3	3:L:591:ASP:HB3	1.91	0.53
3:K:65:THR:H	3:K:69:ALA:H	1.56	0.53
3:K:237:ALA:O	3:K:245:SER:OG	2.27	0.53
3:N:359:ALA:HB2	3:N:392:GLN:HE22	1.74	0.53
3:N:365:ASN:HB2	3:N:384:VAL:HG21	1.90	0.53
3:N:502:GLN:NE2	3:N:513:GLU:O	2.42	0.53
3:A:62:THR:HG23	3:A:64:LYS:HZ3	1.74	0.52
3:A:482:ILE:O	3:A:485:THR:OG1	2.24	0.52
2:B:137:ASP:HA	2:B:140:LYS:HD2	1.90	0.52
2:B:196:GLU:O	2:B:200:VAL:HG23	2.09	0.52
3:D:344:GLY:O	3:D:446:ARG:NH2	2.41	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:G:144:GLN:HG2	2:F:141:MET:HG2	1.91	0.52
2:F:61:SER:O	2:F:65:LYS:HG2	2.08	0.52
3:J:438:LYS:HB3	3:J:623:TYR:HB3	1.90	0.52
3:L:273:GLU:OE2	3:L:275:SER:OG	2.27	0.52
3:K:147:LYS:O	3:K:165:GLN:NE2	2.27	0.52
3:K:166:PHE:O	3:K:169:THR:OG1	2.24	0.52
3:K:483:ASN:O	3:K:487:GLU:HG2	2.09	0.52
3:K:778:LEU:O	3:K:782:GLU:N	2.33	0.52
3:N:118:THR:HG22	3:N:119:TYR:H	1.73	0.52
3:N:195:GLN:O	3:N:199:THR:HG23	2.10	0.52
1:E:123:GLN:O	1:E:127:GLU:HG2	2.09	0.52
1:O:123:GLN:O	1:O:127:GLU:HG2	2.09	0.52
3:D:685:GLU:CD	3:D:685:GLU:H	2.16	0.52
2:F:127:MET:O	2:F:131:GLU:HG2	2.09	0.52
3:L:700:GLN:HA	3:L:703:CYS:SG	2.49	0.52
3:K:197:PHE:HA	3:K:200:ILE:HG22	1.91	0.52
3:N:289:ILE:O	3:N:293:ILE:HG12	2.09	0.52
1:O:203:VAL:N	1:O:207:GLU:OE2	2.33	0.52
1:Q:290:ASP:OD2	1:R:64:ARG:NE	2.42	0.52
2:C:64:VAL:HG13	2:B:64:VAL:HG22	1.91	0.52
3:A:114:TRP:HZ3	3:A:689:PRO:HB2	1.75	0.52
3:L:195:GLN:O	3:L:199:THR:HG23	2.10	0.52
3:K:118:THR:HG22	3:K:119:TYR:H	1.74	0.52
3:K:234:PHE:O	3:K:436:TYR:OH	2.27	0.52
3:K:439:MET:HA	3:K:623:TYR:CE1	2.44	0.52
3:N:65:THR:H	3:N:69:ALA:H	1.57	0.52
3:N:234:PHE:CD1	3:N:289:ILE:HG13	2.44	0.52
2:B:158:SER:HA	2:B:161:LYS:HG2	1.91	0.52
3:D:485:THR:HG22	3:D:663:LEU:HD12	1.91	0.52
3:L:90:GLU:OE2	3:L:110:ARG:NH1	2.42	0.52
3:K:379:PRO:HG3	3:K:400:LEU:HD13	1.91	0.52
3:N:166:PHE:O	3:N:169:THR:OG1	2.23	0.52
3:N:222:ASP:OD1	3:N:223:GLN:N	2.42	0.52
3:N:232:GLU:O	3:N:236:ASN:HB2	2.09	0.52
3:N:553:LYS:HE2	3:N:557:TYR:CZ	2.44	0.52
1:Q:288:ASP:OD2	1:R:41:ARG:NH2	2.42	0.52
3:K:297:LYS:HZ1	3:K:334:MET:CB	2.22	0.52
3:K:573:ALA:O	3:K:574:LYS:HG2	2.10	0.52
3:N:175:SER:O	3:N:676:HIS:N	2.43	0.52
1:R:153:ILE:HD13	1:R:284:ILE:HD11	1.92	0.52
2:B:81:ALA:O	2:B:85:VAL:HG12	2.10	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:D:234:PHE:O	3:D:436:TYR:OH	2.26	0.52
3:D:319:GLN:N	3:D:319:GLN:OE1	2.42	0.52
3:J:84:PRO:HA	3:J:87:ASP:HB2	1.91	0.52
3:J:145:ARG:NH1	3:J:161:ASP:OD1	2.37	0.52
3:L:174:GLN:HG3	3:L:674:HIS:HB3	1.92	0.52
3:N:176:ILE:N	3:N:462:GLY:O	2.40	0.52
3:A:83:PRO:HG2	3:A:86:TYR:HB2	1.92	0.52
3:D:510:ILE:HG12	3:D:765:LYS:HG2	1.92	0.52
2:F:198:LYS:O	2:F:202:ASN:ND2	2.43	0.52
3:J:120:SER:HB2	3:J:123:PHE:HB2	1.92	0.52
3:N:766:PHE:HA	3:N:771:VAL:HA	1.91	0.52
1:E:7:THR:OG1	1:E:8:THR:N	2.41	0.52
1:O:306:THR:O	1:O:337:ARG:NH1	2.42	0.52
1:Q:113:ASN:OD1	1:Q:179:ARG:NH1	2.31	0.52
1:Q:359:ILE:HG12	1:Q:376:CYS:HB3	1.90	0.52
2:C:182:ARG:NH1	2:B:179:SER:OG	2.39	0.52
2:C:182:ARG:HA	2:C:185:VAL:HG22	1.91	0.52
1:P:203:VAL:N	1:P:207:GLU:OE2	2.34	0.52
3:A:145:ARG:NH1	3:A:161:ASP:OD1	2.39	0.52
3:A:679:ARG:HD2	3:A:704:ASN:HB3	1.92	0.52
3:J:235:GLY:C	3:J:236:ASN:HD22	2.17	0.52
3:L:118:THR:HB	3:L:125:VAL:HG13	1.92	0.52
3:L:469:PHE:HB3	3:L:703:CYS:HA	1.92	0.52
3:K:717:PHE:O	3:K:720:ARG:NH1	2.33	0.52
3:K:731:LYS:HG3	3:K:735:ALA:HA	1.91	0.52
1:E:36:ILE:HD12	1:E:69:LEU:HD13	1.91	0.52
1:O:302:SER:O	1:O:306:THR:OG1	2.21	0.52
1:P:336:GLU:OE1	1:P:336:GLU:N	2.39	0.52
1:P:371:ILE:HD12	1:P:374:ARG:HH11	1.74	0.52
3:A:269:THR:HG21	3:A:440:PHE:CE2	2.44	0.52
2:B:196:GLU:HA	2:B:199:ILE:HD12	1.92	0.52
2:G:93:GLN:O	2:G:97:GLU:HG2	2.10	0.52
2:F:138:GLU:HA	2:F:141:MET:HE3	1.92	0.52
3:J:231:LEU:HD23	3:J:443:MET:HE1	1.91	0.52
3:L:711:ARG:O	3:L:714:ARG:HG2	2.10	0.52
3:K:21:SER:N	3:K:24:GLU:OE2	2.43	0.52
3:N:439:MET:HA	3:N:623:TYR:CE1	2.45	0.52
3:N:573:ALA:O	3:N:574:LYS:HG2	2.10	0.52
1:Q:8:THR:HG21	3:L:646:LYS:H	1.75	0.52
1:Q:229:MET:SD	1:Q:254:ASN:ND2	2.75	0.52
3:A:747:LYS:O	3:A:750:SER:OG	2.23	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:147:GLN:HA	2:B:150:GLU:HG3	1.92	0.52
2:G:106:LEU:HD13	2:F:105:ARG:HE	1.75	0.52
3:J:322:ILE:HG13	3:J:323:THR:H	1.75	0.52
3:L:94:MET:HE1	3:L:720:ARG:HB2	1.92	0.52
3:L:291:TYR:CE1	3:L:322:ILE:HG22	2.43	0.52
3:K:458:GLN:HG2	3:K:459:TYR:H	1.75	0.52
1:Q:157:SER:HB2	1:Q:162:THR:HG23	1.91	0.51
3:A:134:PRO:HB2	3:A:137:ASN:HD21	1.75	0.51
3:A:297:LYS:NZ	3:A:334:MET:HB2	2.17	0.51
3:N:120:SER:HB2	3:N:123:PHE:HB2	1.91	0.51
3:A:20:LYS:HG2	3:A:115:MET:HE2	1.91	0.51
3:A:438:LYS:HB3	3:A:623:TYR:HB3	1.91	0.51
3:D:664:ASN:O	3:D:668:THR:HG22	2.11	0.51
3:J:108:LYS:NZ	3:J:692:MET:SD	2.72	0.51
3:L:348:ASP:HA	3:L:351:VAL:HG12	1.92	0.51
3:K:765:LYS:O	3:K:772:PHE:N	2.30	0.51
1:P:352:SER:N	3:K:540:GLU:OE2	2.41	0.51
2:B:54:GLU:O	2:B:58:GLU:HG2	2.10	0.51
2:G:106:LEU:HD13	2:F:105:ARG:NE	2.24	0.51
2:F:107:ALA:HA	2:F:110:LEU:HD12	1.92	0.51
3:J:176:ILE:N	3:J:462:GLY:O	2.36	0.51
3:L:65:THR:HG22	3:L:69:ALA:H	1.76	0.51
3:L:96:THR:OG1	3:L:775:ALA:O	2.17	0.51
3:N:17:TYR:CE2	3:N:135:VAL:HG12	2.45	0.51
2:C:147:GLN:NE2	2:B:144:GLN:HG3	2.25	0.51
1:P:216:GLU:HG2	4:P:401:ADP:C5	2.46	0.51
1:R:216:GLU:HG2	4:R:401:ADP:C5	2.44	0.51
3:A:192:ARG:HH11	3:A:195:GLN:HE22	1.57	0.51
3:D:145:ARG:HD2	3:D:146:GLY:H	1.76	0.51
3:D:241:ARG:HE	3:D:242:ASN:HB3	1.75	0.51
3:D:289:ILE:O	3:D:293:ILE:HG12	2.11	0.51
3:D:300:ASP:OD1	3:D:301:LEU:N	2.42	0.51
2:G:122:GLU:O	2:G:125:ARG:HD3	2.11	0.51
3:J:170:ASP:N	3:J:170:ASP:OD1	2.43	0.51
3:J:553:LYS:HE2	3:J:557:TYR:CZ	2.45	0.51
3:J:763:GLN:HA	3:J:774:LYS:HE2	1.92	0.51
3:L:184:ALA:HB1	3:L:682:ILE:HD11	1.91	0.51
3:L:273:GLU:OE1	3:L:276:ARG:HG2	2.10	0.51
3:L:292:GLN:O	3:L:333:LEU:HD11	2.11	0.51
3:L:618:MET:HB2	3:L:620:THR:HG23	1.92	0.51
3:L:678:VAL:O	3:L:679:ARG:NH1	2.43	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:K:91:ASP:OD1	3:K:92:MET:N	2.43	0.51
3:N:171:ARG:HG3	3:N:459:TYR:CE1	2.45	0.51
3:N:503:GLU:N	3:N:503:GLU:OE1	2.44	0.51
3:N:707:LEU:HA	3:N:710:ILE:HG12	1.92	0.51
3:A:82:ASN:ND2	3:A:95:MET:SD	2.83	0.51
3:D:747:LYS:O	3:D:750:SER:OG	2.22	0.51
3:J:499:VAL:HG13	3:J:500:LEU:HD12	1.91	0.51
3:L:722:LEU:HG	3:L:770:LYS:HE2	1.92	0.51
3:K:20:LYS:HB3	3:K:24:GLU:HG3	1.91	0.51
3:K:33:PHE:CD1	3:K:84:PRO:HD3	2.45	0.51
3:K:171:ARG:HG3	3:K:459:TYR:CE1	2.46	0.51
3:N:51:ALA:HB1	3:N:63:ALA:HB1	1.92	0.51
3:N:237:ALA:O	3:N:245:SER:OG	2.29	0.51
2:B:68:GLN:HA	2:B:71:LEU:HD12	1.92	0.51
3:D:348:ASP:HA	3:D:351:VAL:HG12	1.92	0.51
2:G:144:GLN:HA	2:G:147:GLN:HG3	1.93	0.51
3:J:243:ASP:OD2	3:J:326:SER:OG	2.28	0.51
3:L:328:ASP:OD1	3:L:329:ASP:N	2.43	0.51
3:K:700:GLN:HA	3:K:703:CYS:SG	2.51	0.51
3:N:781:LEU:O	3:N:785:ARG:N	2.33	0.51
2:B:64:VAL:HG12	2:B:68:GLN:NE2	2.17	0.51
2:B:90:ARG:O	2:B:93:GLN:NE2	2.38	0.51
3:J:747:LYS:O	3:J:750:SER:OG	2.23	0.51
3:K:41:VAL:HG23	3:K:73:VAL:HG21	1.93	0.51
2:C:176:LEU:HD13	2:B:176:LEU:HG	1.92	0.51
3:D:274:LYS:HG3	3:D:433:LYS:HB3	1.93	0.51
2:G:189:LYS:NZ	2:F:187:GLU:HA	2.26	0.51
3:J:191:LYS:HA	3:J:194:ILE:HG12	1.91	0.51
3:L:322:ILE:HG13	3:L:323:THR:H	1.76	0.51
3:N:90:GLU:HA	3:N:110:ARG:HH12	1.76	0.51
1:R:36:ILE:HD12	1:R:69:LEU:HD13	1.92	0.51
3:D:40:PHE:HB2	3:D:79:PHE:HB2	1.92	0.51
3:D:524:CYS:SG	3:D:585:HIS:ND1	2.83	0.51
3:L:74:LYS:HB2	3:L:77:GLN:HE22	1.75	0.51
3:L:186:LYS:HD3	3:L:189:ASN:HD22	1.75	0.51
3:L:294:MET:HE1	3:L:309:THR:C	2.36	0.51
3:K:80:PRO:HB2	3:K:97:HIS:HE2	1.76	0.51
3:K:722:LEU:HG	3:K:770:LYS:HE2	1.93	0.51
3:A:610:VAL:HG12	3:A:614:GLN:NE2	2.26	0.51
3:D:175:SER:N	3:D:674:HIS:O	2.44	0.51
3:D:238:LYS:O	3:D:284:GLU:HB2	2.11	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:G:95:VAL:HB	2:F:95:VAL:HG11	1.93	0.51
3:J:336:THR:O	3:J:340:ILE:HG13	2.11	0.51
3:J:439:MET:HA	3:J:623:TYR:CE1	2.46	0.51
3:J:483:ASN:O	3:J:487:GLU:HG2	2.11	0.51
3:K:96:THR:HB	3:K:778:LEU:HB2	1.93	0.51
3:K:147:LYS:NZ	3:K:158:SER:HB2	2.26	0.51
3:K:482:ILE:O	3:K:485:THR:OG1	2.25	0.51
3:N:104:LEU:HD11	3:N:694:HIS:CD2	2.46	0.51
1:E:275:GLY:O	1:E:279:THR:HG23	2.11	0.50
3:A:272:LEU:HD23	3:A:437:GLU:HG2	1.92	0.50
3:D:584:VAL:HA	3:D:589:THR:HA	1.92	0.50
2:F:64:VAL:HG12	2:F:68:GLN:NE2	2.21	0.50
2:F:101:ARG:HA	2:F:104:GLU:HG3	1.93	0.50
3:K:105:TYR:HA	3:K:108:LYS:HB3	1.91	0.50
3:N:31:LYS:HE2	3:N:32:PRO:HD2	1.93	0.50
3:N:192:ARG:HH11	3:N:195:GLN:HE22	1.58	0.50
3:N:197:PHE:HA	3:N:200:ILE:HG22	1.94	0.50
3:N:285:ARG:HB2	3:N:291:TYR:CZ	2.46	0.50
1:P:123:GLN:O	1:P:127:GLU:HG2	2.11	0.50
3:A:300:ASP:OD1	3:A:301:LEU:N	2.44	0.50
2:G:91:ARG:O	2:G:95:VAL:HG22	2.11	0.50
2:G:126:GLY:O	2:G:130:ILE:HG23	2.11	0.50
3:J:278:THR:O	3:J:319:GLN:NE2	2.45	0.50
3:L:701:LEU:HG	3:L:707:LEU:HD22	1.93	0.50
3:L:719:SER:HB2	3:L:773:PHE:HB2	1.92	0.50
3:K:177:LEU:N	3:K:676:HIS:O	2.39	0.50
3:N:11:PHE:HE2	3:N:14:ALA:HB3	1.76	0.50
1:E:359:ILE:HG12	1:E:376:CYS:HB3	1.93	0.50
1:O:7:THR:OG1	3:J:646:LYS:NZ	2.37	0.50
3:A:101:PRO:HA	3:A:104:LEU:HB3	1.92	0.50
2:G:49:LYS:HG2	2:F:50:LEU:HD11	1.92	0.50
3:J:171:ARG:HG3	3:J:459:TYR:CE1	2.45	0.50
3:K:761:HIS:HA	3:K:764:TYR:CE1	2.47	0.50
3:N:721:ILE:HD11	3:N:773:PHE:HE2	1.76	0.50
1:E:153:ILE:HD13	1:E:284:ILE:HD11	1.93	0.50
1:P:7:THR:HA	3:K:646:LYS:HE3	1.93	0.50
1:R:234:SER:OG	1:R:235:SER:N	2.45	0.50
3:A:178:ILE:HG22	3:A:678:VAL:HB	1.94	0.50
3:A:348:ASP:HA	3:A:351:VAL:HG12	1.94	0.50
2:B:47:GLN:O	2:B:51:LYS:HG2	2.12	0.50
2:B:64:VAL:O	2:B:68:GLN:NE2	2.44	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:124:GLU:HG3	2:B:128:LYS:NZ	2.26	0.50
3:L:438:LYS:HD3	3:L:623:TYR:HB3	1.91	0.50
3:L:516:ASP:OD1	3:L:518:GLY:N	2.44	0.50
3:N:488:LYS:HB3	3:N:667:MET:HE2	1.93	0.50
3:N:733:LEU:HG	3:N:757:ILE:HG23	1.92	0.50
1:O:115:LYS:HG3	1:R:197:GLU:HB2	1.92	0.50
1:Q:306:THR:O	1:Q:337:ARG:NH1	2.44	0.50
2:C:124:GLU:HA	2:C:127:MET:HG2	1.93	0.50
2:C:144:GLN:HG2	2:B:141:MET:HG2	1.94	0.50
3:A:439:MET:HA	3:A:623:TYR:CE1	2.46	0.50
3:D:343:LEU:HG	3:D:447:ILE:HD12	1.93	0.50
3:D:765:LYS:O	3:D:772:PHE:N	2.38	0.50
3:J:197:PHE:HA	3:J:200:ILE:HG22	1.92	0.50
3:N:175:SER:N	3:N:674:HIS:O	2.45	0.50
3:N:319:GLN:OE1	3:N:319:GLN:N	2.44	0.50
1:H:10:LEU:HD13	1:H:103:HIS:HB3	1.93	0.50
1:O:290:ASP:OD2	1:P:64:ARG:NE	2.44	0.50
3:A:577:VAL:HG13	3:A:578:GLU:H	1.77	0.50
2:G:60:TYR:O	2:G:64:VAL:HG23	2.11	0.50
3:L:251:PHE:O	3:L:268:GLU:N	2.44	0.50
3:N:60:LYS:HG3	3:N:72:THR:HG23	1.94	0.50
2:B:45:ALA:HB3	2:B:47:GLN:HE22	1.77	0.50
2:B:124:GLU:O	2:B:128:LYS:HG3	2.12	0.50
2:G:179:SER:O	2:G:182:ARG:HD3	2.12	0.50
2:F:166:ALA:HA	2:F:169:LEU:HD12	1.94	0.50
3:J:527:LEU:HD21	3:J:567:PHE:HB2	1.93	0.50
3:K:174:GLN:O	3:K:462:GLY:N	2.45	0.50
3:K:176:ILE:N	3:K:462:GLY:O	2.40	0.50
3:K:270:TYR:CG	3:K:666:LEU:HD11	2.47	0.50
3:N:164:TYR:O	3:N:167:MET:HG2	2.11	0.50
1:P:148:GLY:C	3:K:545:PRO:HB3	2.37	0.50
3:A:90:GLU:OE2	3:A:110:ARG:NH1	2.45	0.50
3:D:169:THR:O	3:D:171:ARG:NH1	2.45	0.50
3:D:297:LYS:HZ1	3:D:334:MET:H	1.59	0.50
3:D:516:ASP:OD1	3:D:517:PHE:N	2.44	0.50
2:G:50:LEU:HD22	2:F:50:LEU:HD13	1.92	0.50
2:G:73:GLN:HA	2:G:76:LYS:HE2	1.94	0.50
3:J:261:LYS:HB3	3:J:455:GLN:HE22	1.77	0.50
3:L:439:MET:HA	3:L:623:TYR:CE1	2.47	0.50
3:N:238:LYS:O	3:N:284:GLU:HB2	2.12	0.50
1:O:61:GLN:NE2	1:O:64:ARG:HD3	2.27	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:O:153:ILE:HD13	1:O:284:ILE:HD11	1.93	0.50
3:A:188:VAL:HG13	3:A:191:LYS:HE3	1.93	0.50
3:A:710:ILE:O	3:A:714:ARG:HB3	2.12	0.50
3:D:722:LEU:HD23	3:D:770:LYS:HG2	1.93	0.50
3:D:723:TYR:HA	3:D:726:PHE:HB3	1.94	0.50
3:J:233:ALA:HB2	3:J:336:THR:HG21	1.94	0.50
3:N:271:LEU:HA	3:N:662:ASN:HD21	1.77	0.50
1:Q:8:THR:H	3:L:646:LYS:HZ3	1.58	0.49
3:A:140:VAL:HA	3:A:143:ALA:HB3	1.94	0.49
3:D:778:LEU:HA	3:D:781:LEU:HD12	1.93	0.49
3:J:79:PHE:HD2	3:J:99:HIS:HB3	1.76	0.49
3:J:147:LYS:NZ	3:J:158:SER:HB2	2.26	0.49
3:J:667:MET:HB3	3:J:671:ARG:HH12	1.77	0.49
3:J:701:LEU:HD11	3:J:707:LEU:HB3	1.94	0.49
3:L:685:GLU:CD	3:L:685:GLU:H	2.18	0.49
3:K:293:ILE:HD12	3:K:301:LEU:HD13	1.94	0.49
3:N:234:PHE:O	3:N:436:TYR:OH	2.29	0.49
3:N:234:PHE:CE2	3:N:443:MET:HG3	2.47	0.49
3:N:266:ASP:HB3	3:N:448:ASN:HD21	1.77	0.49
3:N:468:GLY:N	3:N:470:GLU:OE2	2.44	0.49
1:O:10:LEU:HB2	1:O:105:THR:HG22	1.94	0.49
3:D:148:LYS:HE3	3:D:151:GLU:HB3	1.93	0.49
2:F:196:GLU:O	2:F:200:VAL:HG23	2.12	0.49
3:J:507:LYS:HD2	3:J:508:GLU:HG2	1.94	0.49
3:L:254:ILE:HB	3:L:461:ILE:HG22	1.94	0.49
3:L:443:MET:O	3:L:447:ILE:HG12	2.12	0.49
3:L:573:ALA:O	3:L:574:LYS:HG2	2.11	0.49
3:K:88:LYS:O	3:K:110:ARG:NH1	2.39	0.49
3:N:251:PHE:O	3:N:268:GLU:N	2.38	0.49
3:N:264:SER:HB3	3:N:457:ARG:HE	1.76	0.49
3:N:610:VAL:HG12	3:N:614:GLN:HE21	1.77	0.49
1:H:8:THR:OG1	3:D:646:LYS:NZ	2.27	0.49
1:Q:148:GLY:C	3:L:545:PRO:HB3	2.38	0.49
2:C:136:LYS:HB3	2:C:140:LYS:HE2	1.93	0.49
1:P:308:TYR:CE1	4:P:401:ADP:H2	2.30	0.49
3:A:343:LEU:HD13	3:A:447:ILE:HD12	1.92	0.49
3:D:322:ILE:HG13	3:D:323:THR:H	1.77	0.49
2:G:101:ARG:HA	2:G:104:GLU:CD	2.37	0.49
2:F:96:GLU:O	2:F:99:LEU:HG	2.11	0.49
2:F:159:ASP:O	2:F:163:GLU:HG2	2.12	0.49
3:L:610:VAL:HG13	3:L:624:LEU:HD23	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:L:648:LYS:HB3	3:L:652:PHE:HB2	1.94	0.49
2:C:108:THR:HA	2:C:111:GLN:HE21	1.78	0.49
1:R:148:GLY:C	3:N:545:PRO:HB3	2.38	0.49
1:R:217:LYS:HD2	1:R:242:TYR:HE1	1.77	0.49
3:D:179:THR:OG1	3:D:704:ASN:ND2	2.44	0.49
3:D:269:THR:HG21	3:D:440:PHE:HE2	1.77	0.49
3:D:711:ARG:HA	3:D:714:ARG:HB3	1.94	0.49
2:G:165:VAL:HG12	2:G:168:LYS:HE2	1.95	0.49
3:L:289:ILE:O	3:L:293:ILE:HG12	2.12	0.49
3:K:8:MET:O	3:K:19:ARG:NH2	2.39	0.49
3:K:290:PHE:O	3:K:294:MET:HG2	2.12	0.49
3:N:82:ASN:HD21	3:N:102:ALA:HB1	1.76	0.49
3:N:173:ASN:OD1	3:N:460:PHE:N	2.35	0.49
3:A:164:TYR:O	3:A:167:MET:HG2	2.12	0.49
2:G:56:GLU:HA	2:G:59:LYS:HE3	1.94	0.49
2:G:157:ASP:O	2:G:160:ARG:HD3	2.12	0.49
2:F:58:GLU:O	2:F:61:SER:OG	2.29	0.49
2:F:82:GLU:HA	2:F:85:VAL:HG12	1.95	0.49
2:F:181:GLU:O	2:F:185:VAL:HG23	2.12	0.49
3:J:516:ASP:HB3	3:J:519:MET:HG2	1.95	0.49
3:K:99:HIS:HB3	3:K:101:PRO:HD2	1.93	0.49
3:N:718:PRO:HD2	3:N:774:LYS:HA	1.93	0.49
3:N:720:ARG:HG3	3:N:772:PHE:CD1	2.47	0.49
1:H:203:VAL:N	1:H:207:GLU:OE2	2.27	0.49
1:P:234:SER:OG	1:P:235:SER:N	2.45	0.49
3:A:15:ALA:O	3:A:19:ARG:N	2.42	0.49
3:A:290:PHE:O	3:A:294:MET:HG2	2.13	0.49
3:D:37:SER:OG	3:D:53:VAL:O	2.24	0.49
3:D:224:ILE:H	3:D:224:ILE:HD12	1.78	0.49
2:G:160:ARG:HH12	2:G:161:LYS:HD3	1.78	0.49
3:J:175:SER:O	3:J:676:HIS:N	2.45	0.49
3:L:251:PHE:HB2	3:L:464:LEU:HD12	1.94	0.49
3:L:566:ASN:HA	3:L:584:VAL:HG22	1.94	0.49
3:L:720:ARG:HG3	3:L:772:PHE:HD1	1.78	0.49
3:L:765:LYS:O	3:L:772:PHE:N	2.31	0.49
3:K:65:THR:HG23	3:K:67:GLY:H	1.77	0.49
3:A:118:THR:HB	3:A:125:VAL:HG13	1.95	0.49
3:D:720:ARG:HG3	3:D:772:PHE:CD1	2.48	0.49
2:G:171:ILE:O	2:G:175:GLU:HG2	2.11	0.49
2:F:157:ASP:C	2:F:161:LYS:HZ2	2.21	0.49
3:J:340:ILE:HG21	3:J:350:ARG:HG2	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:J:365:ASN:HB2	3:J:384:VAL:HG21	1.95	0.49
3:L:488:LYS:HB3	3:L:667:MET:HE2	1.95	0.49
3:K:147:LYS:HZ2	3:K:158:SER:HB2	1.77	0.49
3:N:33:PHE:HB2	3:N:84:PRO:HG3	1.94	0.49
3:N:170:ASP:N	3:N:170:ASP:OD1	2.45	0.49
3:N:403:LEU:HD22	3:N:609:VAL:HG11	1.93	0.49
2:C:132:ASN:O	2:C:136:LYS:HG3	2.12	0.49
2:C:177:GLU:HG3	2:C:178:ARG:H	1.77	0.49
2:B:168:LYS:O	2:B:172:LEU:HG	2.13	0.49
3:J:524:CYS:SG	3:J:585:HIS:ND1	2.86	0.49
3:L:147:LYS:NZ	3:L:158:SER:HB2	2.28	0.49
3:L:599:ASP:N	3:L:599:ASP:OD1	2.36	0.49
3:L:717:PHE:HB3	3:L:772:PHE:HB3	1.94	0.49
3:K:536:SER:O	3:K:540:GLU:HG2	2.13	0.49
3:A:584:VAL:HA	3:A:589:THR:HA	1.95	0.49
3:D:90:GLU:OE2	3:D:110:ARG:NH1	2.45	0.49
3:D:761:HIS:HA	3:D:764:TYR:CE1	2.46	0.49
3:L:527:LEU:HD21	3:L:567:PHE:HB2	1.93	0.49
3:J:164:TYR:HB2	3:J:197:PHE:HE1	1.78	0.49
3:N:61:VAL:HG22	3:N:73:VAL:H	1.77	0.49
3:N:104:LEU:HD21	3:N:694:HIS:CD2	2.48	0.49
2:C:165:VAL:HG21	2:B:162:TYR:HD1	1.78	0.48
3:A:54:GLN:HG2	3:A:62:THR:HG22	1.95	0.48
3:A:276:ARG:HH12	3:A:284:GLU:CD	2.20	0.48
3:A:722:LEU:HG	3:A:770:LYS:HE2	1.94	0.48
3:D:165:GLN:HA	3:D:168:LEU:HD12	1.95	0.48
3:D:241:ARG:HH21	3:D:242:ASN:ND2	2.11	0.48
2:F:45:ALA:HB3	2:F:47:GLN:HE22	1.77	0.48
2:F:47:GLN:O	2:F:51:LYS:HG2	2.12	0.48
2:F:163:GLU:HB3	2:F:167:ARG:HH12	1.78	0.48
3:J:161:ASP:HB2	3:J:196:TYR:OH	2.12	0.48
3:J:297:LYS:HZ1	3:J:334:MET:CB	2.25	0.48
3:K:82:ASN:CG	3:K:97:HIS:HB2	2.38	0.48
3:K:255:HIS:N	3:K:264:SER:OG	2.26	0.48
3:N:37:SER:HA	3:N:53:VAL:HG12	1.95	0.48
1:H:232:ALA:HB2	1:H:238:LEU:HD12	1.95	0.48
3:A:402:ALA:HB1	3:A:608:THR:OG1	2.13	0.48
3:A:490:GLN:HE21	3:A:494:ASN:HB2	1.77	0.48
3:A:669:ASN:OD1	3:A:670:LEU:N	2.45	0.48
3:D:365:ASN:HB2	3:D:384:VAL:HG21	1.93	0.48
3:J:119:TYR:HB3	3:J:149:ARG:HH22	1.77	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:J:610:VAL:HG12	3:J:614:GLN:NE2	2.27	0.48
3:J:732:VAL:HG23	3:J:733:LEU:HD22	1.96	0.48
3:K:238:LYS:HZ3	3:K:321:GLU:HB2	1.78	0.48
3:K:488:LYS:HG3	3:K:663:LEU:HD21	1.95	0.48
3:N:664:ASN:O	3:N:668:THR:HG22	2.13	0.48
1:H:148:GLY:C	3:D:545:PRO:HB3	2.38	0.48
3:D:469:PHE:HA	3:D:486:ASN:HD21	1.78	0.48
2:G:197:LEU:HD22	2:F:193:LEU:HD11	1.95	0.48
3:J:75:ASP:N	3:J:75:ASP:OD1	2.45	0.48
3:N:443:MET:O	3:N:447:ILE:HG12	2.14	0.48
3:N:593:ASN:O	3:N:597:TRP:NE1	2.47	0.48
3:N:616:SER:OG	3:N:617:SER:N	2.44	0.48
3:A:164:TYR:HA	3:A:167:MET:HE3	1.93	0.48
3:A:181:GLU:N	3:A:181:GLU:OE1	2.45	0.48
2:B:161:LYS:HA	2:B:164:GLU:CD	2.39	0.48
2:G:176:LEU:HD22	2:F:172:LEU:HB3	1.95	0.48
3:J:319:GLN:OE1	3:J:319:GLN:N	2.45	0.48
3:L:773:PHE:CD1	3:L:777:LEU:HD11	2.48	0.48
3:K:40:PHE:HB2	3:K:79:PHE:HB2	1.95	0.48
3:N:145:ARG:HD2	3:N:146:GLY:H	1.78	0.48
1:E:148:GLY:C	3:A:545:PRO:HB3	2.38	0.48
1:Q:234:SER:OG	1:Q:235:SER:N	2.45	0.48
1:Q:275:GLY:O	1:Q:279:THR:HG23	2.13	0.48
1:P:108:THR:OG1	1:P:139:GLN:NE2	2.42	0.48
3:A:359:ALA:HB2	3:A:392:GLN:HE22	1.78	0.48
3:D:237:ALA:O	3:D:245:SER:OG	2.31	0.48
3:D:539:GLU:OE1	3:D:660:ARG:NH1	2.46	0.48
2:G:75:GLU:HG2	3:N:373:ARG:HH21	1.77	0.48
2:F:54:GLU:O	2:F:58:GLU:HG2	2.13	0.48
3:J:164:TYR:O	3:J:167:MET:HG2	2.13	0.48
3:J:175:SER:N	3:J:674:HIS:O	2.45	0.48
3:N:363:TYR:OH	3:N:613:TYR:OH	2.23	0.48
2:C:165:VAL:HG12	2:C:168:LYS:HE2	1.95	0.48
1:R:308:TYR:CE1	4:R:401:ADP:H2	2.31	0.48
3:D:56:ARG:HH12	3:D:78:VAL:HG21	1.78	0.48
3:D:512:TRP:HE3	3:D:513:GLU:HG3	1.78	0.48
3:D:610:VAL:HG12	3:D:614:GLN:NE2	2.25	0.48
2:F:150:GLU:O	2:F:154:ILE:HG12	2.13	0.48
3:J:490:GLN:HE21	3:J:494:ASN:HB2	1.78	0.48
3:L:26:ILE:HG23	3:L:30:ASN:ND2	2.29	0.48
3:L:165:GLN:HA	3:L:168:LEU:HD12	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:K:314:TYR:HD1	3:K:365:ASN:HD21	1.61	0.48
3:N:765:LYS:O	3:N:772:PHE:N	2.32	0.48
2:C:159:ASP:O	2:C:163:GLU:HG3	2.14	0.48
3:A:291:TYR:HE1	3:A:322:ILE:HG22	1.79	0.48
3:A:469:PHE:HB3	3:A:703:CYS:HA	1.94	0.48
3:A:717:PHE:CD1	3:A:774:LYS:HD3	2.48	0.48
3:D:297:LYS:NZ	3:D:334:MET:HB2	2.19	0.48
2:F:60:TYR:O	2:F:63:SER:OG	2.26	0.48
3:J:293:ILE:HD11	3:J:301:LEU:HB2	1.95	0.48
3:L:279:PHE:HA	3:L:319:GLN:HE21	1.78	0.48
3:L:314:TYR:O	3:L:318:SER:OG	2.31	0.48
3:L:503:GLU:HA	3:L:506:LYS:HE3	1.95	0.48
3:K:92:MET:HG3	3:K:95:MET:SD	2.54	0.48
3:N:701:LEU:HG	3:N:707:LEU:HD22	1.95	0.48
2:C:47:GLN:HG3	2:B:46:LEU:HD11	1.96	0.48
2:C:171:ILE:O	2:C:175:GLU:HG2	2.13	0.48
1:P:192:MET:HG3	1:P:211:VAL:HG11	1.96	0.48
2:B:159:ASP:O	2:B:163:GLU:HG2	2.14	0.48
2:G:60:TYR:CE2	2:F:57:VAL:HG13	2.49	0.48
3:L:233:ALA:HB2	3:L:336:THR:HG21	1.95	0.48
3:L:248:PHE:HB3	3:L:272:LEU:HD13	1.96	0.48
3:K:603:ASP:OD1	3:K:603:ASP:N	2.46	0.48
3:N:179:THR:OG1	3:N:704:ASN:ND2	2.46	0.48
1:E:8:THR:HG23	3:A:646:LYS:HD3	1.95	0.48
1:O:288:ASP:OD2	1:P:41:ARG:NH2	2.46	0.48
2:C:101:ARG:HA	2:C:104:GLU:CD	2.38	0.48
2:C:163:GLU:O	2:C:167:ARG:HG3	2.14	0.48
3:D:65:THR:HG23	3:D:67:GLY:H	1.78	0.48
3:J:54:GLN:HE22	3:J:57:GLU:HB2	1.78	0.48
3:J:178:ILE:HD12	3:J:186:LYS:HD2	1.95	0.48
3:J:254:ILE:HB	3:J:461:ILE:HG22	1.96	0.48
3:L:176:ILE:N	3:L:462:GLY:O	2.33	0.48
3:L:241:ARG:NH1	3:L:470:GLU:OE1	2.46	0.48
3:L:490:GLN:HE21	3:L:494:ASN:HB2	1.79	0.48
3:K:720:ARG:HG3	3:K:772:PHE:CD1	2.49	0.48
3:N:565:ASN:OD1	3:N:566:ASN:N	2.45	0.48
3:A:22:GLU:HA	3:A:25:ARG:HD2	1.95	0.48
3:A:516:ASP:OD1	3:A:517:PHE:N	2.47	0.48
3:A:708:GLU:O	3:A:711:ARG:HG3	2.13	0.48
3:D:482:ILE:O	3:D:485:THR:OG1	2.24	0.48
3:D:525:ILE:O	3:D:529:GLU:HG3	2.14	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:D:667:MET:O	3:D:671:ARG:NH1	2.39	0.48
2:G:92:ILE:HD11	2:F:88:LEU:HB3	1.95	0.48
2:G:157:ASP:O	2:G:160:ARG:NH1	2.47	0.48
3:L:582:SER:HA	3:L:591:ASP:HA	1.96	0.48
3:K:643:LYS:HG3	3:K:645:ALA:H	1.79	0.48
1:Q:178:MET:HG3	1:Q:283:SER:HB2	1.96	0.47
3:A:33:PHE:CG	3:A:84:PRO:HD3	2.49	0.47
3:D:92:MET:SD	3:D:103:VAL:HG13	2.54	0.47
3:J:99:HIS:HB3	3:J:101:PRO:HD2	1.96	0.47
3:J:180:GLY:HA3	3:J:186:LYS:HB2	1.96	0.47
3:J:443:MET:O	3:J:447:ILE:HG12	2.14	0.47
3:L:591:ASP:OD1	3:L:591:ASP:N	2.46	0.47
3:K:222:ASP:OD1	3:K:223:GLN:N	2.47	0.47
3:N:99:HIS:HB3	3:N:101:PRO:HD2	1.96	0.47
3:N:526:GLU:HA	3:N:530:LYS:HG2	1.96	0.47
3:N:548:THR:HG23	3:N:551:SER:H	1.79	0.47
3:N:727:LYS:HE3	3:N:749:ALA:HB3	1.95	0.47
1:E:234:SER:OG	1:E:235:SER:N	2.47	0.47
1:H:302:SER:O	1:H:306:THR:OG1	2.29	0.47
1:P:217:LYS:HD2	1:P:242:TYR:HE1	1.79	0.47
3:A:667:MET:HB3	3:A:671:ARG:HH12	1.79	0.47
2:B:175:GLU:HA	2:B:178:ARG:CD	2.44	0.47
3:J:147:LYS:HZ2	3:J:158:SER:HB2	1.79	0.47
3:L:25:ARG:O	3:L:29:GLN:HB2	2.14	0.47
3:L:45:LYS:HD2	3:L:46:GLU:HG2	1.95	0.47
3:L:118:THR:HG22	3:L:119:TYR:H	1.79	0.47
3:L:308:THR:HG22	3:L:314:TYR:CE2	2.49	0.47
3:K:674:HIS:CD2	3:K:675:PRO:HD2	2.47	0.47
3:N:482:ILE:O	3:N:485:THR:OG1	2.27	0.47
1:E:216:GLU:HG2	4:E:401:ADP:C5	2.49	0.47
2:C:164:GLU:O	2:C:168:LYS:HG3	2.13	0.47
3:A:117:TYR:HB3	3:A:155:HIS:HA	1.95	0.47
3:A:307:ILE:HG21	3:A:361:MET:HE3	1.96	0.47
2:B:47:GLN:CD	2:B:47:GLN:H	2.21	0.47
3:D:96:THR:OG1	3:D:775:ALA:O	2.22	0.47
3:D:281:LEU:HD23	3:D:281:LEU:H	1.79	0.47
3:D:708:GLU:O	3:D:711:ARG:HG3	2.14	0.47
2:F:98:GLU:O	2:F:101:ARG:HD3	2.14	0.47
3:L:33:PHE:CG	3:L:84:PRO:HD3	2.50	0.47
3:K:85:LYS:HG3	3:K:86:TYR:HD1	1.80	0.47
3:K:192:ARG:HH11	3:K:195:GLN:NE2	2.12	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:N:147:LYS:NZ	3:N:158:SER:HB2	2.29	0.47
1:E:308:TYR:CE1	4:E:401:ADP:H2	2.32	0.47
3:A:175:SER:N	3:A:674:HIS:O	2.46	0.47
3:L:497:MET:HE1	3:L:712:ILE:HG21	1.95	0.47
3:L:730:TYR:HD2	3:L:757:ILE:HD12	1.79	0.47
3:K:79:PHE:HD2	3:K:99:HIS:HB3	1.78	0.47
1:H:19:VAL:HG23	1:H:35:SER:HB3	1.95	0.47
1:H:113:ASN:OD1	1:H:179:ARG:NH1	2.32	0.47
1:H:234:SER:OG	1:H:235:SER:N	2.47	0.47
1:O:234:SER:OG	1:O:235:SER:N	2.46	0.47
2:C:147:GLN:HA	2:C:150:GLU:HG3	1.95	0.47
2:C:195:GLU:O	2:C:199:ILE:HG13	2.15	0.47
3:A:16:PRO:O	3:A:20:LYS:NZ	2.33	0.47
3:A:165:GLN:HA	3:A:168:LEU:HD12	1.95	0.47
3:A:171:ARG:HG3	3:A:459:TYR:CE1	2.50	0.47
3:A:273:GLU:OE1	3:A:276:ARG:HG2	2.14	0.47
3:A:493:PHE:HB2	3:A:677:PHE:CZ	2.48	0.47
2:B:98:GLU:O	2:B:101:ARG:HD3	2.15	0.47
2:B:100:ASP:O	2:B:103:GLN:NE2	2.47	0.47
2:B:138:GLU:HA	2:B:141:MET:HE3	1.94	0.47
3:D:8:MET:O	3:D:19:ARG:NH2	2.47	0.47
3:D:43:ASP:OD2	3:D:49:VAL:N	2.47	0.47
3:D:573:ALA:O	3:D:574:LYS:HG2	2.14	0.47
2:G:138:GLU:O	2:G:141:MET:HG2	2.14	0.47
2:F:161:LYS:HA	2:F:164:GLU:CD	2.40	0.47
3:L:508:GLU:HB3	3:L:772:PHE:HZ	1.79	0.47
3:L:667:MET:HB3	3:L:671:ARG:HH12	1.77	0.47
1:E:375:LYS:HD2	1:E:375:LYS:HA	1.65	0.47
3:K:52:THR:N	3:K:64:LYS:O	2.48	0.47
3:K:763:GLN:HA	3:K:774:LYS:HE2	1.97	0.47
3:N:502:GLN:NE2	3:N:512:TRP:O	2.36	0.47
1:E:10:LEU:HB2	1:E:105:THR:HG22	1.97	0.47
2:C:122:GLU:O	2:C:125:ARG:HD3	2.13	0.47
2:C:151:ALA:HB2	2:B:148:LEU:HD13	1.96	0.47
3:D:86:TYR:CD2	3:D:95:MET:HA	2.50	0.47
3:D:88:LYS:HD2	3:D:110:ARG:HG2	1.96	0.47
3:D:582:SER:HA	3:D:591:ASP:HA	1.97	0.47
2:F:53:THR:HA	2:F:56:GLU:HG2	1.96	0.47
3:J:165:GLN:O	3:J:169:THR:HG23	2.13	0.47
3:J:297:LYS:HD3	3:J:330:GLN:HB3	1.96	0.47
3:L:33:PHE:HZ	3:L:81:MET:HB3	1.80	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:L:284:GLU:O	3:L:320:GLY:HA3	2.14	0.47
3:L:732:VAL:HG23	3:L:733:LEU:HD22	1.97	0.47
3:K:55:SER:OG	3:K:56:ARG:N	2.48	0.47
3:K:697:VAL:O	3:K:701:LEU:N	2.44	0.47
3:N:498:PHE:HB2	3:N:517:PHE:CG	2.49	0.47
3:N:614:GLN:HG2	3:N:624:LEU:O	2.14	0.47
3:N:747:LYS:O	3:N:750:SER:OG	2.25	0.47
2:C:157:ASP:O	2:C:160:ARG:HD3	2.14	0.47
2:C:201:THR:O	2:C:205:LYS:HD3	2.15	0.47
3:A:251:PHE:O	3:A:268:GLU:N	2.46	0.47
3:D:54:GLN:NE2	3:D:57:GLU:HB2	2.29	0.47
3:D:65:THR:HG22	3:D:69:ALA:H	1.79	0.47
3:D:619:LYS:HD3	3:D:619:LYS:HA	1.62	0.47
2:G:169:LEU:HD13	2:F:169:LEU:HG	1.96	0.47
2:F:106:LEU:O	2:F:110:LEU:HG	2.15	0.47
2:F:138:GLU:O	2:F:142:GLU:HG3	2.14	0.47
3:J:251:PHE:HB2	3:J:464:LEU:HD12	1.96	0.47
3:L:232:GLU:O	3:L:236:ASN:HB2	2.14	0.47
3:L:234:PHE:CD2	3:L:443:MET:HE3	2.50	0.47
3:L:319:GLN:N	3:L:319:GLN:OE1	2.48	0.47
3:L:343:LEU:HD13	3:L:447:ILE:HD12	1.95	0.47
3:L:442:TRP:HB3	3:L:623:TYR:CE1	2.48	0.47
3:N:51:ALA:HA	3:N:65:THR:HA	1.97	0.47
3:N:165:GLN:O	3:N:169:THR:HG23	2.15	0.47
3:N:778:LEU:O	3:N:782:GLU:N	2.33	0.47
1:E:10:LEU:HD13	1:E:103:HIS:HB3	1.97	0.47
1:O:275:GLY:O	1:O:279:THR:HG23	2.14	0.47
1:P:255:GLU:OE1	1:P:255:GLU:N	2.34	0.47
3:A:730:TYR:HD2	3:A:757:ILE:HD12	1.80	0.47
2:G:72:GLU:O	2:G:76:LYS:HG3	2.14	0.47
2:G:183:ALA:O	2:F:182:ARG:NH1	2.41	0.47
3:J:155:HIS:O	3:J:158:SER:OG	2.18	0.47
3:J:577:VAL:HG13	3:J:578:GLU:H	1.80	0.47
3:L:11:PHE:HZ	3:L:15:ALA:N	2.12	0.47
3:L:190:THR:O	3:L:194:ILE:HG23	2.15	0.47
3:K:348:ASP:HA	3:K:351:VAL:HG12	1.97	0.47
1:H:61:GLN:OE1	1:H:64:ARG:HD3	2.15	0.47
1:O:192:MET:HG2	1:O:211:VAL:HG21	1.95	0.47
2:C:102:ALA:HA	2:C:105:ARG:NE	2.29	0.47
2:C:196:GLU:HA	2:C:199:ILE:HD12	1.96	0.47
3:A:155:HIS:O	3:A:158:SER:OG	2.20	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:443:MET:O	3:A:447:ILE:HG12	2.15	0.47
2:F:195:GLU:O	2:F:199:ILE:HG13	2.15	0.47
3:N:34:ASP:OD2	3:N:37:SER:HB3	2.14	0.47
3:N:118:THR:HB	3:N:125:VAL:HG13	1.97	0.47
3:N:130:TYR:HB2	3:N:689:PRO:HD3	1.97	0.47
2:C:130:ILE:HG22	2:C:133:ARG:NH2	2.30	0.46
1:P:255:GLU:HA	1:P:258:ARG:HB2	1.97	0.46
3:A:162:ASN:HA	3:A:165:GLN:HE21	1.80	0.46
3:A:684:ASN:OD1	3:A:684:ASN:N	2.47	0.46
3:J:292:GLN:C	3:J:333:LEU:HD21	2.40	0.46
3:L:327:ILE:HG22	3:L:328:ASP:O	2.15	0.46
3:K:383:GLU:O	3:K:387:LYS:HG3	2.14	0.46
1:E:178:MET:HG3	1:E:283:SER:HB2	1.97	0.46
3:A:43:ASP:HB2	3:A:46:GLU:O	2.16	0.46
3:A:145:ARG:HD2	3:A:146:GLY:H	1.80	0.46
3:A:253:ARG:HG2	3:A:460:PHE:CD1	2.50	0.46
3:A:278:THR:OG1	3:A:433:LYS:HE2	2.14	0.46
3:A:285:ARG:HD2	3:A:291:TYR:CE2	2.50	0.46
3:D:94:MET:HE1	3:D:720:ARG:H	1.80	0.46
2:G:88:LEU:HD22	2:F:89:ASN:HB3	1.98	0.46
2:G:162:TYR:HA	2:G:165:VAL:HG22	1.97	0.46
2:F:175:GLU:HA	2:F:178:ARG:CD	2.45	0.46
3:J:98:LEU:O	3:J:714:ARG:NE	2.43	0.46
3:J:761:HIS:HA	3:J:764:TYR:CE1	2.50	0.46
3:L:81:MET:HE3	3:L:82:ASN:HB2	1.96	0.46
3:L:162:ASN:HA	3:L:165:GLN:HE21	1.80	0.46
3:L:170:ASP:OD1	3:L:170:ASP:N	2.48	0.46
3:L:267:ILE:H	3:L:448:ASN:ND2	2.13	0.46
3:K:174:GLN:HG3	3:K:676:HIS:HE1	1.81	0.46
3:K:195:GLN:O	3:K:199:THR:HG23	2.15	0.46
3:K:577:VAL:HG22	3:K:578:GLU:HG2	1.98	0.46
3:N:16:PRO:O	3:N:20:LYS:NZ	2.44	0.46
3:N:525:ILE:O	3:N:529:GLU:HG3	2.15	0.46
3:N:701:LEU:HD11	3:N:707:LEU:HB3	1.98	0.46
1:E:173:LEU:HD12	1:E:287:CYS:SG	2.55	0.46
1:Q:307:MET:SD	1:Q:337:ARG:NH1	2.88	0.46
3:A:80:PRO:HB2	3:A:97:HIS:NE2	2.29	0.46
3:A:255:HIS:HA	3:A:460:PHE:HA	1.97	0.46
3:A:483:ASN:O	3:A:487:GLU:HG2	2.15	0.46
2:G:99:LEU:HD13	2:F:95:VAL:HG13	1.97	0.46
3:J:65:THR:HG23	3:J:67:GLY:H	1.80	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:L:65:THR:OG1	3:L:66:GLU:N	2.49	0.46
3:L:145:ARG:HD2	3:L:146:GLY:H	1.81	0.46
3:L:482:ILE:O	3:L:485:THR:OG1	2.27	0.46
3:N:254:ILE:HB	3:N:461:ILE:HG22	1.96	0.46
3:N:439:MET:O	3:N:443:MET:HG2	2.15	0.46
1:E:155:LEU:HD11	1:E:276:ILE:HG23	1.97	0.46
1:O:308:TYR:CE1	4:O:401:ADP:H2	2.34	0.46
2:C:142:GLU:O	2:C:146:MET:HG2	2.14	0.46
1:P:353:THR:O	1:P:356:GLN:NE2	2.48	0.46
1:R:7:THR:HA	3:N:646:LYS:HE3	1.96	0.46
3:A:169:THR:O	3:A:171:ARG:NH1	2.47	0.46
3:D:297:LYS:NZ	3:D:334:MET:H	2.13	0.46
3:D:548:THR:HG23	3:D:551:SER:H	1.80	0.46
3:J:111:TYR:HD2	3:J:692:MET:HE3	1.81	0.46
3:L:723:TYR:HA	3:L:726:PHE:HB3	1.97	0.46
3:K:96:THR:OG1	3:K:779:GLY:N	2.42	0.46
3:K:175:SER:N	3:K:674:HIS:O	2.48	0.46
3:K:269:THR:HG21	3:K:440:PHE:HE1	1.81	0.46
3:K:492:PHE:HB2	3:K:667:MET:HE1	1.98	0.46
3:N:255:HIS:HB3	3:N:457:ARG:HB2	1.96	0.46
3:N:610:VAL:O	3:N:614:GLN:HG3	2.15	0.46
1:H:216:GLU:HG2	4:H:401:ADP:C5	2.50	0.46
3:D:290:PHE:O	3:D:294:MET:HG2	2.15	0.46
2:G:60:TYR:HE2	2:F:57:VAL:HG13	1.81	0.46
3:J:184:ALA:HA	3:J:682:ILE:HD11	1.97	0.46
3:K:701:LEU:HD11	3:K:707:LEU:HB3	1.98	0.46
3:N:383:GLU:O	3:N:387:LYS:HG3	2.16	0.46
2:C:167:ARG:O	2:C:170:VAL:HG12	2.15	0.46
3:D:105:TYR:HA	3:D:108:LYS:HB3	1.97	0.46
3:D:176:ILE:N	3:D:462:GLY:O	2.36	0.46
3:D:773:PHE:CD1	3:D:777:LEU:HD11	2.51	0.46
2:G:99:LEU:HB2	2:F:95:VAL:HG13	1.96	0.46
3:J:82:ASN:ND2	3:J:95:MET:SD	2.88	0.46
3:K:543:MET:HE2	3:K:543:MET:HA	1.97	0.46
3:K:664:ASN:O	3:K:668:THR:HG22	2.15	0.46
2:C:53:THR:HG22	2:B:53:THR:HG22	1.98	0.46
1:P:149:ARG:NH1	1:P:332:ILE:HG13	2.31	0.46
3:A:438:LYS:HD3	3:A:623:TYR:HB3	1.98	0.46
3:D:119:TYR:CE1	3:D:154:PRO:HB3	2.51	0.46
3:J:232:GLU:O	3:J:236:ASN:HB2	2.15	0.46
3:L:114:TRP:HZ3	3:L:689:PRO:HB2	1.80	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Q:145:TYR:CE2	1:Q:348:LEU:HD12	2.51	0.46
3:A:62:THR:HG23	3:A:64:LYS:NZ	2.30	0.46
3:A:293:ILE:O	3:A:302:ILE:HD11	2.16	0.46
3:D:618:MET:HB2	3:D:620:THR:HG23	1.97	0.46
2:F:124:GLU:HG3	2:F:128:LYS:NZ	2.31	0.46
3:J:20:LYS:O	3:J:25:ARG:NE	2.43	0.46
3:L:77:GLN:HA	3:L:79:PHE:HE1	1.80	0.46
3:L:297:LYS:HD3	3:L:330:GLN:C	2.40	0.46
3:K:521:LEU:HD21	3:K:586:TYR:HB3	1.97	0.46
3:N:174:GLN:O	3:N:462:GLY:N	2.49	0.46
1:O:10:LEU:HD13	1:O:103:HIS:HB3	1.97	0.46
1:Q:153:ILE:HD11	1:Q:280:THR:HG23	1.97	0.46
1:Q:314:ARG:NE	1:Q:318:GLU:OE2	2.32	0.46
1:P:157:SER:HB2	1:P:162:THR:HG23	1.97	0.46
3:A:11:PHE:HZ	3:A:15:ALA:N	2.14	0.46
3:A:118:THR:HG22	3:A:119:TYR:H	1.80	0.46
3:J:45:LYS:HD2	3:J:46:GLU:HG2	1.98	0.46
3:J:248:PHE:HB3	3:J:272:LEU:HD13	1.96	0.46
3:K:145:ARG:HH11	3:K:146:GLY:H	1.64	0.46
3:K:468:GLY:HA2	3:K:486:ASN:HD21	1.81	0.46
3:N:234:PHE:HE2	3:N:443:MET:HG3	1.81	0.46
3:N:298:LYS:HG2	3:N:333:LEU:HD23	1.98	0.46
3:N:330:GLN:O	3:N:333:LEU:HB2	2.16	0.46
1:H:157:SER:HB2	1:H:162:THR:HG23	1.98	0.46
2:C:72:GLU:HA	2:C:75:GLU:HG3	1.97	0.46
1:R:302:SER:HA	1:R:337:ARG:HB2	1.98	0.46
3:A:104:LEU:HD11	3:A:694:HIS:CD2	2.51	0.46
3:A:526:GLU:HA	3:A:530:LYS:HG2	1.97	0.46
2:G:164:GLU:O	2:G:168:LYS:HG3	2.16	0.46
3:J:711:ARG:HA	3:J:714:ARG:HB3	1.98	0.46
3:L:402:ALA:HB1	3:L:608:THR:OG1	2.15	0.46
3:K:167:MET:HB3	3:K:174:GLN:NE2	2.31	0.46
3:K:238:LYS:O	3:K:284:GLU:HB2	2.16	0.46
3:N:311:PRO:HG2	3:N:322:ILE:HD12	1.97	0.46
1:H:308:TYR:CE1	4:H:401:ADP:H2	2.34	0.45
1:Q:149:ARG:NH1	1:Q:332:ILE:HG13	2.31	0.45
1:Q:243:GLU:OE2	1:Q:247:GLY:HA2	2.17	0.45
2:C:127:MET:O	2:C:130:ILE:HG12	2.17	0.45
3:A:478:GLU:H	3:A:478:GLU:CD	2.24	0.45
3:A:732:VAL:HG23	3:A:733:LEU:HD22	1.98	0.45
2:G:99:LEU:HG	2:G:103:GLN:NE2	2.31	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:G:108:THR:HA	2:G:111:GLN:NE2	2.31	0.45
2:G:142:GLU:O	2:G:146:MET:HG2	2.16	0.45
2:G:163:GLU:O	2:G:167:ARG:HG3	2.17	0.45
3:J:334:MET:HE3	3:J:337:ASP:HB3	1.98	0.45
3:J:438:LYS:HD3	3:J:623:TYR:HB3	1.96	0.45
3:L:95:MET:HE1	3:L:106:ASN:HB2	1.98	0.45
3:L:238:LYS:O	3:L:284:GLU:HB2	2.16	0.45
3:L:584:VAL:HA	3:L:589:THR:HA	1.96	0.45
3:N:516:ASP:OD1	3:N:517:PHE:N	2.49	0.45
3:N:685:GLU:H	3:N:685:GLU:CD	2.22	0.45
1:O:217:LYS:HD2	1:O:242:TYR:HE1	1.80	0.45
2:C:106:LEU:CD1	2:B:105:ARG:HE	2.30	0.45
2:C:108:THR:HG1	2:C:109:ALA:H	1.63	0.45
2:C:179:SER:O	2:C:182:ARG:HD3	2.16	0.45
1:R:115:LYS:HB3	1:R:373:HIS:CE1	2.51	0.45
3:A:52:THR:HB	3:A:64:LYS:HB2	1.97	0.45
3:A:57:GLU:HB3	3:A:60:LYS:O	2.16	0.45
3:D:251:PHE:HD1	3:D:464:LEU:HB2	1.81	0.45
3:D:347:SER:HA	3:D:350:ARG:HD2	1.99	0.45
3:D:717:PHE:HB3	3:D:772:PHE:HB3	1.99	0.45
2:G:179:SER:HA	2:G:182:ARG:NE	2.31	0.45
2:F:193:LEU:HA	2:F:196:GLU:OE1	2.17	0.45
3:J:108:LYS:HG3	3:J:692:MET:SD	2.56	0.45
3:L:307:ILE:HG21	3:L:361:MET:HE3	1.97	0.45
3:L:614:GLN:HG2	3:L:624:LEU:O	2.16	0.45
3:K:179:THR:OG1	3:K:679:ARG:NE	2.45	0.45
3:K:420:THR:HG22	3:K:423:GLN:OE1	2.16	0.45
3:N:132:TRP:CD1	3:N:134:PRO:HD3	2.52	0.45
3:N:623:TYR:HB2	3:N:624:LEU:HD12	1.99	0.45
1:Q:203:VAL:N	1:Q:207:GLU:OE2	2.36	0.45
2:C:147:GLN:HE22	2:B:144:GLN:HG3	1.80	0.45
1:P:149:ARG:HH12	1:P:332:ILE:HG13	1.80	0.45
3:A:28:ALA:O	3:A:84:PRO:HB2	2.16	0.45
3:A:37:SER:HA	3:A:53:VAL:HG22	1.96	0.45
3:A:49:VAL:HA	3:A:105:TYR:OH	2.17	0.45
3:A:120:SER:O	3:A:123:PHE:N	2.48	0.45
2:B:53:THR:HA	2:B:56:GLU:HG2	1.97	0.45
3:D:285:ARG:HB2	3:D:291:TYR:OH	2.17	0.45
3:D:512:TRP:CE3	3:D:513:GLU:HG3	2.52	0.45
3:J:623:TYR:HB2	3:J:624:LEU:HD12	1.98	0.45
3:L:720:ARG:HG3	3:L:772:PHE:CD1	2.52	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:K:527:LEU:HD22	3:K:566:ASN:HB2	1.98	0.45
3:N:94:MET:HE1	3:N:720:ARG:HB2	1.98	0.45
1:Q:276:ILE:HD13	1:Q:276:ILE:HA	1.83	0.45
1:Q:364:TYR:HH	1:Q:369:PRO:HG3	1.81	0.45
1:P:178:MET:HE2	1:P:178:MET:HB3	1.77	0.45
2:B:162:TYR:HA	2:B:165:VAL:HG22	1.99	0.45
3:J:297:LYS:HB3	3:J:333:LEU:HD12	1.99	0.45
3:L:161:ASP:HB2	3:L:196:TYR:OH	2.16	0.45
3:L:553:LYS:HE2	3:L:557:TYR:CZ	2.52	0.45
3:K:164:TYR:HB2	3:K:197:PHE:HE1	1.82	0.45
3:K:258:THR:HG23	3:K:259:THR:HG23	1.99	0.45
3:K:266:ASP:HB3	3:K:448:ASN:HD21	1.82	0.45
3:K:747:LYS:O	3:K:750:SER:OG	2.25	0.45
1:Q:307:MET:HA	1:Q:337:ARG:NH1	2.31	0.45
3:A:43:ASP:OD1	3:A:49:VAL:HG22	2.17	0.45
3:A:605:LEU:O	3:A:650:SER:HB2	2.17	0.45
2:B:209:ALA:O	2:B:210:GLN:HG3	2.17	0.45
3:D:99:HIS:H	3:D:102:ALA:HB3	1.81	0.45
3:D:667:MET:HB3	3:D:671:ARG:HH12	1.82	0.45
2:G:104:GLU:O	2:G:108:THR:HG23	2.17	0.45
3:J:548:THR:HG23	3:J:551:SER:H	1.81	0.45
3:J:593:ASN:O	3:J:597:TRP:NE1	2.49	0.45
3:L:344:GLY:O	3:L:446:ARG:NH2	2.45	0.45
3:L:510:ILE:HG21	3:L:765:LYS:HG2	1.98	0.45
3:L:616:SER:OG	3:L:617:SER:N	2.48	0.45
3:K:225:ILE:HA	3:K:228:ASN:HB2	1.99	0.45
3:K:267:ILE:H	3:K:448:ASN:ND2	2.15	0.45
3:N:23:LYS:HE2	3:N:24:GLU:OE2	2.17	0.45
3:N:281:LEU:HD23	3:N:281:LEU:H	1.80	0.45
1:E:327:MET:HE3	1:O:246:ASP:HA	1.98	0.45
1:O:353:THR:O	1:O:356:GLN:NE2	2.49	0.45
3:A:247:ARG:HA	3:A:247:ARG:HD2	1.81	0.45
3:D:92:MET:HE3	3:D:120:SER:HB2	1.98	0.45
3:D:104:LEU:HD11	3:D:694:HIS:CD2	2.51	0.45
3:D:339:ALA:O	3:D:343:LEU:HD23	2.17	0.45
2:F:168:LYS:HA	2:F:171:ILE:HG12	1.99	0.45
3:L:49:VAL:HA	3:L:105:TYR:OH	2.17	0.45
3:L:297:LYS:NZ	3:L:334:MET:H	2.15	0.45
3:L:330:GLN:O	3:L:333:LEU:HB2	2.16	0.45
3:K:223:GLN:HB3	3:K:451:LEU:HG	1.99	0.45
3:N:420:THR:HG22	3:N:423:GLN:OE1	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:N:723:TYR:HA	3:N:726:PHE:HB3	1.97	0.45
1:E:171:TYR:CD2	1:O:66:ILE:HD12	2.51	0.45
2:C:124:GLU:O	2:C:127:MET:HG2	2.17	0.45
1:P:153:ILE:HG22	1:P:166:PRO:HB3	1.97	0.45
3:A:497:MET:HE1	3:A:712:ILE:HG23	1.99	0.45
2:B:175:GLU:O	2:B:178:ARG:NH1	2.49	0.45
3:D:82:ASN:OD1	3:D:97:HIS:HB2	2.16	0.45
3:D:292:GLN:O	3:D:333:LEU:HD11	2.17	0.45
3:D:506:LYS:HG3	3:D:507:LYS:N	2.31	0.45
3:J:238:LYS:HE3	3:J:284:GLU:HA	1.99	0.45
3:L:300:ASP:OD1	3:L:301:LEU:N	2.49	0.45
3:L:664:ASN:O	3:L:668:THR:HG22	2.16	0.45
3:L:761:HIS:HA	3:L:764:TYR:HE1	1.82	0.45
3:K:54:GLN:HG2	3:K:55:SER:N	2.31	0.45
3:K:170:ASP:N	3:K:170:ASP:OD1	2.48	0.45
3:K:610:VAL:HG12	3:K:614:GLN:NE2	2.24	0.45
3:N:77:GLN:OE1	3:N:77:GLN:N	2.49	0.45
1:E:161:VAL:HG22	1:E:162:THR:H	1.81	0.45
1:H:168:TYR:HD2	1:Q:66:ILE:HD13	1.82	0.45
1:H:319:ILE:HG23	1:H:329:ILE:HG21	1.99	0.45
1:O:145:TYR:CE2	1:O:348:LEU:HD12	2.52	0.45
2:C:140:LYS:HB3	2:B:141:MET:SD	2.56	0.45
2:C:145:GLU:HB3	2:C:149:LYS:NZ	2.31	0.45
2:C:175:GLU:O	2:C:178:ARG:HD3	2.16	0.45
1:R:352:SER:N	3:N:540:GLU:OE1	2.25	0.45
3:A:176:ILE:N	3:A:462:GLY:O	2.24	0.45
3:A:754:LEU:HD12	3:A:755:GLY:N	2.30	0.45
3:D:582:SER:HB3	3:D:591:ASP:HB3	1.99	0.45
3:J:40:PHE:HB3	3:J:48:PHE:HD2	1.82	0.45
3:J:77:GLN:HA	3:J:79:PHE:HE1	1.82	0.45
3:J:344:GLY:O	3:J:446:ARG:NH2	2.42	0.45
3:J:722:LEU:HD23	3:J:770:LYS:HG2	1.98	0.45
3:J:747:LYS:HG3	3:J:766:PHE:HE2	1.82	0.45
3:L:501:GLU:HG2	3:L:505:TYR:CE2	2.52	0.45
3:K:98:LEU:HD23	3:K:98:LEU:HA	1.83	0.45
3:K:270:TYR:HB3	3:K:666:LEU:HD11	1.98	0.45
3:K:349:GLU:HG3	3:K:442:TRP:HH2	1.81	0.45
3:N:708:GLU:O	3:N:711:ARG:HG3	2.17	0.45
1:E:232:ALA:HB2	1:E:238:LEU:HD12	1.98	0.45
1:O:149:ARG:NH1	1:O:332:ILE:HG13	2.31	0.45
2:C:134:ALA:O	2:C:138:GLU:HG2	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:165:VAL:HA	2:C:168:LYS:HE2	1.99	0.45
1:P:263:LEU:O	1:P:276:ILE:HG12	2.16	0.45
3:A:40:PHE:HB2	3:A:79:PHE:HB2	1.97	0.45
3:A:234:PHE:CD2	3:A:443:MET:HE3	2.52	0.45
2:B:163:GLU:O	2:B:167:ARG:HG2	2.17	0.45
2:G:53:THR:HG21	2:F:50:LEU:HD12	1.98	0.45
3:J:402:ALA:HB1	3:J:608:THR:OG1	2.17	0.45
3:L:253:ARG:HG2	3:L:460:PHE:CD1	2.52	0.45
3:L:469:PHE:HA	3:L:486:ASN:HD21	1.82	0.45
3:L:707:LEU:HA	3:L:710:ILE:HG12	1.99	0.45
3:L:708:GLU:O	3:L:711:ARG:HG3	2.17	0.45
1:H:171:TYR:CD2	1:Q:66:ILE:HD12	2.52	0.45
3:A:192:ARG:O	3:A:195:GLN:HG2	2.17	0.45
3:A:525:ILE:O	3:A:529:GLU:HG3	2.17	0.45
3:D:247:ARG:HA	3:D:247:ARG:HD2	1.82	0.45
3:J:17:TYR:CD2	3:J:135:VAL:HG12	2.50	0.45
3:J:169:THR:O	3:J:171:ARG:NH1	2.50	0.45
3:J:698:LEU:O	3:J:701:LEU:HB3	2.17	0.45
3:K:43:ASP:HB2	3:K:46:GLU:O	2.16	0.45
3:N:728:GLN:HE22	3:N:729:ARG:HH21	1.65	0.45
1:R:61:GLN:O	1:R:64:ARG:HG3	2.17	0.44
3:A:102:ALA:O	3:A:106:ASN:HB2	2.16	0.44
3:A:285:ARG:HB3	3:A:321:GLU:O	2.17	0.44
3:A:322:ILE:HG13	3:A:323:THR:N	2.31	0.44
3:D:85:LYS:HG3	3:D:86:TYR:CD1	2.48	0.44
3:L:297:LYS:HZ1	3:L:334:MET:H	1.64	0.44
3:K:593:ASN:O	3:K:597:TRP:NE1	2.49	0.44
3:N:490:GLN:HE21	3:N:494:ASN:HB2	1.82	0.44
1:Q:35:SER:O	1:Q:35:SER:OG	2.31	0.44
3:A:297:LYS:HZ1	3:A:334:MET:H	1.64	0.44
3:A:532:MET:HE2	3:A:559:GLN:HE21	1.83	0.44
3:D:75:ASP:OD1	3:D:75:ASP:N	2.47	0.44
3:D:170:ASP:OD1	3:D:170:ASP:N	2.50	0.44
3:D:356:LEU:HD11	3:D:620:THR:HG22	1.98	0.44
3:D:584:VAL:HG12	3:D:589:THR:HB	2.00	0.44
2:G:47:GLN:HG3	2:F:46:LEU:HD11	1.99	0.44
2:G:158:SER:HB2	2:F:158:SER:OG	2.16	0.44
2:F:70:LYS:HE3	3:N:372:GLN:HB3	1.99	0.44
3:J:174:GLN:HG3	3:J:674:HIS:HB3	1.99	0.44
3:J:526:GLU:HA	3:J:530:LYS:HG2	1.98	0.44
3:J:648:LYS:HA	3:J:648:LYS:HD2	1.81	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:L:282:LYS:NZ	3:L:319:GLN:O	2.39	0.44
3:L:356:LEU:HD21	3:L:620:THR:HG22	1.99	0.44
3:L:571:LYS:HD3	3:L:572:PRO:HD2	2.00	0.44
3:K:269:THR:HG21	3:K:440:PHE:CE1	2.53	0.44
3:K:395:ASN:OD1	3:K:396:SER:N	2.50	0.44
3:K:537:ILE:HG22	3:K:552:PHE:HE1	1.83	0.44
3:K:759:ILE:HD11	3:K:763:GLN:HG3	1.99	0.44
3:N:43:ASP:HB2	3:N:46:GLU:O	2.16	0.44
3:N:490:GLN:NE2	3:N:490:GLN:O	2.48	0.44
3:N:537:ILE:HG22	3:N:552:PHE:HE1	1.83	0.44
1:E:64:ARG:HG2	1:E:69:LEU:HD11	2.00	0.44
1:H:140:ALA:HB1	1:H:154:VAL:CG1	2.47	0.44
1:Q:61:GLN:OE1	1:Q:64:ARG:HD3	2.17	0.44
1:Q:193:LYS:O	1:Q:196:THR:OG1	2.30	0.44
1:Q:353:THR:O	1:Q:356:GLN:NE2	2.50	0.44
1:Q:369:PRO:O	1:Q:372:VAL:HG23	2.17	0.44
1:R:61:GLN:OE1	1:R:64:ARG:HD3	2.17	0.44
3:D:31:LYS:HD2	3:D:31:LYS:HA	1.84	0.44
3:D:376:GLN:NE2	3:D:404:CYS:O	2.50	0.44
3:D:490:GLN:HE21	3:D:494:ASN:HB2	1.82	0.44
2:G:207:LEU:HD21	2:F:204:LEU:HD22	2.00	0.44
3:J:117:TYR:CE1	3:J:135:VAL:HG21	2.52	0.44
3:J:664:ASN:O	3:J:668:THR:HG22	2.16	0.44
3:K:133:LEU:HD23	3:K:133:LEU:HA	1.83	0.44
3:K:297:LYS:HB3	3:K:333:LEU:HD12	2.00	0.44
3:K:717:PHE:HB3	3:K:772:PHE:HB3	1.99	0.44
1:Q:307:MET:HE2	1:Q:338:LYS:HB2	1.99	0.44
2:C:68:GLN:NE2	2:B:67:ALA:HB2	2.33	0.44
1:P:148:GLY:HA2	3:K:545:PRO:HB3	2.00	0.44
3:D:101:PRO:HA	3:D:104:LEU:HB3	1.99	0.44
3:D:164:TYR:HB2	3:D:197:PHE:HE1	1.81	0.44
3:D:439:MET:HA	3:D:623:TYR:CZ	2.52	0.44
2:F:180:GLU:O	2:F:184:GLU:HG3	2.17	0.44
3:L:17:TYR:CD2	3:L:135:VAL:HG12	2.51	0.44
3:K:117:TYR:HE1	3:K:135:VAL:HG21	1.81	0.44
3:K:403:LEU:HD22	3:K:609:VAL:HG11	1.99	0.44
3:K:710:ILE:O	3:K:714:ARG:CB	2.61	0.44
1:H:359:ILE:HG12	1:H:376:CYS:HB3	1.99	0.44
1:P:202:PHE:HB3	1:P:207:GLU:HG3	1.99	0.44
1:R:140:ALA:HB1	1:R:154:VAL:CG1	2.47	0.44
3:A:75:ASP:OD1	3:A:75:ASP:N	2.48	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:114:TRP:CZ3	3:A:689:PRO:HB2	2.51	0.44
3:A:256:PHE:HB3	3:A:261:LYS:H	1.81	0.44
3:A:586:TYR:HD1	3:A:708:GLU:HG3	1.82	0.44
2:B:119:ALA:O	2:B:122:GLU:HG3	2.18	0.44
2:B:137:ASP:O	2:B:141:MET:HG3	2.17	0.44
3:D:233:ALA:O	3:D:289:ILE:HG12	2.17	0.44
3:D:454:LYS:N	3:D:454:LYS:HD2	2.33	0.44
2:G:78:ALA:O	2:G:82:GLU:HG2	2.18	0.44
3:J:11:PHE:HZ	3:J:15:ALA:N	2.15	0.44
3:J:92:MET:SD	3:J:92:MET:N	2.91	0.44
3:J:420:THR:HG22	3:J:423:GLN:OE1	2.18	0.44
3:J:667:MET:HB3	3:J:671:ARG:NH1	2.31	0.44
3:L:50:LYS:HD2	3:L:50:LYS:HA	1.77	0.44
3:K:87:ASP:OD1	3:K:88:LYS:N	2.50	0.44
3:N:345:PHE:HB3	3:N:350:ARG:HE	1.82	0.44
3:N:707:LEU:O	3:N:710:ILE:HG12	2.18	0.44
2:C:148:LEU:HD12	2:B:144:GLN:HB2	2.00	0.44
1:P:223:LEU:O	1:P:317:LYS:NZ	2.44	0.44
1:P:307:MET:HA	1:P:337:ARG:NH1	2.32	0.44
3:A:96:THR:HB	3:A:778:LEU:HB2	2.00	0.44
3:A:442:TRP:HB3	3:A:623:TYR:HE1	1.83	0.44
3:D:190:THR:O	3:D:194:ILE:HG23	2.18	0.44
3:J:123:PHE:HE1	3:J:679:ARG:HH11	1.66	0.44
3:L:241:ARG:HH21	3:L:242:ASN:ND2	2.15	0.44
3:L:281:LEU:HD23	3:L:281:LEU:H	1.83	0.44
3:L:712:ILE:HD12	3:L:715:LYS:HE3	1.99	0.44
3:N:577:VAL:HG13	3:N:578:GLU:H	1.83	0.44
3:N:582:SER:HB3	3:N:591:ASP:HB3	2.00	0.44
3:N:748:LYS:HA	3:N:751:GLU:CD	2.43	0.44
1:E:157:SER:HB2	1:E:162:THR:HG23	1.99	0.44
1:E:352:SER:N	3:A:540:GLU:OE2	2.50	0.44
1:H:158:GLY:O	1:H:305:THR:OG1	2.31	0.44
1:O:155:LEU:HD11	1:O:276:ILE:HG23	2.00	0.44
1:R:353:THR:O	1:R:356:GLN:NE2	2.51	0.44
3:A:60:LYS:HA	3:A:72:THR:HG23	1.99	0.44
3:A:99:HIS:H	3:A:102:ALA:HB3	1.82	0.44
3:A:177:LEU:HD12	3:A:677:PHE:CE1	2.53	0.44
2:B:163:GLU:HB3	2:B:167:ARG:HH12	1.83	0.44
3:D:119:TYR:HB3	3:D:149:ARG:HH22	1.81	0.44
3:D:192:ARG:O	3:D:195:GLN:HG2	2.18	0.44
3:D:498:PHE:HB2	3:D:517:PHE:CD2	2.52	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:G:49:LYS:HD2	2:F:50:LEU:HD21	1.99	0.44
2:G:145:GLU:HB3	2:G:149:LYS:NZ	2.33	0.44
3:J:62:THR:O	3:J:62:THR:HG23	2.17	0.44
3:J:74:LYS:HE2	3:J:77:GLN:HE22	1.83	0.44
3:J:395:ASN:OD1	3:J:396:SER:N	2.50	0.44
3:L:164:TYR:HB2	3:L:197:PHE:HE1	1.81	0.44
3:L:192:ARG:O	3:L:195:GLN:HG2	2.18	0.44
3:L:234:PHE:CD1	3:L:289:ILE:HG13	2.46	0.44
3:L:725:ASP:OD2	3:L:785:ARG:NH2	2.51	0.44
3:K:685:GLU:H	3:K:685:GLU:CD	2.26	0.44
1:O:61:GLN:O	1:O:64:ARG:HG3	2.18	0.44
1:Q:308:TYR:CE1	4:Q:401:ADP:H2	2.35	0.44
1:P:37:VAL:HG21	1:P:83:ASP:HB3	2.00	0.44
1:R:150:THR:HG23	1:R:151:THR:HG23	2.00	0.44
3:A:29:GLN:HA	3:A:85:LYS:HA	1.99	0.44
3:A:98:LEU:O	3:A:714:ARG:NE	2.51	0.44
3:A:220:LEU:HD23	3:A:221:GLU:N	2.33	0.44
3:A:541:GLU:OE1	3:A:551:SER:OG	2.29	0.44
3:D:284:GLU:O	3:D:320:GLY:HA3	2.18	0.44
3:D:576:LYS:NZ	3:D:578:GLU:O	2.50	0.44
3:D:732:VAL:HG23	3:D:733:LEU:HD22	2.00	0.44
3:J:81:MET:HG3	3:J:82:ASN:O	2.18	0.44
3:J:778:LEU:O	3:J:782:GLU:N	2.37	0.44
3:L:176:ILE:HD12	3:L:676:HIS:C	2.43	0.44
3:L:274:LYS:HG3	3:L:433:LYS:HB3	1.99	0.44
3:L:438:LYS:HB3	3:L:623:TYR:HB3	1.99	0.44
3:N:686:THR:OG1	3:N:687:LYS:N	2.51	0.44
1:E:140:ALA:HB1	1:E:154:VAL:CG1	2.48	0.44
1:O:153:ILE:HG23	1:O:295:LEU:HD22	2.00	0.44
2:C:145:GLU:HB3	2:C:149:LYS:HZ3	1.83	0.44
2:C:146:MET:HA	2:C:149:LYS:HD2	1.99	0.44
1:R:281:TYR:O	1:R:285:MET:HG2	2.18	0.44
3:A:524:CYS:SG	3:A:585:HIS:ND1	2.91	0.44
2:B:82:GLU:HA	2:B:85:VAL:HG12	1.99	0.44
2:B:108:THR:HA	2:B:111:GLN:HE21	1.83	0.44
2:B:122:GLU:O	2:B:125:ARG:HG2	2.18	0.44
2:B:165:VAL:HA	2:B:168:LYS:HB2	1.99	0.44
3:D:363:TYR:HH	3:D:613:TYR:HH	1.66	0.44
3:D:438:LYS:HD3	3:D:623:TYR:HB3	1.99	0.44
3:J:47:SER:OG	3:J:48:PHE:N	2.51	0.44
3:J:267:ILE:H	3:J:448:ASN:ND2	2.15	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:J:419:GLN:OE1	3:J:423:GLN:HB3	2.18	0.44
3:J:683:PRO:HA	3:J:697:VAL:HG22	1.99	0.44
3:J:754:LEU:HD13	3:J:764:TYR:OH	2.18	0.44
3:L:62:THR:HG23	3:L:62:THR:O	2.18	0.44
3:L:256:PHE:O	3:L:458:GLN:N	2.50	0.44
3:L:341:ASP:HA	3:L:350:ARG:NH1	2.33	0.44
3:N:292:GLN:O	3:N:333:LEU:HD11	2.18	0.44
3:N:766:PHE:HD1	3:N:771:VAL:HB	1.82	0.44
1:E:334:PRO:O	1:E:337:ARG:NH1	2.51	0.43
1:O:140:ALA:HB1	1:O:154:VAL:CG1	2.48	0.43
2:C:60:TYR:CE2	2:B:57:VAL:HG13	2.43	0.43
1:P:319:ILE:HG23	1:P:329:ILE:HG21	2.00	0.43
3:A:164:TYR:HB2	3:A:197:PHE:HE1	1.83	0.43
3:A:370:GLN:HG2	3:A:371:LYS:O	2.18	0.43
3:A:442:TRP:HB3	3:A:623:TYR:CE1	2.52	0.43
3:D:120:SER:HB3	3:D:123:PHE:HB2	2.00	0.43
3:D:698:LEU:HA	3:D:701:LEU:HB3	1.99	0.43
2:G:99:LEU:HD21	2:F:98:GLU:CD	2.43	0.43
3:J:133:LEU:HD23	3:J:133:LEU:HA	1.84	0.43
3:J:392:GLN:HG3	3:J:618:MET:HE2	1.99	0.43
3:N:284:GLU:O	3:N:320:GLY:HA3	2.17	0.43
1:E:195:LEU:HD23	1:E:195:LEU:HA	1.81	0.43
1:Q:140:ALA:HB1	1:Q:154:VAL:CG1	2.47	0.43
1:Q:155:LEU:HD11	1:Q:276:ILE:HG23	2.00	0.43
1:Q:161:VAL:HG22	1:Q:162:THR:H	1.83	0.43
2:C:58:GLU:O	2:C:61:SER:OG	2.35	0.43
2:C:100:ASP:O	2:C:104:GLU:HG3	2.17	0.43
1:P:140:ALA:HB1	1:P:154:VAL:CG1	2.48	0.43
1:R:19:VAL:HG23	1:R:35:SER:HB3	2.00	0.43
3:A:255:HIS:CG	3:A:460:PHE:HB3	2.53	0.43
3:D:54:GLN:OE1	3:D:55:SER:OG	2.29	0.43
2:G:167:ARG:HA	2:G:170:VAL:HG12	2.00	0.43
3:J:65:THR:HG23	3:J:67:GLY:N	2.33	0.43
3:J:392:GLN:HA	3:J:618:MET:HE2	2.00	0.43
3:K:65:THR:HG22	3:K:69:ALA:H	1.82	0.43
3:K:297:LYS:HZ1	3:K:334:MET:H	1.65	0.43
3:K:306:LEU:HB3	3:K:387:LYS:HE2	2.00	0.43
3:N:251:PHE:HB2	3:N:464:LEU:HD12	2.00	0.43
2:C:47:GLN:O	2:C:51:LYS:HG2	2.18	0.43
1:R:155:LEU:HD11	1:R:276:ILE:HG23	2.01	0.43
1:R:263:LEU:O	1:R:276:ILE:HG12	2.17	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:33:PHE:CD1	3:A:84:PRO:HD3	2.53	0.43
3:A:238:LYS:O	3:A:284:GLU:HB2	2.18	0.43
3:A:706:VAL:O	3:A:710:ILE:HG23	2.18	0.43
3:D:119:TYR:CD1	3:D:154:PRO:HB3	2.53	0.43
3:D:605:LEU:O	3:D:650:SER:HB2	2.18	0.43
3:J:43:ASP:HB2	3:J:46:GLU:O	2.17	0.43
3:J:612:LEU:HD23	3:J:615:LYS:HZ3	1.82	0.43
3:L:148:LYS:HD2	3:L:150:GLN:H	1.83	0.43
3:L:222:ASP:N	3:L:222:ASP:OD1	2.50	0.43
3:K:271:LEU:HA	3:K:662:ASN:HD21	1.84	0.43
3:N:117:TYR:HE1	3:N:135:VAL:HG21	1.82	0.43
1:E:302:SER:HA	1:E:337:ARG:HB2	2.01	0.43
1:Q:108:THR:OG1	1:Q:139:GLN:NE2	2.43	0.43
1:R:315:MET:O	1:R:319:ILE:HG22	2.18	0.43
1:R:371:ILE:HA	1:R:374:ARG:NH1	2.33	0.43
3:A:43:ASP:HB2	3:A:46:GLU:C	2.44	0.43
2:B:58:GLU:O	2:B:62:GLU:HG2	2.18	0.43
3:D:61:VAL:HG11	3:D:78:VAL:HG11	1.99	0.43
3:D:161:ASP:HB2	3:D:196:TYR:OH	2.19	0.43
3:D:177:LEU:HD21	3:D:670:LEU:HD21	2.00	0.43
3:D:438:LYS:NZ	3:D:624:LEU:HG	2.33	0.43
3:D:681:ILE:H	3:D:681:ILE:HD12	1.82	0.43
3:J:28:ALA:O	3:J:84:PRO:HB2	2.17	0.43
3:J:31:LYS:HE2	3:J:32:PRO:HD2	2.01	0.43
3:J:527:LEU:HD22	3:J:566:ASN:HB2	2.00	0.43
3:N:52:THR:HB	3:N:64:LYS:HB2	2.01	0.43
3:N:481:CYS:O	3:N:485:THR:HG23	2.18	0.43
1:P:229:MET:SD	1:P:254:ASN:ND2	2.91	0.43
3:A:161:ASP:HB2	3:A:196:TYR:OH	2.18	0.43
3:A:170:ASP:OD1	3:A:170:ASP:N	2.49	0.43
3:D:121:GLY:O	3:D:149:ARG:NH2	2.50	0.43
3:D:266:ASP:HB3	3:D:448:ASN:HD21	1.83	0.43
2:G:130:ILE:HG13	2:G:131:GLU:N	2.34	0.43
2:F:132:ASN:O	2:F:136:LYS:HG2	2.18	0.43
3:J:251:PHE:O	3:J:268:GLU:N	2.40	0.43
3:J:300:ASP:N	3:J:300:ASP:OD1	2.50	0.43
3:L:596:GLY:O	3:L:600:LYS:HB2	2.18	0.43
3:N:75:ASP:O	3:N:78:VAL:HG22	2.19	0.43
3:N:665:LYS:HE3	3:N:665:LYS:HB2	1.81	0.43
1:H:217:LYS:HD2	1:H:242:TYR:HE1	1.84	0.43
2:C:144:GLN:HA	2:C:147:GLN:CG	2.48	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:P:43:GLN:OE1	1:P:43:GLN:N	2.42	0.43
1:P:195:LEU:HD23	1:P:195:LEU:HA	1.85	0.43
1:R:302:SER:O	1:R:306:THR:OG1	2.33	0.43
3:D:43:ASP:HB2	3:D:46:GLU:O	2.18	0.43
3:D:269:THR:HG21	3:D:440:PHE:CE2	2.54	0.43
3:D:402:ALA:HB1	3:D:608:THR:OG1	2.19	0.43
3:D:446:ARG:NH1	3:D:449:GLN:OE1	2.52	0.43
2:G:88:LEU:CD2	2:F:85:VAL:HG23	2.49	0.43
2:G:140:LYS:HB3	2:F:141:MET:SD	2.59	0.43
2:G:148:LEU:HA	2:F:147:GLN:NE2	2.34	0.43
2:F:101:ARG:O	2:F:104:GLU:HG3	2.19	0.43
3:K:478:GLU:H	3:K:478:GLU:CD	2.26	0.43
3:N:308:THR:OG1	3:N:309:THR:N	2.51	0.43
3:N:754:LEU:HD13	3:N:764:TYR:OH	2.18	0.43
1:O:314:ARG:O	1:O:318:GLU:HG2	2.19	0.43
1:Q:88:TRP:HH2	1:Q:121:MET:HG3	1.84	0.43
1:Q:195:LEU:HD23	1:Q:195:LEU:HA	1.82	0.43
2:C:162:TYR:HA	2:C:165:VAL:HG22	2.00	0.43
1:P:35:SER:O	1:P:35:SER:OG	2.34	0.43
3:A:120:SER:HB2	3:A:123:PHE:HB2	1.99	0.43
3:A:497:MET:HB3	3:A:497:MET:HE2	1.76	0.43
3:D:192:ARG:HH11	3:D:195:GLN:NE2	2.15	0.43
2:G:165:VAL:HA	2:G:168:LYS:HE2	1.99	0.43
2:G:196:GLU:HA	2:G:199:ILE:HD12	2.00	0.43
2:F:47:GLN:O	2:F:50:LEU:HB3	2.18	0.43
2:F:108:THR:HA	2:F:111:GLN:HE21	1.83	0.43
3:L:499:VAL:O	3:L:503:GLU:HB2	2.18	0.43
3:L:610:VAL:HG12	3:L:614:GLN:NE2	2.24	0.43
3:L:669:ASN:OD1	3:L:670:LEU:N	2.52	0.43
3:K:76:ASP:OD2	3:K:76:ASP:N	2.47	0.43
3:N:45:LYS:HD2	3:N:46:GLU:HG2	1.99	0.43
3:N:402:ALA:HB1	3:N:608:THR:OG1	2.18	0.43
3:N:420:THR:O	3:N:424:VAL:HG23	2.19	0.43
1:H:153:ILE:HG22	1:H:166:PRO:HA	2.01	0.43
1:H:229:MET:HE2	1:H:229:MET:HB2	1.86	0.43
1:R:371:ILE:HD12	1:R:374:ARG:HH11	1.83	0.43
3:D:83:PRO:HG2	3:D:86:TYR:HB2	2.01	0.43
3:J:605:LEU:O	3:J:650:SER:HB2	2.19	0.43
3:L:247:ARG:HA	3:L:247:ARG:HD2	1.80	0.43
3:L:443:MET:SD	3:L:444:VAL:HG23	2.59	0.43
3:L:747:LYS:O	3:L:750:SER:OG	2.24	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:K:300:ASP:O	3:K:303:GLU:HG2	2.19	0.43
3:K:765:LYS:HD3	3:K:765:LYS:HA	1.78	0.43
3:N:395:ASN:OD1	3:N:396:SER:N	2.52	0.43
3:A:8:MET:SD	3:A:22:GLU:HG3	2.59	0.43
3:A:441:LEU:HA	3:A:441:LEU:HD23	1.75	0.43
3:A:490:GLN:O	3:A:490:GLN:NE2	2.51	0.43
3:A:512:TRP:CZ3	3:A:716:GLY:HA3	2.54	0.43
3:D:60:LYS:HB3	3:D:72:THR:HG23	2.00	0.43
2:G:172:LEU:CD2	2:F:172:LEU:HB2	2.49	0.43
3:J:88:LYS:NZ	3:J:109:GLU:HB3	2.33	0.43
3:J:91:ASP:HA	3:J:119:TYR:O	2.19	0.43
3:J:363:TYR:HD2	3:J:432:ALA:HB2	1.84	0.43
3:J:370:GLN:NE2	3:J:374:GLU:O	2.37	0.43
3:J:582:SER:HA	3:J:591:ASP:HA	2.00	0.43
3:L:119:TYR:CE1	3:L:154:PRO:HB3	2.54	0.43
3:K:234:PHE:CE2	3:K:443:MET:HG2	2.54	0.43
3:D:186:LYS:HZ3	3:D:680:CYS:HB2	1.84	0.43
3:D:718:PRO:HA	3:D:720:ARG:NH1	2.34	0.43
2:G:145:GLU:OE1	2:G:149:LYS:NZ	2.50	0.43
3:J:20:LYS:HB3	3:J:24:GLU:HG3	2.00	0.43
3:L:392:GLN:HA	3:L:618:MET:SD	2.59	0.43
3:L:498:PHE:HB2	3:L:517:PHE:CD2	2.54	0.43
3:L:698:LEU:O	3:L:701:LEU:HB3	2.19	0.43
3:L:710:ILE:HA	3:L:713:CYS:SG	2.59	0.43
3:N:148:LYS:HE3	3:N:151:GLU:HB3	1.99	0.43
1:H:153:ILE:HD13	1:H:284:ILE:HD11	2.00	0.42
1:H:352:SER:H	3:D:540:GLU:CD	2.27	0.42
3:A:65:THR:HG23	3:A:67:GLY:H	1.84	0.42
3:J:82:ASN:OD1	3:J:97:HIS:N	2.51	0.42
3:L:395:ASN:OD1	3:L:396:SER:N	2.52	0.42
3:N:83:PRO:HB3	3:N:782:GLU:CD	2.43	0.42
3:N:100:GLU:OE2	3:N:698:LEU:HD21	2.19	0.42
3:N:241:ARG:HE	3:N:242:ASN:HB3	1.83	0.42
3:N:253:ARG:HH12	3:N:268:GLU:HG3	1.84	0.42
1:H:195:LEU:HA	1:H:195:LEU:HD23	1.81	0.42
1:Q:140:ALA:HB1	1:Q:154:VAL:HG11	1.99	0.42
2:C:128:LYS:O	2:C:131:GLU:HG3	2.19	0.42
3:A:125:VAL:HG23	3:A:681:ILE:HD11	2.01	0.42
3:A:498:PHE:HB2	3:A:517:PHE:CG	2.54	0.42
3:A:667:MET:HB3	3:A:671:ARG:NH1	2.34	0.42
3:D:62:THR:HG23	3:D:62:THR:O	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:D:359:ALA:HB2	3:D:392:GLN:HE22	1.84	0.42
3:D:383:GLU:O	3:D:387:LYS:HG3	2.19	0.42
3:D:481:CYS:O	3:D:485:THR:HG23	2.18	0.42
2:F:113:LEU:HB3	3:L:373:ARG:NH1	2.34	0.42
3:J:327:ILE:HG12	3:J:328:ASP:O	2.19	0.42
3:J:383:GLU:O	3:J:387:LYS:HG3	2.18	0.42
3:J:420:THR:O	3:J:424:VAL:HG23	2.19	0.42
3:L:43:ASP:HB2	3:L:46:GLU:O	2.18	0.42
3:L:110:ARG:O	3:L:115:MET:N	2.51	0.42
3:L:167:MET:HB3	3:L:174:GLN:NE2	2.34	0.42
3:K:757:ILE:O	3:K:757:ILE:HG22	2.19	0.42
3:N:698:LEU:HD23	3:N:698:LEU:HA	1.73	0.42
1:H:375:LYS:HD2	1:H:375:LYS:HA	1.80	0.42
1:Q:75:HIS:C	1:Q:77:ILE:H	2.26	0.42
2:C:90:ARG:NH2	2:C:93:GLN:OE1	2.52	0.42
3:A:685:GLU:OE1	3:A:685:GLU:N	2.49	0.42
2:B:120:ALA:O	2:B:123:SER:OG	2.31	0.42
3:D:439:MET:HA	3:D:623:TYR:CE1	2.54	0.42
2:G:129:VAL:HA	2:G:132:ASN:HD22	1.84	0.42
2:G:201:THR:O	2:G:205:LYS:HD3	2.18	0.42
2:F:194:GLU:O	2:F:198:LYS:HG2	2.19	0.42
3:J:145:ARG:HD2	3:J:146:GLY:H	1.85	0.42
3:J:773:PHE:CD2	3:J:778:LEU:HD11	2.54	0.42
3:L:308:THR:OG1	3:L:309:THR:N	2.52	0.42
3:L:710:ILE:O	3:L:714:ARG:HB3	2.19	0.42
3:K:80:PRO:HB2	3:K:97:HIS:NE2	2.33	0.42
3:K:241:ARG:HH21	3:K:242:ASN:CG	2.26	0.42
3:K:781:LEU:HA	3:K:784:MET:HG3	2.01	0.42
3:N:174:GLN:HG3	3:N:674:HIS:HB3	2.01	0.42
3:N:186:LYS:NZ	3:N:678:VAL:HG12	2.34	0.42
3:N:192:ARG:HH11	3:N:195:GLN:NE2	2.17	0.42
3:N:273:GLU:OE2	3:N:275:SER:OG	2.28	0.42
1:H:307:MET:HA	1:H:337:ARG:NH1	2.34	0.42
1:Q:171:TYR:CD2	1:R:66:ILE:HD12	2.54	0.42
1:R:148:GLY:HA2	3:N:545:PRO:HB3	2.01	0.42
3:A:148:LYS:HE3	3:A:151:GLU:HB3	2.01	0.42
3:A:167:MET:HB3	3:A:174:GLN:NE2	2.35	0.42
3:A:297:LYS:NZ	3:A:334:MET:H	2.17	0.42
3:A:341:ASP:HA	3:A:350:ARG:NH1	2.34	0.42
3:D:11:PHE:HZ	3:D:15:ALA:N	2.16	0.42
3:D:498:PHE:HB2	3:D:517:PHE:HB2	2.00	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:D:508:GLU:O	3:D:767:GLY:HA3	2.19	0.42
3:D:662:ASN:OD1	3:D:663:LEU:N	2.52	0.42
2:G:169:LEU:HD12	2:G:169:LEU:HA	1.86	0.42
3:J:162:ASN:HA	3:J:165:GLN:HE21	1.84	0.42
3:J:253:ARG:HG2	3:J:460:PHE:CD1	2.54	0.42
3:L:383:GLU:O	3:L:387:LYS:HG3	2.18	0.42
3:L:474:PHE:HB2	3:L:576:LYS:HE2	2.01	0.42
3:K:498:PHE:HB2	3:K:517:PHE:CG	2.53	0.42
3:N:54:GLN:HE22	3:N:57:GLU:HB2	1.84	0.42
3:N:147:LYS:HZ2	3:N:158:SER:HB2	1.83	0.42
3:N:693:GLU:H	3:N:693:GLU:CD	2.27	0.42
1:O:7:THR:OG1	1:O:8:THR:N	2.51	0.42
1:Q:327:MET:HE3	1:R:246:ASP:HA	2.01	0.42
2:C:88:LEU:CD2	2:B:85:VAL:HG23	2.45	0.42
1:R:149:ARG:NH1	1:R:332:ILE:HG13	2.34	0.42
3:A:105:TYR:CE1	3:A:108:LYS:HD3	2.55	0.42
3:A:188:VAL:O	3:A:191:LYS:HG2	2.19	0.42
2:B:101:ARG:NH1	2:B:105:ARG:HH22	2.17	0.42
3:D:65:THR:HG23	3:D:67:GLY:N	2.34	0.42
3:D:86:TYR:HD2	3:D:95:MET:HA	1.84	0.42
3:D:282:LYS:HD3	3:D:282:LYS:HA	1.88	0.42
3:D:285:ARG:HB3	3:D:321:GLU:O	2.20	0.42
2:G:148:LEU:HD12	2:F:144:GLN:CB	2.49	0.42
2:G:172:LEU:CD2	2:F:169:LEU:HA	2.49	0.42
2:F:56:GLU:HB2	2:F:60:TYR:CZ	2.55	0.42
3:J:179:THR:HG23	3:J:679:ARG:NH2	2.34	0.42
3:J:284:GLU:O	3:J:320:GLY:HA3	2.19	0.42
3:J:557:TYR:OH	3:J:580:HIS:O	2.27	0.42
3:J:591:ASP:OD1	3:J:591:ASP:N	2.51	0.42
3:J:763:GLN:O	3:J:774:LYS:HG2	2.20	0.42
3:K:119:TYR:CE1	3:K:159:ILE:HD11	2.54	0.42
3:K:255:HIS:CG	3:K:460:PHE:HB3	2.54	0.42
1:H:307:MET:SD	1:H:337:ARG:NH1	2.93	0.42
1:O:307:MET:HA	1:O:337:ARG:NH1	2.35	0.42
1:O:319:ILE:HG23	1:O:329:ILE:HG21	2.02	0.42
2:C:157:ASP:O	2:C:160:ARG:NH1	2.53	0.42
1:R:123:GLN:O	1:R:127:GLU:HG2	2.19	0.42
3:A:266:ASP:HA	3:A:448:ASN:OD1	2.20	0.42
2:B:96:GLU:O	2:B:99:LEU:HG	2.19	0.42
2:B:195:GLU:O	2:B:199:ILE:HG13	2.19	0.42
3:D:294:MET:HG3	3:D:311:PRO:HB3	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:J:473:ASP:OD1	3:J:473:ASP:N	2.53	0.42
3:L:255:HIS:HB2	3:L:457:ARG:HG2	2.01	0.42
3:K:304:MET:HE2	3:K:304:MET:HB3	1.92	0.42
3:K:402:ALA:HB1	3:K:608:THR:OG1	2.19	0.42
3:K:707:LEU:O	3:K:710:ILE:HG12	2.19	0.42
3:K:732:VAL:HG23	3:K:733:LEU:HD22	2.01	0.42
3:N:251:PHE:HD2	3:N:268:GLU:HB2	1.83	0.42
3:N:558:GLU:O	3:N:563:LYS:NZ	2.39	0.42
1:H:140:ALA:HB1	1:H:154:VAL:HG11	2.00	0.42
1:P:271:MET:HE2	1:P:271:MET:HB3	1.77	0.42
1:R:337:ARG:HA	1:R:340:SER:OG	2.18	0.42
3:A:616:SER:OG	3:A:617:SER:N	2.51	0.42
3:D:176:ILE:HD12	3:D:676:HIS:C	2.45	0.42
3:J:297:LYS:HZ1	3:J:334:MET:HB2	1.85	0.42
3:L:83:PRO:HB3	3:L:782:GLU:CD	2.44	0.42
3:K:65:THR:HG23	3:K:67:GLY:N	2.34	0.42
3:K:526:GLU:HA	3:K:530:LYS:HG2	2.02	0.42
3:K:550:THR:HG22	3:K:554:ASN:HD21	1.85	0.42
1:E:75:HIS:C	1:E:77:ILE:H	2.28	0.42
1:H:73:ILE:HG12	1:H:78:ILE:HG13	2.02	0.42
1:O:315:MET:O	1:O:319:ILE:HG22	2.20	0.42
1:P:109:GLU:OE2	1:P:118:ARG:NE	2.52	0.42
3:A:294:MET:HE2	3:A:311:PRO:HA	2.01	0.42
3:D:33:PHE:HZ	3:D:81:MET:HB3	1.84	0.42
3:D:65:THR:HG22	3:D:69:ALA:N	2.35	0.42
3:D:93:ALA:HA	3:D:98:LEU:HD21	2.02	0.42
3:D:232:GLU:O	3:D:236:ASN:HB2	2.19	0.42
3:J:98:LEU:O	3:J:99:HIS:ND1	2.51	0.42
3:J:167:MET:HB3	3:J:174:GLN:NE2	2.35	0.42
3:L:481:CYS:O	3:L:485:THR:HG23	2.20	0.42
3:L:577:VAL:HG13	3:L:578:GLU:H	1.85	0.42
3:L:598:LEU:HD23	3:L:598:LEU:HA	1.91	0.42
3:K:157:PHE:HA	3:K:160:SER:OG	2.20	0.42
3:K:512:TRP:CE2	3:K:717:PHE:HB2	2.54	0.42
3:K:527:LEU:HD21	3:K:567:PHE:HB2	2.01	0.42
3:N:605:LEU:O	3:N:650:SER:HB2	2.20	0.42
1:E:288:ASP:OD1	1:E:289:ILE:N	2.53	0.42
1:Q:319:ILE:HG23	1:Q:329:ILE:HG21	2.02	0.42
1:P:19:VAL:HG23	1:P:35:SER:HB3	2.01	0.42
1:P:315:MET:O	1:P:319:ILE:HG22	2.19	0.42
1:R:49:MET:HG2	3:L:544:PHE:HZ	1.84	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:99:LEU:O	2:B:103:GLN:HG3	2.19	0.42
3:D:49:VAL:HA	3:D:105:TYR:OH	2.19	0.42
3:D:440:PHE:O	3:D:443:MET:HG3	2.19	0.42
3:D:754:LEU:HD12	3:D:755:GLY:N	2.34	0.42
2:F:75:GLU:O	2:F:79:THR:HG23	2.20	0.42
3:J:192:ARG:HH11	3:J:195:GLN:HE22	1.68	0.42
3:J:512:TRP:HE3	3:J:513:GLU:HG3	1.85	0.42
3:L:117:TYR:HE1	3:L:135:VAL:HG21	1.84	0.42
3:L:305:LEU:HD22	3:L:355:LYS:HA	2.00	0.42
3:L:441:LEU:HD23	3:L:441:LEU:HA	1.84	0.42
3:L:526:GLU:HA	3:L:530:LYS:HG2	2.01	0.42
3:L:726:PHE:CE2	3:L:750:SER:HA	2.55	0.42
3:K:370:GLN:HG2	3:K:371:LYS:O	2.20	0.42
3:N:33:PHE:CG	3:N:84:PRO:HD3	2.55	0.42
1:Q:229:MET:HE2	1:Q:229:MET:HB2	1.90	0.42
1:P:281:TYR:O	1:P:285:MET:HG2	2.20	0.42
1:R:369:PRO:O	1:R:372:VAL:HG23	2.20	0.42
3:A:11:PHE:HE2	3:A:14:ALA:HB3	1.85	0.42
3:A:65:THR:HG23	3:A:67:GLY:N	2.34	0.42
3:A:74:LYS:HB2	3:A:77:GLN:HE22	1.85	0.42
3:A:284:GLU:O	3:A:320:GLY:HA3	2.20	0.42
3:A:417:LYS:HB3	3:A:417:LYS:HE3	1.88	0.42
3:D:41:VAL:HG12	3:D:51:ALA:HB2	2.01	0.42
3:D:285:ARG:HB2	3:D:291:TYR:CZ	2.54	0.42
3:D:487:GLU:OE2	3:D:521:LEU:HD12	2.19	0.42
2:G:70:LYS:HE3	2:G:70:LYS:HB2	1.75	0.42
2:F:140:LYS:O	2:F:144:GLN:HG2	2.19	0.42
3:J:117:TYR:HE1	3:J:135:VAL:HG21	1.83	0.42
3:J:177:LEU:HD13	3:J:677:PHE:CE1	2.54	0.42
3:J:706:VAL:O	3:J:710:ILE:HG23	2.20	0.42
3:L:130:TYR:HB2	3:L:689:PRO:HD3	2.02	0.42
3:K:577:VAL:HG13	3:K:578:GLU:N	2.35	0.42
3:N:327:ILE:HG12	3:N:328:ASP:O	2.20	0.42
3:N:438:LYS:HZ3	3:N:624:LEU:HA	1.84	0.42
3:N:490:GLN:HG2	3:N:586:TYR:CG	2.55	0.42
3:N:580:HIS:ND1	3:N:594:ILE:HG22	2.34	0.42
1:E:149:ARG:NH1	1:E:332:ILE:HG13	2.35	0.41
1:E:175:HIS:CD2	1:Q:270:GLY:HA3	2.55	0.41
1:Q:168:TYR:HD2	1:R:66:ILE:HD13	1.85	0.41
1:P:182:LEU:HA	1:P:186:ASP:OD2	2.20	0.41
3:A:192:ARG:HH11	3:A:195:GLN:NE2	2.18	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:251:PHE:CE2	3:A:253:ARG:HG3	2.55	0.41
2:B:60:TYR:O	2:B:63:SER:OG	2.24	0.41
3:D:710:ILE:HA	3:D:713:CYS:SG	2.60	0.41
2:G:165:VAL:HG11	2:F:162:TYR:CE2	2.55	0.41
2:F:137:ASP:HA	2:F:140:LYS:HD2	2.00	0.41
3:J:179:THR:OG1	3:J:679:ARG:NE	2.51	0.41
3:L:605:LEU:O	3:L:650:SER:HB2	2.19	0.41
3:N:164:TYR:HB2	3:N:197:PHE:HE1	1.85	0.41
1:R:271:MET:HE2	1:R:271:MET:HB3	1.82	0.41
3:A:457:ARG:HD3	3:A:457:ARG:H	1.84	0.41
3:A:711:ARG:HA	3:A:714:ARG:CG	2.44	0.41
3:A:723:TYR:HA	3:A:726:PHE:HB3	2.01	0.41
2:B:178:ARG:NH1	2:B:179:SER:HB2	2.35	0.41
3:D:380:ASP:OD1	3:D:380:ASP:N	2.50	0.41
3:D:537:ILE:HG23	3:D:555:LYS:HD2	2.02	0.41
3:D:577:VAL:HG13	3:D:578:GLU:N	2.34	0.41
2:G:193:LEU:HD12	2:F:190:CYS:HB3	2.01	0.41
2:F:86:ALA:HB1	2:F:90:ARG:NH1	2.36	0.41
3:L:65:THR:HG22	3:L:69:ALA:N	2.35	0.41
3:L:345:PHE:HB3	3:L:350:ARG:HE	1.86	0.41
3:L:359:ALA:HB2	3:L:392:GLN:HE22	1.85	0.41
3:K:498:PHE:HB2	3:K:517:PHE:CB	2.49	0.41
3:N:88:LYS:NZ	3:N:109:GLU:HB3	2.34	0.41
3:N:251:PHE:CE2	3:N:253:ARG:HG3	2.56	0.41
3:N:612:LEU:HD23	3:N:615:LYS:NZ	2.34	0.41
1:H:144:LEU:HA	1:H:144:LEU:HD12	1.82	0.41
1:P:254:ASN:ND2	1:P:258:ARG:HH11	2.19	0.41
3:A:91:ASP:HB2	3:A:150:GLN:HE22	1.85	0.41
3:A:248:PHE:HB3	3:A:272:LEU:HD13	2.01	0.41
3:D:497:MET:HE1	3:D:712:ILE:CG2	2.50	0.41
2:G:100:ASP:O	2:G:104:GLU:HG3	2.21	0.41
3:J:174:GLN:O	3:J:462:GLY:N	2.52	0.41
3:J:363:TYR:OH	3:J:613:TYR:OH	2.26	0.41
3:L:220:LEU:HD23	3:L:221:GLU:N	2.35	0.41
3:L:612:LEU:HD23	3:L:615:LYS:NZ	2.35	0.41
3:L:618:MET:HE2	3:L:618:MET:HB3	1.93	0.41
3:L:763:GLN:HG3	3:L:777:LEU:HD22	2.01	0.41
3:K:710:ILE:HA	3:K:713:CYS:SG	2.60	0.41
3:K:748:LYS:HA	3:K:751:GLU:CD	2.46	0.41
3:K:773:PHE:CG	3:K:777:LEU:HD11	2.54	0.41
3:N:53:VAL:HA	3:N:63:ALA:HA	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:155:LEU:HD11	1:H:276:ILE:HG23	2.02	0.41
1:O:109:GLU:OE2	1:O:118:ARG:NH2	2.54	0.41
1:O:328:LYS:HA	1:O:328:LYS:HD3	1.82	0.41
2:C:181:GLU:O	2:C:184:GLU:HG3	2.21	0.41
1:R:153:ILE:HG22	1:R:166:PRO:HB3	2.01	0.41
2:B:103:GLN:HA	2:B:106:LEU:HB3	2.02	0.41
3:D:164:TYR:HB2	3:D:197:PHE:CE1	2.55	0.41
3:D:763:GLN:H	3:D:763:GLN:HG2	1.74	0.41
2:G:49:LYS:HE3	2:G:49:LYS:HB2	1.85	0.41
3:J:710:ILE:HA	3:J:713:CYS:SG	2.60	0.41
3:L:778:LEU:O	3:L:782:GLU:N	2.40	0.41
3:K:201:ALA:HB2	3:K:262:LEU:HD13	2.03	0.41
3:K:730:TYR:CE2	3:K:781:LEU:HD13	2.48	0.41
3:N:297:LYS:HB2	3:N:330:GLN:HB3	2.03	0.41
3:N:683:PRO:HA	3:N:697:VAL:HG22	2.01	0.41
1:H:13:ASP:HB3	1:H:20:LYS:HG3	2.03	0.41
1:O:75:HIS:C	1:O:77:ILE:H	2.29	0.41
2:C:72:GLU:O	2:C:75:GLU:HG3	2.19	0.41
3:A:60:LYS:HG3	3:A:72:THR:HG21	2.02	0.41
3:A:327:ILE:HG22	3:A:328:ASP:O	2.20	0.41
3:A:573:ALA:O	3:A:574:LYS:HG2	2.20	0.41
2:G:82:GLU:HA	2:G:85:VAL:HG22	2.02	0.41
3:J:94:MET:SD	3:J:719:SER:HA	2.60	0.41
3:J:442:TRP:HB3	3:J:623:TYR:CE1	2.56	0.41
3:L:523:ALA:O	3:L:526:GLU:HG3	2.20	0.41
3:L:577:VAL:HG13	3:L:578:GLU:N	2.36	0.41
3:L:593:ASN:O	3:L:597:TRP:NE1	2.53	0.41
3:K:91:ASP:HA	3:K:119:TYR:O	2.21	0.41
3:K:118:THR:HB	3:K:125:VAL:HG13	2.02	0.41
3:K:565:ASN:OD1	3:K:566:ASN:N	2.53	0.41
1:E:353:THR:O	1:E:356:GLN:NE2	2.53	0.41
1:H:335:PRO:HB2	3:D:416:THR:O	2.20	0.41
3:D:278:THR:OG1	3:D:433:LYS:HE2	2.20	0.41
2:F:58:GLU:O	2:F:62:GLU:HG2	2.20	0.41
2:F:154:ILE:O	2:F:158:SER:OG	2.34	0.41
3:J:253:ARG:HH12	3:J:268:GLU:HG3	1.86	0.41
3:L:54:GLN:HE22	3:L:57:GLU:HB2	1.86	0.41
3:L:231:LEU:HD23	3:L:443:MET:HE1	2.02	0.41
3:K:148:LYS:HB3	3:K:151:GLU:OE1	2.21	0.41
3:N:192:ARG:O	3:N:195:GLN:HG2	2.20	0.41
3:N:648:LYS:HB3	3:N:652:PHE:HB2	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:229:MET:HE2	1:E:229:MET:HB2	1.86	0.41
1:H:327:MET:HE3	1:Q:246:ASP:HA	2.03	0.41
3:A:60:LYS:HG3	3:A:72:THR:CG2	2.50	0.41
3:A:273:GLU:OE2	3:A:275:SER:OG	2.39	0.41
3:A:591:ASP:OD1	3:A:591:ASP:N	2.48	0.41
3:D:130:TYR:OH	3:D:683:PRO:HD2	2.20	0.41
3:D:133:LEU:HD23	3:D:133:LEU:HA	1.84	0.41
3:D:373:ARG:HH12	2:G:156:GLU:N	2.18	0.41
3:D:420:THR:O	3:D:424:VAL:HG23	2.20	0.41
2:G:149:LYS:O	2:G:153:HIS:ND1	2.54	0.41
2:F:163:GLU:HB3	2:F:167:ARG:NH1	2.36	0.41
3:J:53:VAL:HG23	3:J:61:VAL:HB	2.02	0.41
3:J:188:VAL:O	3:J:192:ARG:HG2	2.20	0.41
3:J:341:ASP:HA	3:J:350:ARG:CZ	2.50	0.41
3:L:43:ASP:OD1	3:L:49:VAL:HG22	2.21	0.41
3:L:308:THR:HG21	3:L:313:ASP:HB3	2.02	0.41
3:L:476:SER:OG	3:L:600:LYS:NZ	2.54	0.41
3:L:774:LYS:HB2	3:L:777:LEU:HD23	2.03	0.41
3:K:247:ARG:HA	3:K:247:ARG:HD2	1.91	0.41
3:K:516:ASP:OD1	3:K:517:PHE:N	2.53	0.41
3:N:92:MET:N	3:N:92:MET:SD	2.93	0.41
3:N:157:PHE:HA	3:N:160:SER:OG	2.20	0.41
3:N:763:GLN:O	3:N:774:LYS:HG2	2.20	0.41
1:E:314:ARG:O	1:E:318:GLU:HG2	2.21	0.41
1:H:314:ARG:NE	1:H:318:GLU:OE2	2.35	0.41
1:Q:364:TYR:OH	1:Q:369:PRO:HG3	2.21	0.41
1:P:246:ASP:CG	1:P:248:GLN:HE21	2.29	0.41
1:P:371:ILE:HD12	1:P:374:ARG:HD2	2.02	0.41
1:R:276:ILE:HG22	1:R:315:MET:HE1	2.02	0.41
3:A:62:THR:HG23	3:A:62:THR:O	2.20	0.41
3:A:190:THR:O	3:A:194:ILE:HG23	2.20	0.41
3:A:383:GLU:O	3:A:387:LYS:HG3	2.20	0.41
3:A:530:LYS:HA	3:A:530:LYS:HD2	1.89	0.41
3:A:584:VAL:HG12	3:A:589:THR:HB	2.03	0.41
3:A:773:PHE:CD1	3:A:777:LEU:HD11	2.56	0.41
2:B:167:ARG:O	2:B:171:ILE:HG12	2.21	0.41
3:D:718:PRO:HG3	3:D:775:ALA:HB2	2.03	0.41
2:G:177:GLU:O	2:G:181:GLU:HG2	2.20	0.41
3:J:29:GLN:HG2	3:J:85:LYS:HB2	2.02	0.41
3:J:49:VAL:HA	3:J:105:TYR:OH	2.21	0.41
3:J:297:LYS:HZ1	3:J:334:MET:H	1.68	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:L:157:PHE:HA	3:L:160:SER:OG	2.21	0.41
3:L:679:ARG:O	3:L:681:ILE:HD12	2.20	0.41
3:K:222:ASP:HA	3:K:225:ILE:HG22	2.02	0.41
3:K:266:ASP:HA	3:K:448:ASN:OD1	2.20	0.41
3:N:179:THR:OG1	3:N:679:ARG:NE	2.53	0.41
3:N:247:ARG:HA	3:N:247:ARG:HD2	1.82	0.41
1:E:145:TYR:CE2	1:E:348:LEU:HD12	2.56	0.41
1:E:217:LYS:HD2	1:E:242:TYR:HE1	1.86	0.41
1:O:168:TYR:CE2	1:O:169:GLU:HG2	2.56	0.41
1:P:172:ALA:O	1:P:174:PRO:HD3	2.21	0.41
1:P:314:ARG:O	1:P:318:GLU:HG2	2.21	0.41
1:R:75:HIS:C	1:R:77:ILE:H	2.29	0.41
1:R:328:LYS:HD3	1:R:328:LYS:HA	1.83	0.41
3:A:222:ASP:OD1	3:A:222:ASP:N	2.54	0.41
3:A:233:ALA:O	3:A:289:ILE:HG12	2.20	0.41
3:A:348:ASP:OD1	3:A:349:GLU:N	2.53	0.41
3:A:600:LYS:HB3	3:A:600:LYS:HE2	1.90	0.41
3:A:612:LEU:HD23	3:A:615:LYS:NZ	2.35	0.41
2:B:129:VAL:HA	2:B:132:ASN:ND2	2.36	0.41
2:G:132:ASN:O	2:G:136:LYS:HG3	2.21	0.41
2:F:64:VAL:O	2:F:68:GLN:NE2	2.53	0.41
2:F:76:LYS:O	2:F:79:THR:OG1	2.35	0.41
2:F:81:ALA:O	2:F:85:VAL:HG12	2.21	0.41
2:F:136:LYS:HA	2:F:139:GLU:OE2	2.20	0.41
3:J:65:THR:HG22	3:J:69:ALA:H	1.86	0.41
3:J:341:ASP:HA	3:J:350:ARG:NH1	2.35	0.41
3:J:612:LEU:HD23	3:J:615:LYS:NZ	2.36	0.41
3:L:269:THR:HG21	3:L:440:PHE:CE1	2.55	0.41
3:L:667:MET:HB3	3:L:671:ARG:NH1	2.35	0.41
3:L:717:PHE:CB	3:L:772:PHE:HB3	2.51	0.41
3:K:119:TYR:CE1	3:K:154:PRO:HB3	2.56	0.41
3:K:200:ILE:HA	3:K:200:ILE:HD12	1.86	0.41
3:K:343:LEU:HD13	3:K:450:GLN:OE1	2.21	0.41
3:N:43:ASP:OD2	3:N:49:VAL:N	2.53	0.41
3:N:75:ASP:OD1	3:N:76:ASP:N	2.53	0.41
3:N:155:HIS:O	3:N:158:SER:OG	2.19	0.41
3:N:253:ARG:HG2	3:N:460:PHE:CD1	2.55	0.41
3:N:727:LYS:HD3	3:N:753:LEU:HD12	2.03	0.41
1:E:19:VAL:HG23	1:E:35:SER:HB3	2.03	0.41
1:E:168:TYR:HD2	1:O:66:ILE:HD13	1.86	0.41
1:O:18:LEU:HD23	1:O:18:LEU:HA	1.94	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:110:LEU:O	2:C:114:GLU:HG2	2.21	0.41
3:A:725:ASP:OD1	3:A:785:ARG:NH2	2.52	0.41
2:B:112:LYS:HD2	2:B:112:LYS:HA	1.94	0.41
3:D:327:ILE:HG12	3:D:328:ASP:O	2.21	0.41
3:D:521:LEU:O	3:D:525:ILE:HG13	2.21	0.41
3:D:648:LYS:HB3	3:D:652:PHE:HB2	2.03	0.41
2:G:92:ILE:HG23	2:F:91:ARG:HH21	1.86	0.41
2:G:133:ARG:NH2	2:F:130:ILE:HG23	2.35	0.41
2:G:207:LEU:HD13	2:F:207:LEU:HB2	2.02	0.41
3:J:565:ASN:OD1	3:J:566:ASN:N	2.54	0.41
3:K:24:GLU:O	3:K:27:GLU:HG2	2.21	0.41
3:K:179:THR:OG1	3:K:704:ASN:ND2	2.54	0.41
3:K:230:LEU:HD22	3:K:340:ILE:HD13	2.03	0.41
3:K:300:ASP:OD1	3:K:300:ASP:N	2.54	0.41
3:K:613:TYR:HD2	3:K:624:LEU:HD22	1.85	0.41
3:N:8:MET:SD	3:N:22:GLU:HG2	2.60	0.41
3:N:59:GLY:C	3:N:60:LYS:HD2	2.46	0.41
3:N:222:ASP:HA	3:N:225:ILE:HG12	2.02	0.41
1:E:101:GLU:OE1	1:E:101:GLU:N	2.45	0.40
1:H:315:MET:O	1:H:319:ILE:HG22	2.22	0.40
1:Q:271:MET:HE2	1:Q:271:MET:HB3	1.83	0.40
2:C:158:SER:HB2	2:B:158:SER:OG	2.20	0.40
1:P:150:THR:HG23	1:P:151:THR:HG23	2.03	0.40
1:P:371:ILE:HA	1:P:374:ARG:NH1	2.36	0.40
3:A:699:HIS:HA	3:A:702:ARG:HH21	1.86	0.40
2:B:157:ASP:C	2:B:161:LYS:HZ2	2.29	0.40
3:D:175:SER:HA	3:D:462:GLY:H	1.86	0.40
3:D:328:ASP:OD2	3:D:329:ASP:N	2.54	0.40
3:D:442:TRP:HB3	3:D:623:TYR:CE1	2.57	0.40
3:D:603:ASP:OD1	3:D:603:ASP:N	2.52	0.40
3:D:684:ASN:HA	3:D:693:GLU:OE2	2.21	0.40
2:F:147:GLN:HA	2:F:150:GLU:CG	2.50	0.40
3:J:186:LYS:NZ	3:J:678:VAL:HG12	2.37	0.40
3:J:614:GLN:NE2	3:J:626:SER:O	2.53	0.40
3:L:23:LYS:O	3:L:27:GLU:HB2	2.21	0.40
3:K:105:TYR:CE1	3:K:108:LYS:HD3	2.55	0.40
3:A:41:VAL:HA	3:A:78:VAL:HG12	2.02	0.40
3:A:76:ASP:OD1	3:A:76:ASP:N	2.51	0.40
3:A:557:TYR:OH	3:A:580:HIS:O	2.37	0.40
2:B:156:GLU:HB3	2:B:160:ARG:HH12	1.85	0.40
3:D:88:LYS:NZ	3:D:109:GLU:HB3	2.36	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:D:727:LYS:HE3	3:D:749:ALA:HB3	2.02	0.40
2:F:101:ARG:HA	2:F:104:GLU:CG	2.51	0.40
2:F:119:ALA:O	2:F:122:GLU:HG3	2.22	0.40
2:F:137:ASP:O	2:F:141:MET:HG3	2.22	0.40
3:J:192:ARG:HD3	3:J:195:GLN:NE2	2.36	0.40
3:L:498:PHE:HB2	3:L:517:PHE:CG	2.56	0.40
3:L:504:GLU:O	3:L:507:LYS:HG3	2.21	0.40
3:K:167:MET:HG3	3:K:459:TYR:HE2	1.85	0.40
3:K:179:THR:HG23	3:K:679:ARG:NH2	2.36	0.40
3:K:297:LYS:NZ	3:K:334:MET:H	2.19	0.40
3:K:401:LYS:HE3	3:K:401:LYS:HB2	1.90	0.40
3:K:441:LEU:HD13	3:K:441:LEU:HA	1.95	0.40
3:N:305:LEU:HD11	3:N:354:TYR:HB3	2.03	0.40
3:N:726:PHE:HE2	3:N:750:SER:HA	1.86	0.40
1:E:61:GLN:OE1	1:E:64:ARG:HD3	2.20	0.40
1:E:107:LEU:HD11	1:E:125:MET:HE3	2.03	0.40
2:C:115:GLU:HA	2:C:118:LYS:HB3	2.03	0.40
3:A:566:ASN:HA	3:A:584:VAL:HG22	2.03	0.40
3:D:476:SER:N	3:D:479:GLN:HE21	2.19	0.40
2:G:169:LEU:HD22	2:F:165:VAL:HB	2.04	0.40
3:J:96:THR:OG1	3:J:779:GLY:N	2.54	0.40
3:J:247:ARG:HA	3:J:247:ARG:HD2	1.78	0.40
3:J:442:TRP:HB3	3:J:623:TYR:HE1	1.86	0.40
3:J:765:LYS:HD3	3:J:765:LYS:HA	1.86	0.40
3:L:511:GLU:HB2	3:L:514:PHE:CE2	2.55	0.40
3:L:576:LYS:HD2	3:L:577:VAL:H	1.86	0.40
3:L:729:ARG:HA	3:L:729:ARG:HD3	1.93	0.40
3:K:49:VAL:HA	3:K:105:TYR:OH	2.22	0.40
3:K:297:LYS:HD3	3:K:330:GLN:HB3	2.03	0.40
3:K:612:LEU:HD23	3:K:615:LYS:HZ3	1.85	0.40
3:K:707:LEU:HA	3:K:710:ILE:HG12	2.04	0.40
3:N:731:LYS:HG3	3:N:735:ALA:HA	2.02	0.40
1:H:307:MET:HA	1:H:337:ARG:HH12	1.86	0.40
1:O:168:TYR:HD2	1:P:66:ILE:HD13	1.86	0.40
2:C:179:SER:HA	2:C:182:ARG:NE	2.36	0.40
1:P:75:HIS:C	1:P:77:ILE:H	2.30	0.40
3:A:54:GLN:HE22	3:A:57:GLU:HB2	1.87	0.40
3:A:200:ILE:HD12	3:A:200:ILE:HA	1.84	0.40
3:A:297:LYS:HD3	3:A:330:GLN:C	2.47	0.40
3:A:510:ILE:HD12	3:A:510:ILE:HA	1.94	0.40
3:A:698:LEU:O	3:A:701:LEU:HB3	2.22	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:108:THR:O	2:B:111:GLN:NE2	2.54	0.40
3:D:8:MET:SD	3:D:22:GLU:HG2	2.62	0.40
3:D:274:LYS:CG	3:D:433:LYS:HB3	2.51	0.40
3:J:118:THR:HG22	3:J:119:TYR:H	1.86	0.40
3:J:584:VAL:HA	3:J:589:THR:HA	2.03	0.40
3:J:717:PHE:CD1	3:J:774:LYS:HD3	2.56	0.40
3:L:117:TYR:CE1	3:L:135:VAL:HG21	2.57	0.40
3:L:580:HIS:ND1	3:L:594:ILE:HB	2.35	0.40
3:K:20:LYS:HB3	3:K:24:GLU:CG	2.51	0.40
3:K:165:GLN:O	3:K:169:THR:HG23	2.22	0.40
3:K:721:ILE:HD11	3:K:773:PHE:CE2	2.56	0.40
3:N:15:ALA:HB1	3:N:19:ARG:NH1	2.36	0.40
3:N:550:THR:HG22	3:N:554:ASN:HD21	1.86	0.40
3:N:722:LEU:HD23	3:N:770:LYS:HG2	2.03	0.40
2:C:172:LEU:HD12	2:C:172:LEU:HA	1.94	0.40
1:P:61:GLN:O	1:P:64:ARG:HG3	2.21	0.40
1:R:140:ALA:HB1	1:R:154:VAL:HG11	2.03	0.40
3:A:110:ARG:NH2	3:A:118:THR:HG23	2.37	0.40
3:A:133:LEU:HD23	3:A:133:LEU:HA	1.83	0.40
3:A:182:SER:OG	3:A:242:ASN:ND2	2.36	0.40
3:A:274:LYS:CD	3:A:433:LYS:HB3	2.50	0.40
3:A:274:LYS:HE2	3:A:437:GLU:HG3	2.04	0.40
3:D:251:PHE:HB2	3:D:464:LEU:HD12	2.03	0.40
3:D:266:ASP:HA	3:D:448:ASN:OD1	2.21	0.40
3:D:760:ASP:CG	3:D:763:GLN:HE21	2.30	0.40
2:F:86:ALA:O	2:F:90:ARG:NE	2.55	0.40
3:J:80:PRO:HB2	3:J:97:HIS:NE2	2.36	0.40
3:J:226:SER:HB2	3:J:342:ILE:HD11	2.03	0.40
3:J:576:LYS:HZ2	3:J:578:GLU:C	2.29	0.40
3:L:31:LYS:HD2	3:L:31:LYS:HA	1.91	0.40
3:L:192:ARG:HH11	3:L:195:GLN:NE2	2.15	0.40
3:L:439:MET:HA	3:L:623:TYR:CZ	2.55	0.40
3:L:454:LYS:HD2	3:L:454:LYS:N	2.37	0.40
3:N:25:ARG:O	3:N:29:GLN:HB2	2.21	0.40
3:N:179:THR:HG23	3:N:679:ARG:NH2	2.36	0.40
3:N:238:LYS:HG2	3:N:321:GLU:OE2	2.21	0.40
3:N:666:LEU:O	3:N:668:THR:N	2.55	0.40
3:N:698:LEU:O	3:N:701:LEU:HB3	2.21	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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	E	369/371 (100%)	346 (94%)	23 (6%)	0	100	100
1	H	369/371 (100%)	346 (94%)	23 (6%)	0	100	100
1	O	369/371 (100%)	349 (95%)	20 (5%)	0	100	100
1	P	369/371 (100%)	344 (93%)	25 (7%)	0	100	100
1	Q	369/371 (100%)	349 (95%)	20 (5%)	0	100	100
1	R	369/371 (100%)	349 (95%)	20 (5%)	0	100	100
2	B	164/166 (99%)	161 (98%)	3 (2%)	0	100	100
2	C	164/166 (99%)	157 (96%)	7 (4%)	0	100	100
2	F	164/166 (99%)	163 (99%)	1 (1%)	0	100	100
2	G	164/166 (99%)	161 (98%)	3 (2%)	0	100	100
3	A	728/780 (93%)	665 (91%)	63 (9%)	0	100	100
3	D	728/780 (93%)	665 (91%)	63 (9%)	0	100	100
3	J	728/780 (93%)	665 (91%)	63 (9%)	0	100	100
3	K	728/780 (93%)	660 (91%)	68 (9%)	0	100	100
3	L	728/780 (93%)	654 (90%)	74 (10%)	0	100	100
3	N	728/780 (93%)	665 (91%)	63 (9%)	0	100	100
All	All	7238/7570 (96%)	6699 (93%)	539 (7%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	E	314/314 (100%)	314 (100%)	0	100	100
1	H	314/314 (100%)	314 (100%)	0	100	100
1	O	314/314 (100%)	314 (100%)	0	100	100
1	P	314/314 (100%)	314 (100%)	0	100	100
1	Q	314/314 (100%)	314 (100%)	0	100	100
1	R	314/314 (100%)	314 (100%)	0	100	100
2	B	142/142 (100%)	142 (100%)	0	100	100
2	C	142/142 (100%)	142 (100%)	0	100	100
2	F	142/142 (100%)	142 (100%)	0	100	100
2	G	142/142 (100%)	142 (100%)	0	100	100
3	A	637/663 (96%)	637 (100%)	0	100	100
3	D	637/663 (96%)	637 (100%)	0	100	100
3	J	637/663 (96%)	637 (100%)	0	100	100
3	K	637/663 (96%)	637 (100%)	0	100	100
3	L	637/663 (96%)	637 (100%)	0	100	100
3	N	637/663 (96%)	637 (100%)	0	100	100
All	All	6274/6430 (98%)	6274 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (149) such sidechains are listed below:

Mol	Chain	Res	Type
1	E	90	HIS
1	E	94	ASN
1	E	117	ASN
1	E	175	HIS
1	E	227	ASN
1	H	89	HIS
1	H	227	ASN
1	O	89	HIS
1	O	90	HIS
1	O	94	ASN
1	O	175	HIS
1	O	227	ASN
1	Q	89	HIS
1	Q	90	HIS

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Mol	Chain	Res	Type
1	Q	94	ASN
1	Q	175	HIS
1	Q	227	ASN
2	C	103	GLN
2	C	111	GLN
1	P	75	HIS
1	P	89	HIS
1	P	94	ASN
1	P	227	ASN
1	R	61	GLN
1	R	90	HIS
1	R	94	ASN
1	R	103	HIS
1	R	117	ASN
1	R	164	ASN
1	R	227	ASN
3	A	99	HIS
3	A	162	ASN
3	A	189	ASN
3	A	195	GLN
3	A	255	HIS
3	A	392	GLN
3	A	448	ASN
3	A	475	ASN
3	A	490	GLN
3	A	554	ASN
3	A	559	GLN
3	A	593	ASN
3	A	614	GLN
3	A	674	HIS
3	A	676	HIS
3	A	704	ASN
2	B	68	GLN
2	B	103	GLN
2	B	111	GLN
2	B	132	ASN
2	B	144	GLN
3	D	106	ASN
3	D	162	ASN
3	D	165	GLN
3	D	189	ASN
3	D	195	GLN

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Mol	Chain	Res	Type
3	D	228	ASN
3	D	242	ASN
3	D	479	GLN
3	D	490	GLN
3	D	554	ASN
3	D	559	GLN
3	D	614	GLN
3	D	664	ASN
3	D	674	HIS
3	D	704	ASN
3	D	734	ASN
3	D	768	HIS
2	G	68	GLN
2	G	89	ASN
2	G	111	GLN
2	G	132	ASN
2	G	202	ASN
2	F	68	GLN
2	F	132	ASN
2	F	144	GLN
2	F	202	ASN
3	J	162	ASN
3	J	189	ASN
3	J	195	GLN
3	J	236	ASN
3	J	392	GLN
3	J	455	GLN
3	J	458	GLN
3	J	483	ASN
3	J	490	GLN
3	J	491	GLN
3	J	494	ASN
3	J	554	ASN
3	J	614	GLN
3	J	676	HIS
3	J	704	ASN
3	J	734	ASN
3	L	97	HIS
3	L	162	ASN
3	L	189	ASN
3	L	195	GLN
3	L	242	ASN

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Mol	Chain	Res	Type
3	L	255	HIS
3	L	392	GLN
3	L	448	ASN
3	L	458	GLN
3	L	490	GLN
3	L	502	GLN
3	L	554	ASN
3	L	593	ASN
3	L	614	GLN
3	L	674	HIS
3	L	704	ASN
3	L	734	ASN
3	L	763	GLN
3	L	768	HIS
3	K	106	ASN
3	K	162	ASN
3	K	189	ASN
3	K	195	GLN
3	K	365	ASN
3	K	392	GLN
3	K	448	ASN
3	K	483	ASN
3	K	486	ASN
3	K	495	HIS
3	K	560	HIS
3	K	593	ASN
3	K	614	GLN
3	K	674	HIS
3	K	676	HIS
3	K	699	HIS
3	K	704	ASN
3	N	30	ASN
3	N	82	ASN
3	N	106	ASN
3	N	162	ASN
3	N	195	GLN
3	N	228	ASN
3	N	242	ASN
3	N	370	GLN
3	N	392	GLN
3	N	448	ASN
3	N	490	GLN

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Mol	Chain	Res	Type
3	N	495	HIS
3	N	554	ASN
3	N	560	HIS
3	N	614	GLN
3	N	674	HIS
3	N	676	HIS
3	N	704	ASN
3	N	728	GLN
3	N	734	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](#)

6 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# $ Z > 2$	Counts	RMSZ	# $ Z > 2$
4	ADP	Q	401	-	28,29,29	1.38	5 (17%)	43,45,45	1.85	11 (25%)
4	ADP	R	401	-	28,29,29	1.37	5 (17%)	43,45,45	1.83	11 (25%)
4	ADP	P	401	-	28,29,29	1.37	5 (17%)	43,45,45	1.84	10 (23%)
4	ADP	H	401	-	28,29,29	1.37	5 (17%)	43,45,45	1.85	11 (25%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	ADP	E	401	-	28,29,29	1.37	5 (17%)	43,45,45	1.83	10 (23%)
4	ADP	O	401	-	28,29,29	1.37	5 (17%)	43,45,45	1.84	11 (25%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	ADP	Q	401	-	-	3/16/32/32	0/3/3/3
4	ADP	R	401	-	-	2/16/32/32	0/3/3/3
4	ADP	P	401	-	-	1/16/32/32	0/3/3/3
4	ADP	H	401	-	-	3/16/32/32	0/3/3/3
4	ADP	E	401	-	-	3/16/32/32	0/3/3/3
4	ADP	O	401	-	-	1/16/32/32	0/3/3/3

All (30) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	P	401	ADP	C5-C4	4.38	1.46	1.39
4	H	401	ADP	C5-C4	4.37	1.46	1.39
4	E	401	ADP	C5-C4	4.35	1.46	1.39
4	Q	401	ADP	C5-C4	4.35	1.46	1.39
4	R	401	ADP	C5-C4	4.34	1.46	1.39
4	O	401	ADP	C5-C4	4.28	1.46	1.39
4	O	401	ADP	C5-N7	-2.60	1.34	1.39
4	Q	401	ADP	C5-N7	-2.57	1.34	1.39
4	R	401	ADP	C5-N7	-2.57	1.34	1.39
4	P	401	ADP	C5-C6	2.50	1.48	1.41
4	E	401	ADP	C5-C6	2.50	1.48	1.41
4	E	401	ADP	C5-N7	-2.50	1.34	1.39
4	P	401	ADP	C5-N7	-2.50	1.34	1.39
4	H	401	ADP	C5-N7	-2.50	1.34	1.39
4	Q	401	ADP	C5-C6	2.49	1.47	1.41
4	H	401	ADP	C5-C6	2.49	1.47	1.41
4	O	401	ADP	C5-C6	2.48	1.47	1.41
4	R	401	ADP	C5-C6	2.48	1.47	1.41
4	Q	401	ADP	C4-N9	-2.23	1.33	1.37
4	E	401	ADP	C4-N9	-2.19	1.33	1.37
4	O	401	ADP	C4-N9	-2.19	1.33	1.37
4	R	401	ADP	C4-N9	-2.18	1.33	1.37

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	P	401	ADP	C4-N9	-2.16	1.33	1.37
4	H	401	ADP	C8-N7	2.15	1.35	1.31
4	H	401	ADP	C4-N9	-2.14	1.33	1.37
4	Q	401	ADP	C8-N7	2.14	1.35	1.31
4	O	401	ADP	C8-N7	2.14	1.35	1.31
4	R	401	ADP	C8-N7	2.13	1.35	1.31
4	P	401	ADP	C8-N7	2.13	1.35	1.31
4	E	401	ADP	C8-N7	2.09	1.35	1.31

All (64) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	H	401	ADP	C5-C4-N3	-5.82	118.71	126.72
4	P	401	ADP	C5-C4-N3	-5.81	118.71	126.72
4	E	401	ADP	C5-C4-N3	-5.79	118.74	126.72
4	R	401	ADP	C5-C4-N3	-5.77	118.77	126.72
4	O	401	ADP	C5-C4-N3	-5.75	118.81	126.72
4	Q	401	ADP	C5-C4-N3	-5.74	118.81	126.72
4	H	401	ADP	N3-C4-N9	4.59	134.98	127.17
4	P	401	ADP	N3-C4-N9	4.58	134.95	127.17
4	R	401	ADP	N3-C4-N9	4.54	134.88	127.17
4	E	401	ADP	N3-C4-N9	4.53	134.87	127.17
4	Q	401	ADP	N3-C4-N9	4.53	134.87	127.17
4	O	401	ADP	N3-C4-N9	4.51	134.84	127.17
4	H	401	ADP	C2-N3-C4	3.56	120.54	111.83
4	P	401	ADP	C4-C5-N7	-3.54	106.53	110.58
4	E	401	ADP	C4-C5-N7	-3.54	106.54	110.58
4	Q	401	ADP	C2-N3-C4	3.54	120.47	111.83
4	R	401	ADP	C2-N3-C4	3.54	120.47	111.83
4	O	401	ADP	C2-N3-C4	3.53	120.45	111.83
4	P	401	ADP	C2-N3-C4	3.50	120.39	111.83
4	H	401	ADP	C4-C5-N7	-3.50	106.58	110.58
4	Q	401	ADP	C4-C5-N7	-3.50	106.58	110.58
4	R	401	ADP	C4-C5-N7	-3.50	106.58	110.58
4	O	401	ADP	C4-C5-N7	-3.49	106.59	110.58
4	E	401	ADP	C2-N3-C4	3.49	120.35	111.83
4	Q	401	ADP	N3-C2-N1	-2.96	124.09	128.58
4	H	401	ADP	N3-C2-N1	-2.95	124.11	128.58
4	O	401	ADP	N3-C2-N1	-2.93	124.15	128.58
4	R	401	ADP	N3-C2-N1	-2.92	124.17	128.58
4	E	401	ADP	N3-C2-N1	-2.82	124.31	128.58
4	P	401	ADP	N3-C2-N1	-2.82	124.32	128.58

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	Q	401	ADP	C4-N9-C8	2.81	108.69	105.74
4	H	401	ADP	C4-N9-C8	2.78	108.66	105.74
4	P	401	ADP	C4-N9-C8	2.77	108.65	105.74
4	O	401	ADP	C4-N9-C8	2.75	108.63	105.74
4	R	401	ADP	C4-N9-C8	2.70	108.58	105.74
4	E	401	ADP	C4-N9-C8	2.70	108.57	105.74
4	O	401	ADP	C5-N7-C8	2.55	107.47	103.45
4	P	401	ADP	C5-N7-C8	2.54	107.45	103.45
4	Q	401	ADP	C5-N7-C8	2.54	107.44	103.45
4	H	401	ADP	C5-N7-C8	2.54	107.44	103.45
4	E	401	ADP	C5-N7-C8	2.52	107.41	103.45
4	R	401	ADP	C5-N7-C8	2.51	107.39	103.45
4	Q	401	ADP	C2'-C1'-N9	-2.39	107.35	113.30
4	H	401	ADP	C3'-C2'-C1'	2.37	105.95	101.46
4	E	401	ADP	C3'-C2'-C1'	2.36	105.93	101.46
4	O	401	ADP	C3'-C2'-C1'	2.34	105.89	101.46
4	R	401	ADP	C3'-C2'-C1'	2.34	105.88	101.46
4	Q	401	ADP	C3'-C2'-C1'	2.33	105.88	101.46
4	P	401	ADP	C3'-C2'-C1'	2.32	105.86	101.46
4	O	401	ADP	C2'-C1'-N9	-2.31	107.56	113.30
4	E	401	ADP	C2'-C1'-N9	-2.31	107.57	113.30
4	H	401	ADP	C2'-C1'-N9	-2.28	107.63	113.30
4	P	401	ADP	C2'-C1'-N9	-2.11	108.07	113.30
4	O	401	ADP	N9-C8-N7	-2.10	110.96	113.94
4	Q	401	ADP	N9-C8-N7	-2.09	110.96	113.94
4	R	401	ADP	C2'-C1'-N9	-2.09	108.10	113.30
4	H	401	ADP	N9-C8-N7	-2.06	111.01	113.94
4	P	401	ADP	N9-C8-N7	-2.04	111.03	113.94
4	H	401	ADP	C6-C5-N7	2.01	135.96	132.09
4	E	401	ADP	N9-C8-N7	-2.01	111.09	113.94
4	O	401	ADP	O2A-PA-O1A	2.01	121.78	112.44
4	Q	401	ADP	C6-C5-N7	2.00	135.95	132.09
4	R	401	ADP	O2A-PA-O1A	2.00	121.75	112.44
4	R	401	ADP	N9-C8-N7	-2.00	111.10	113.94

There are no chirality outliers.

All (13) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	E	401	ADP	C5'-O5'-PA-O2A
4	E	401	ADP	C5'-O5'-PA-O3A
4	H	401	ADP	C5'-O5'-PA-O2A

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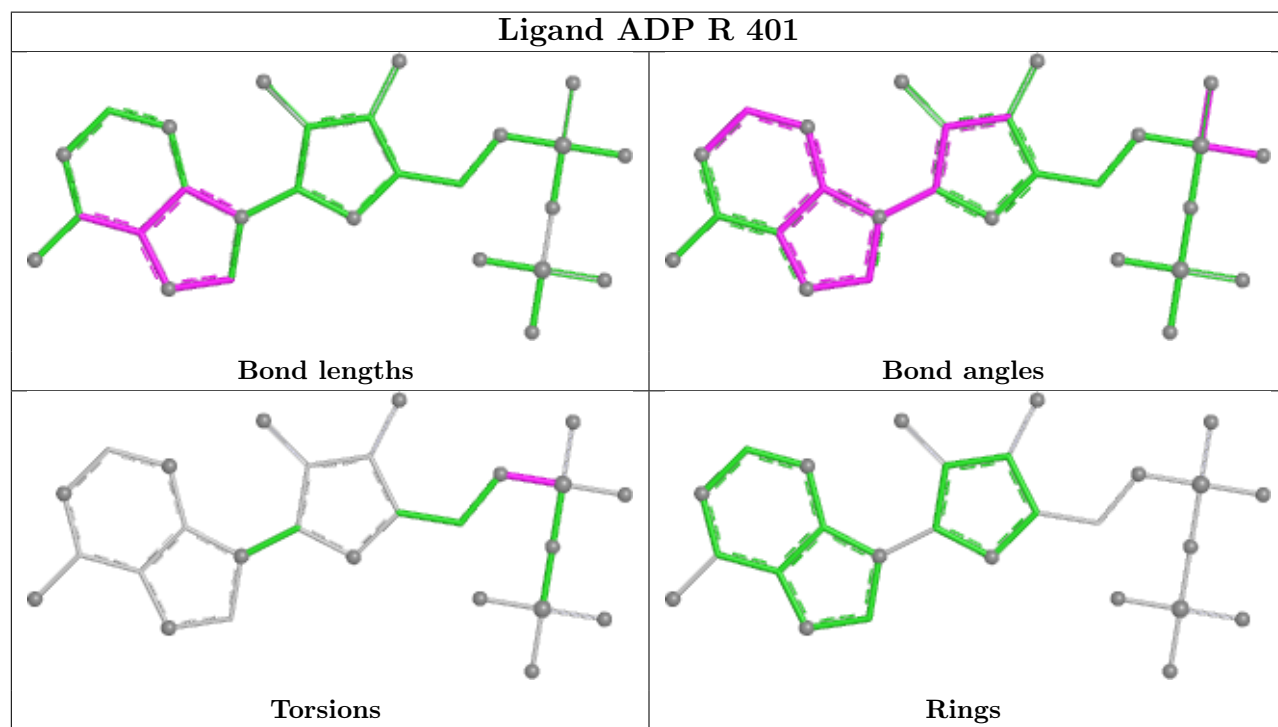
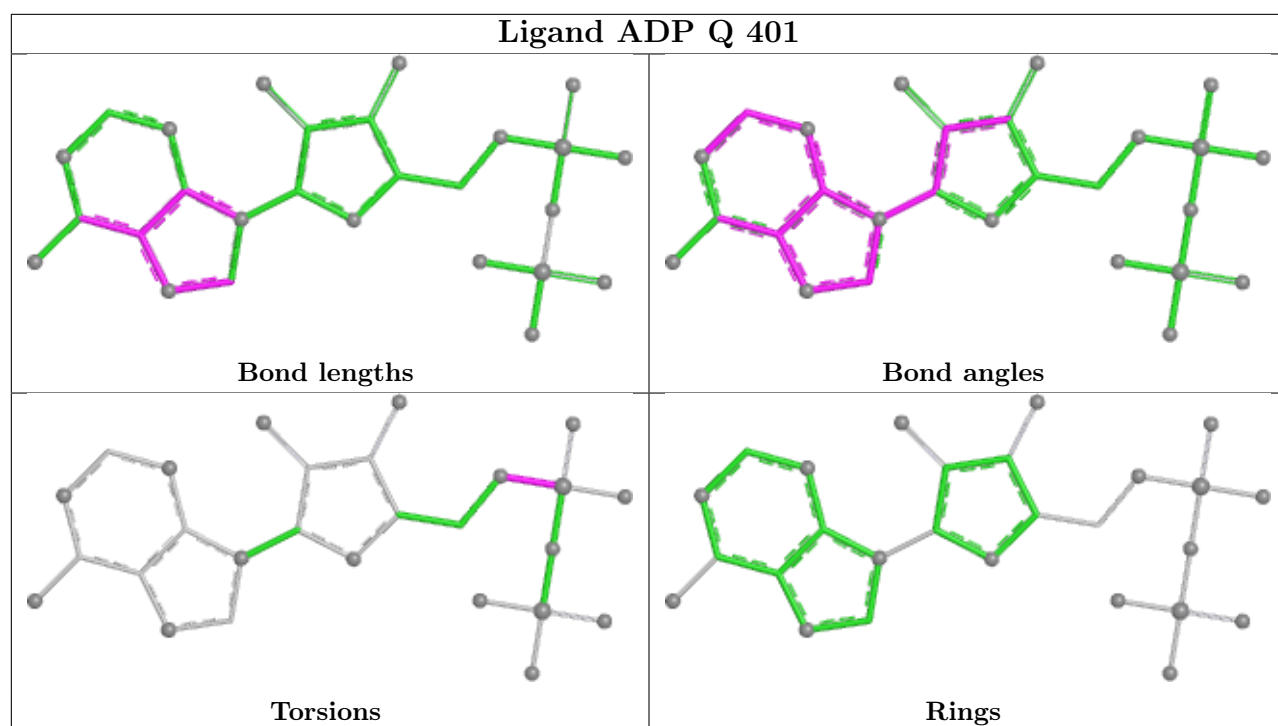
Mol	Chain	Res	Type	Atoms
4	H	401	ADP	C5'-O5'-PA-O3A
4	O	401	ADP	C5'-O5'-PA-O2A
4	Q	401	ADP	C5'-O5'-PA-O2A
4	P	401	ADP	C5'-O5'-PA-O2A
4	R	401	ADP	C5'-O5'-PA-O2A
4	E	401	ADP	C5'-O5'-PA-O1A
4	H	401	ADP	C5'-O5'-PA-O1A
4	Q	401	ADP	C5'-O5'-PA-O1A
4	Q	401	ADP	C5'-O5'-PA-O3A
4	R	401	ADP	C5'-O5'-PA-O3A

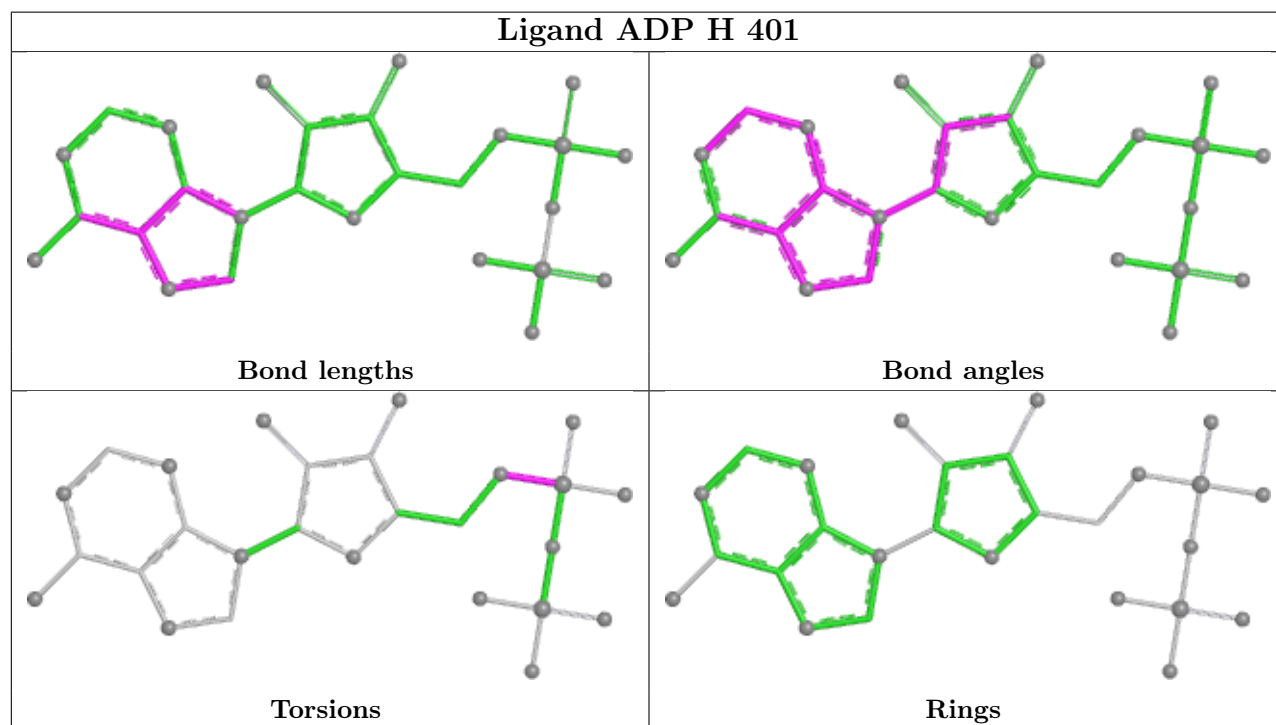
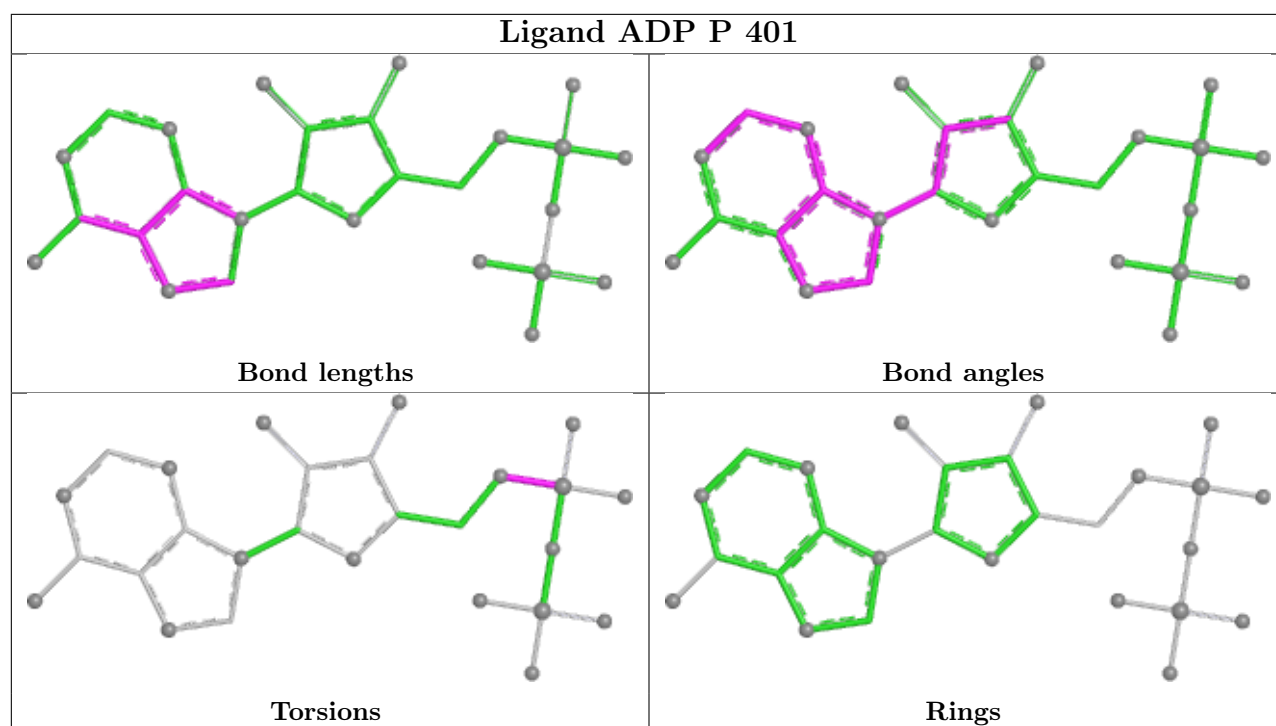
There are no ring outliers.

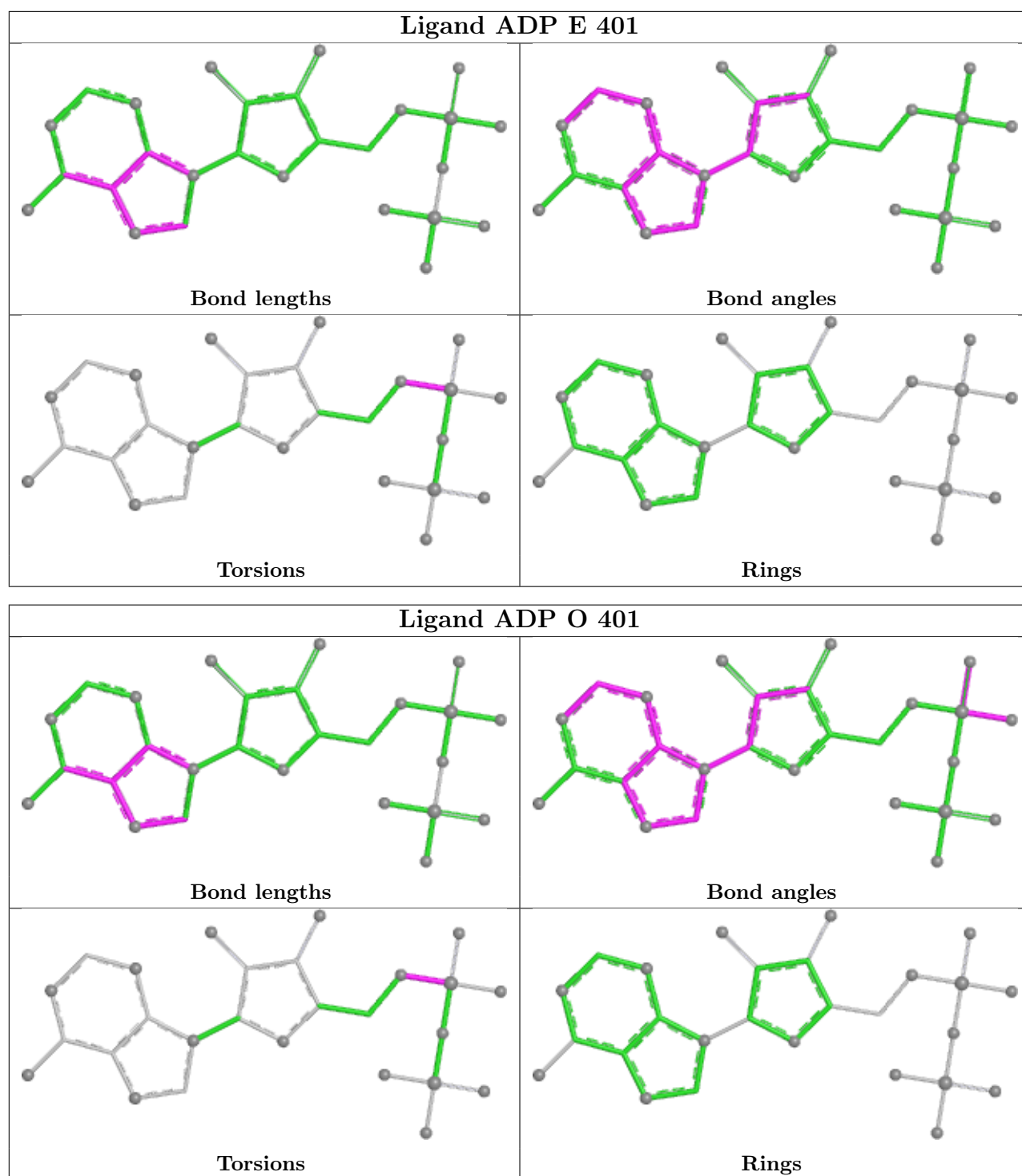
6 monomers are involved in 18 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	Q	401	ADP	3	0
4	R	401	ADP	3	0
4	P	401	ADP	3	0
4	H	401	ADP	3	0
4	E	401	ADP	3	0
4	O	401	ADP	3	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.







5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

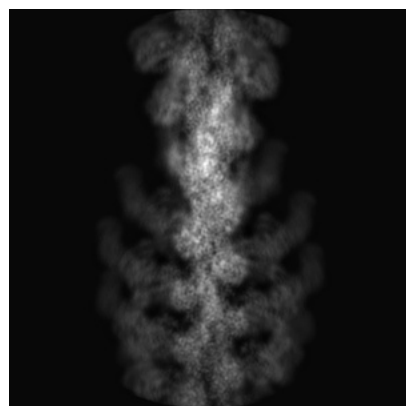
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-39905. These allow visual inspection of the internal detail of the map and identification of artifacts.

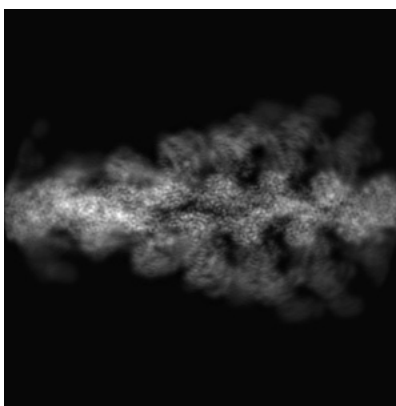
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

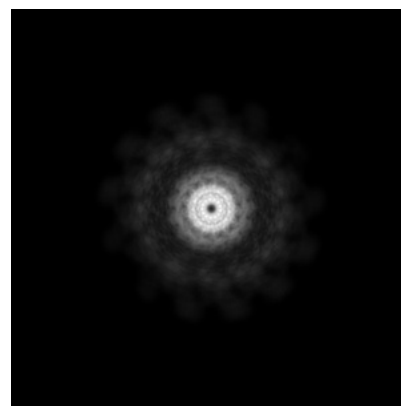
6.1.1 Primary map



X

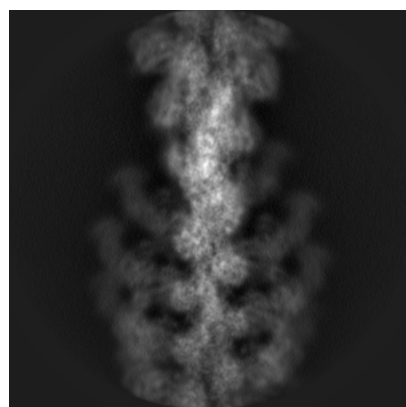


Y

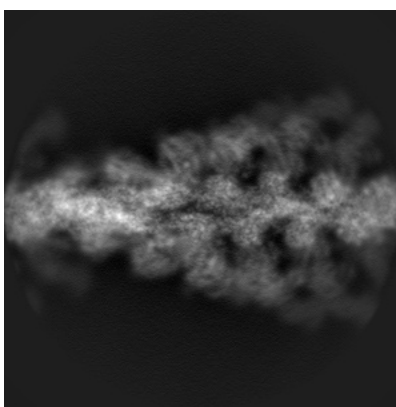


Z

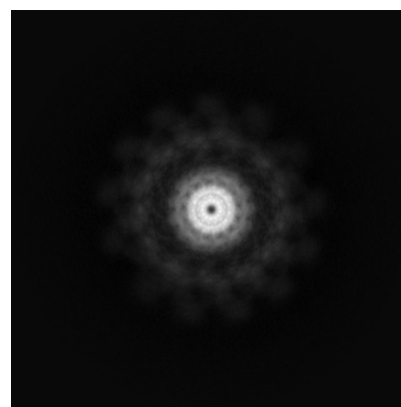
6.1.2 Raw map



X



Y

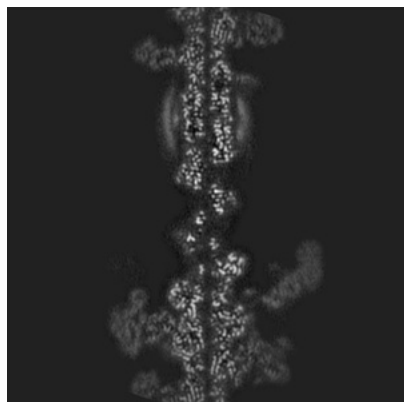


Z

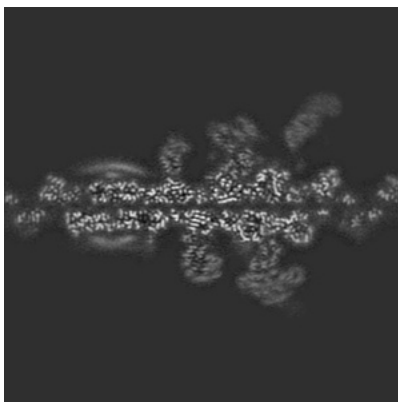
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

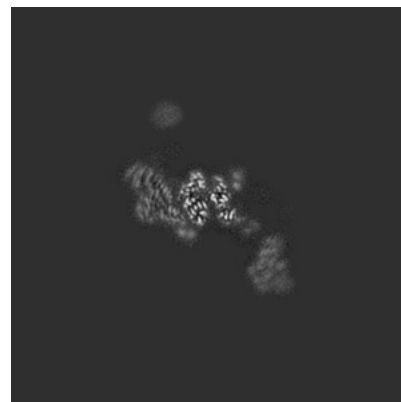
6.2.1 Primary map



X Index: 256

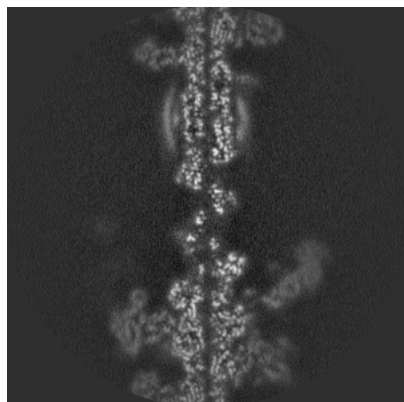


Y Index: 256

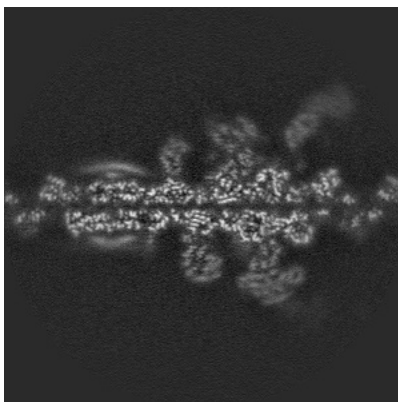


Z Index: 256

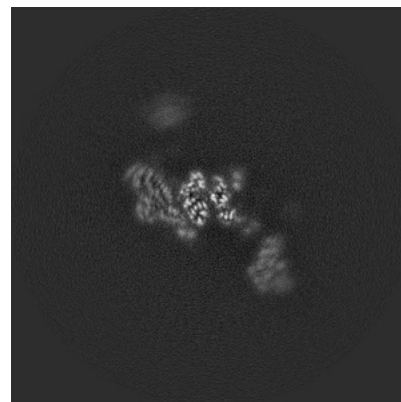
6.2.2 Raw map



X Index: 256



Y Index: 256

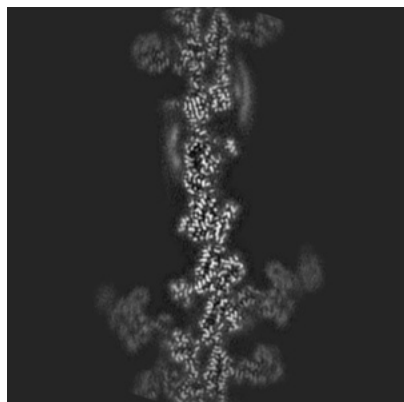


Z Index: 256

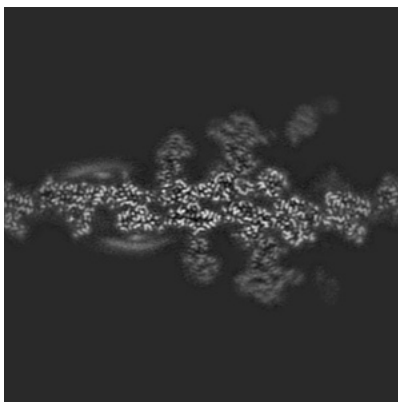
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

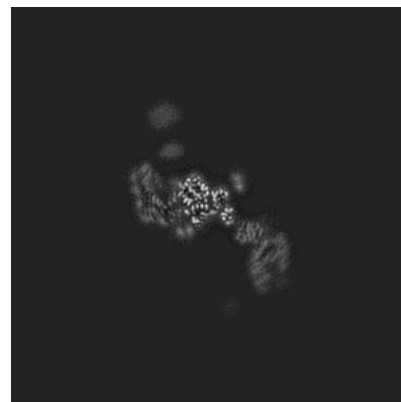
6.3.1 Primary map



X Index: 245

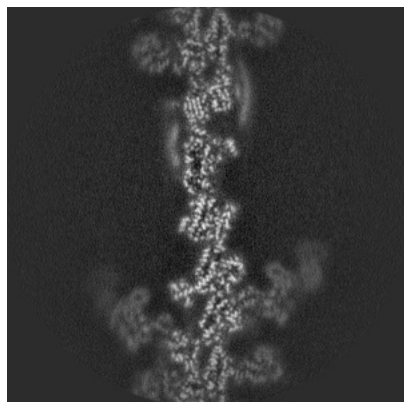


Y Index: 248

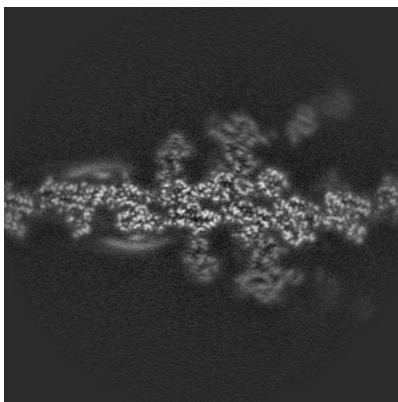


Z Index: 247

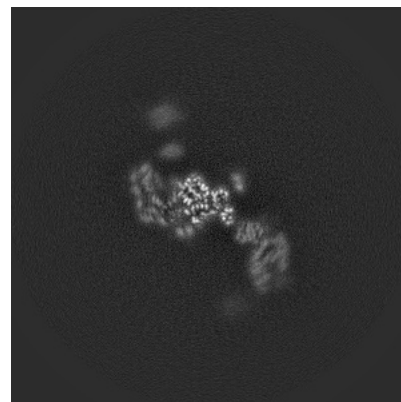
6.3.2 Raw map



X Index: 246



Y Index: 248

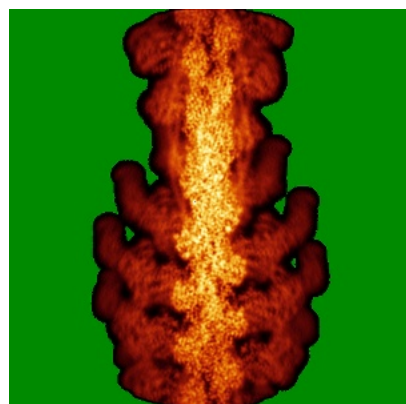


Z Index: 247

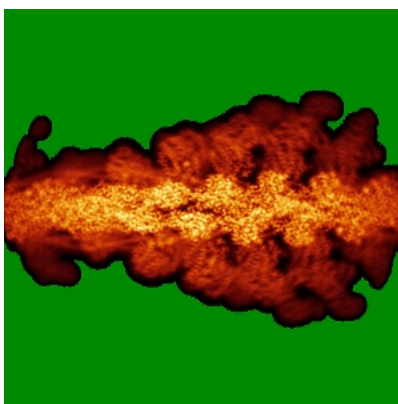
The images above show the largest variance slices of the map in three orthogonal directions.

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

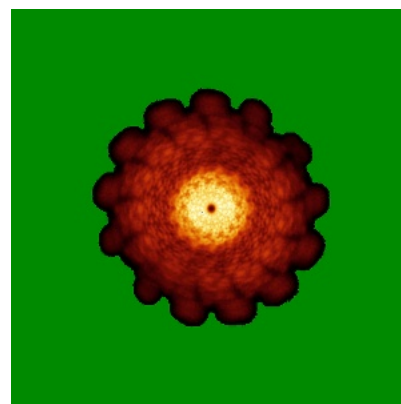
6.4.1 Primary map



X

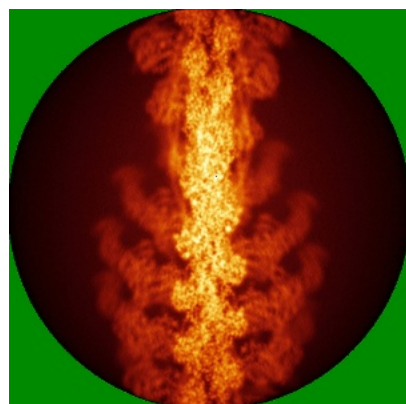


Y

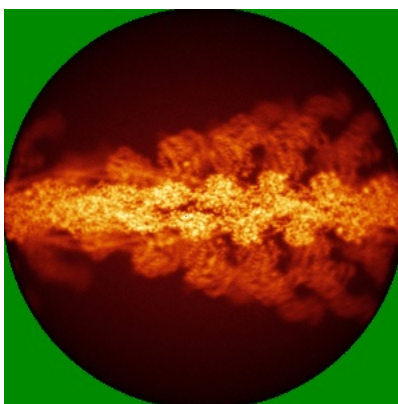


Z

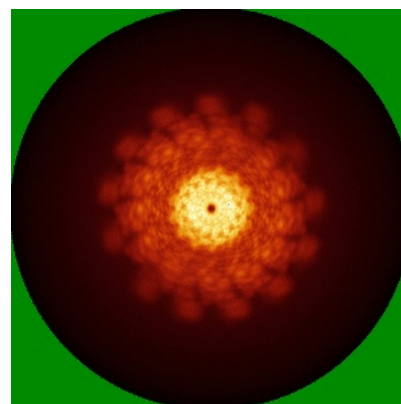
6.4.2 Raw map



X



Y



Z

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

6.5 Orthogonal surface views [i](#)

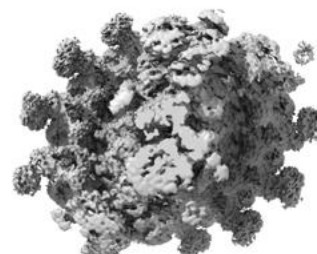
6.5.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.003. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

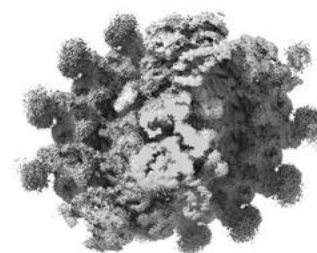
6.5.2 Raw map



X



Y



Z

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

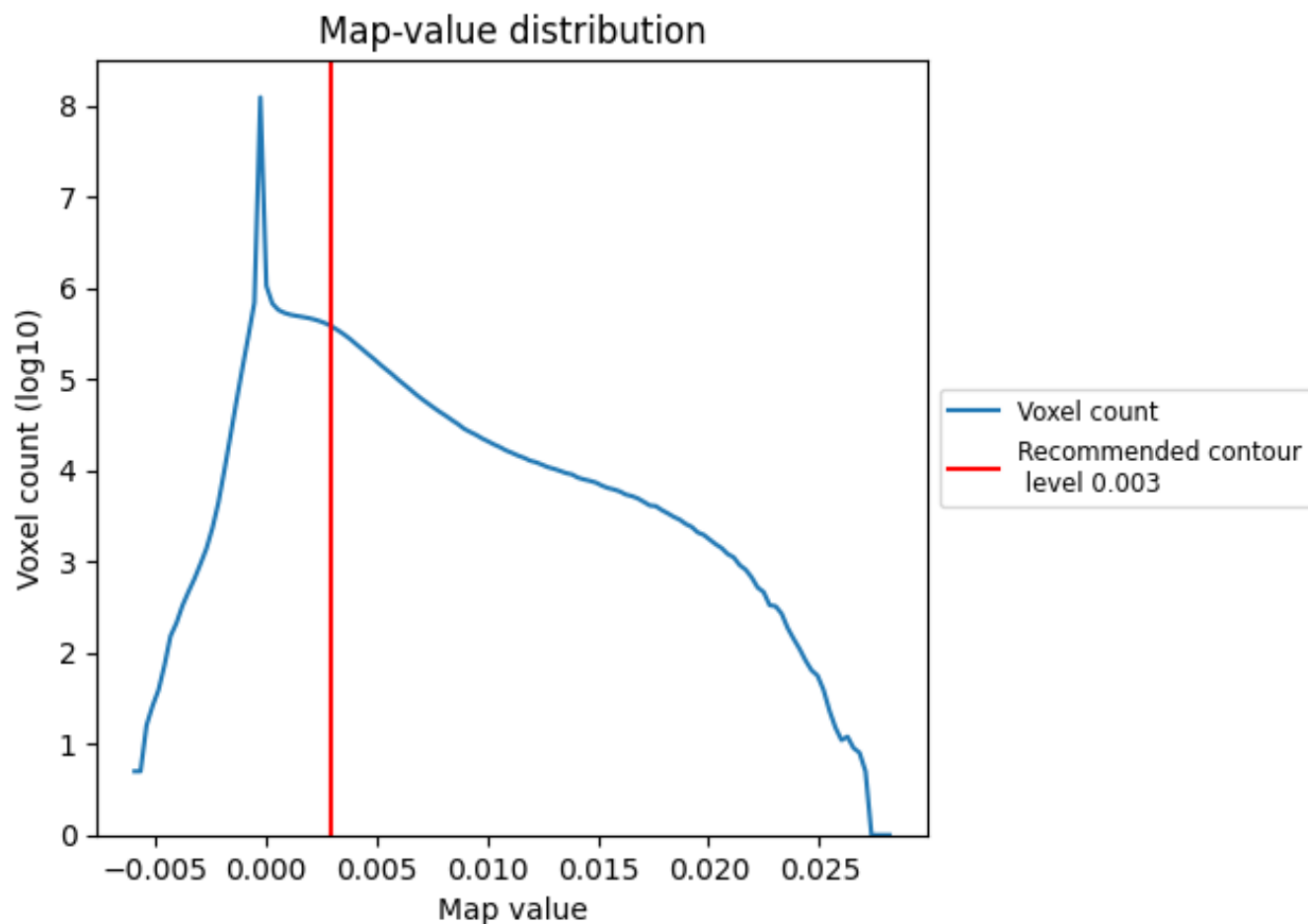
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

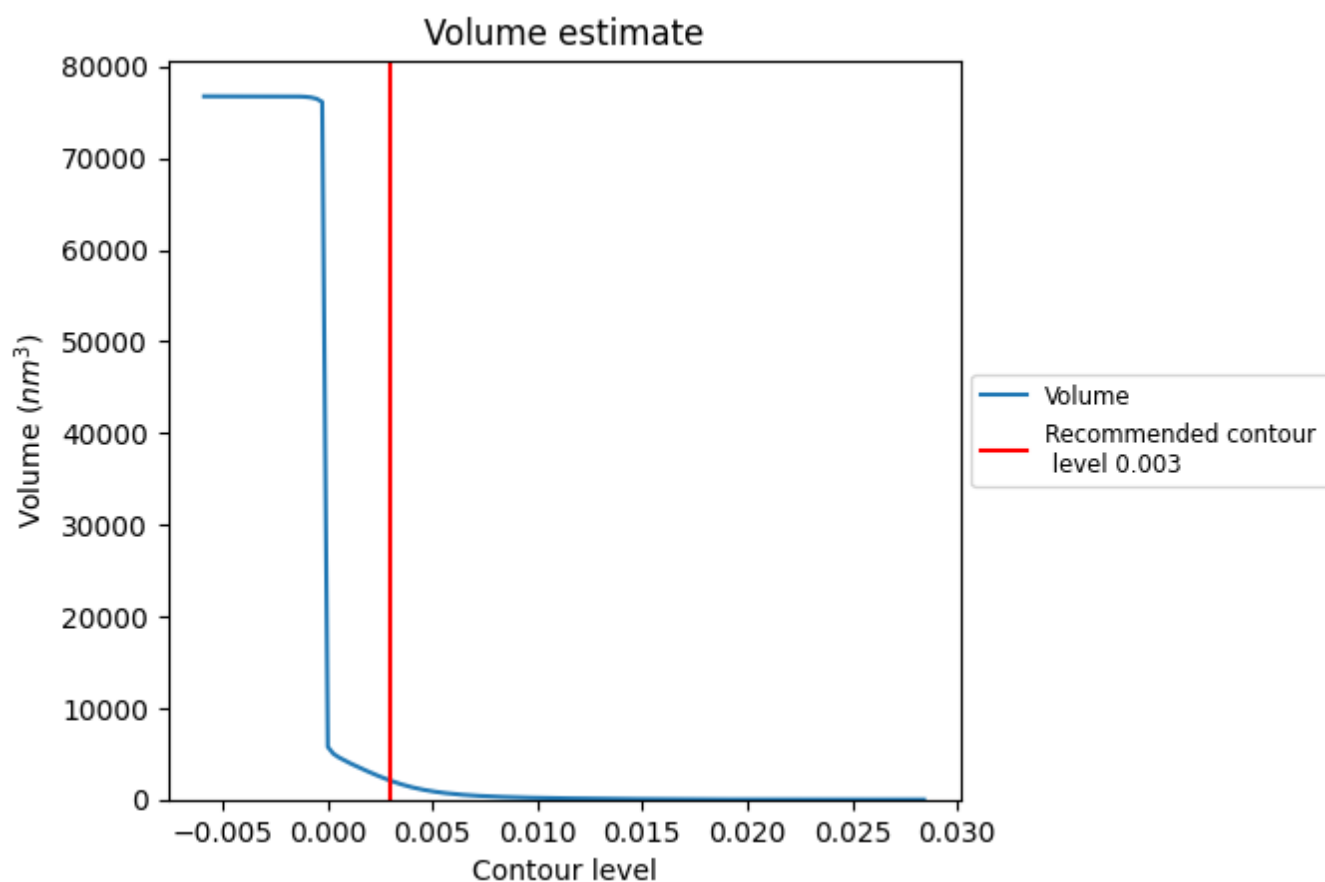
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

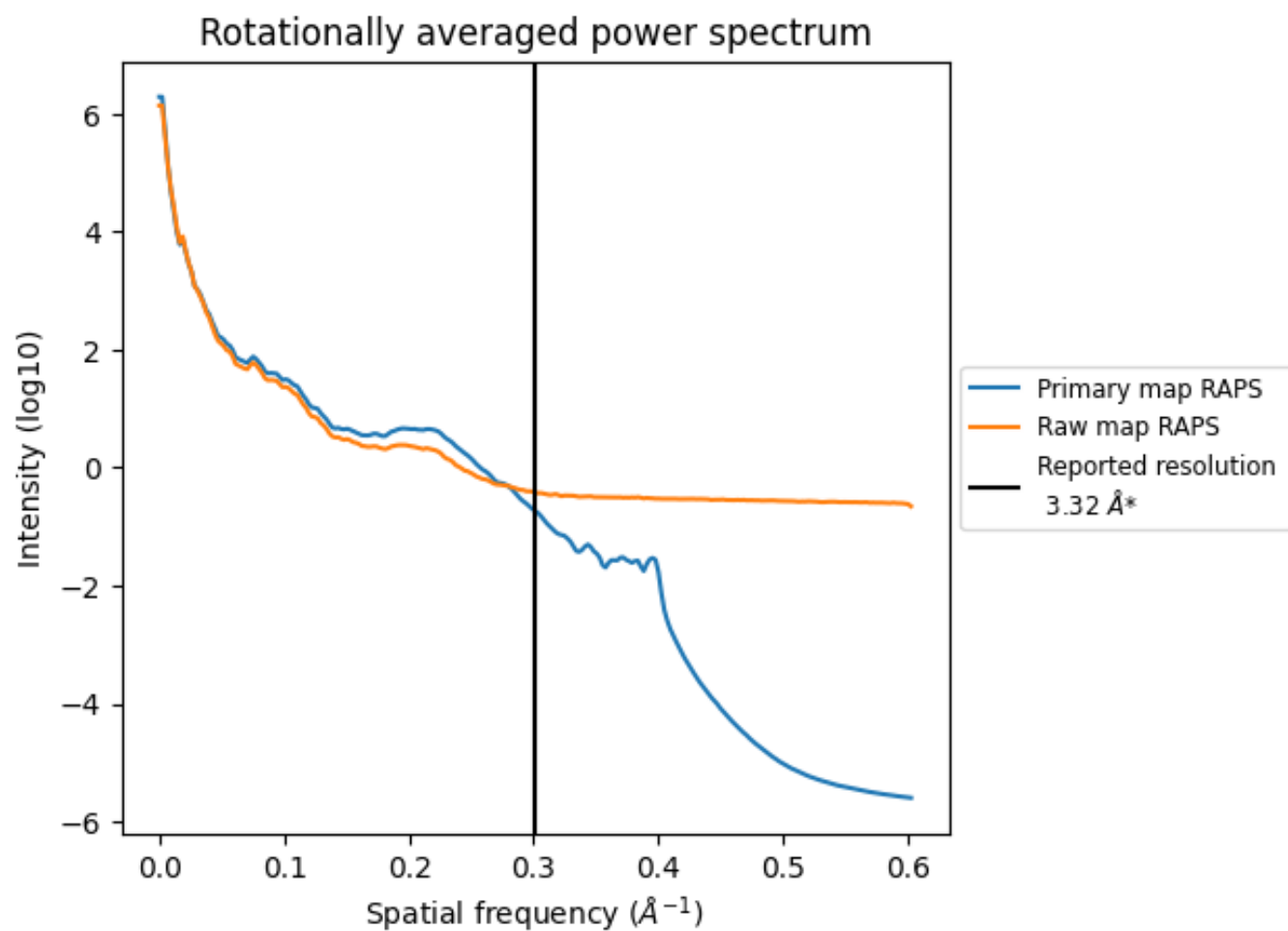
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2063 nm³; this corresponds to an approximate mass of 1863 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 ⓘ

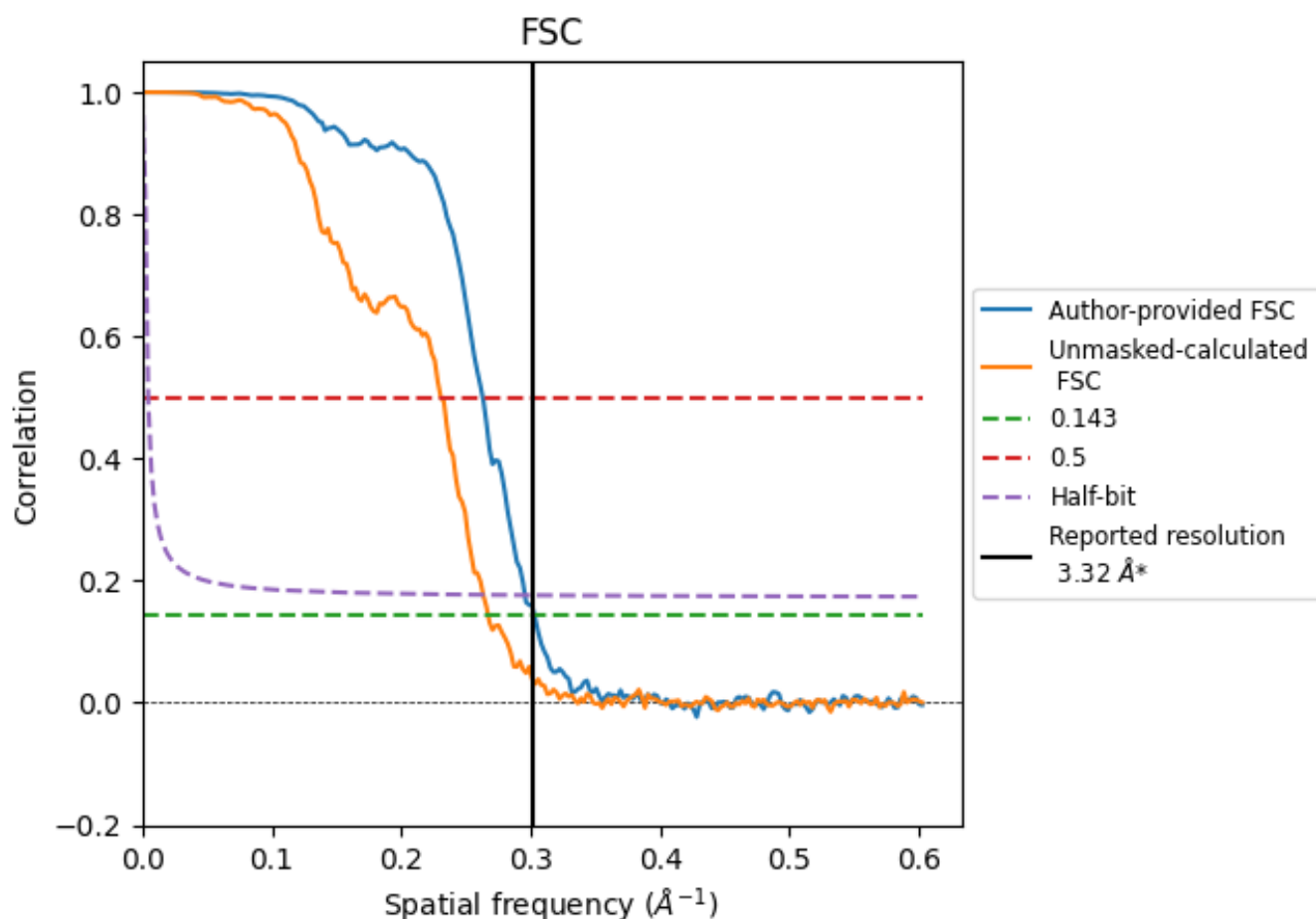


*Reported resolution corresponds to spatial frequency of 0.301 Å⁻¹

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.301 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

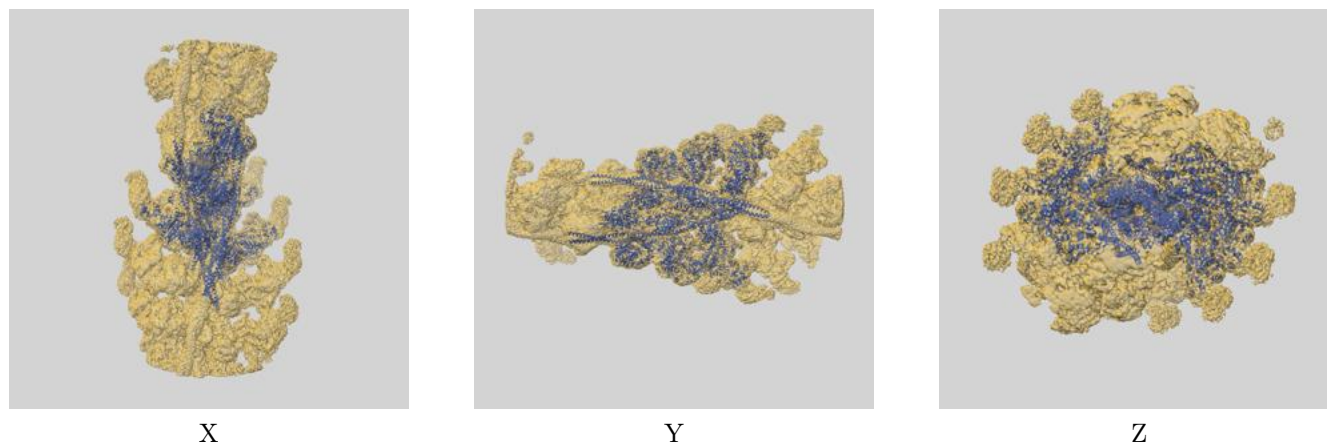
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.32	-	-
Author-provided FSC curve	3.30	3.80	3.38
Unmasked-calculated*	3.74	4.33	3.80

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 3.74 differs from the reported value 3.32 by more than 10 %

9 Map-model fit [i](#)

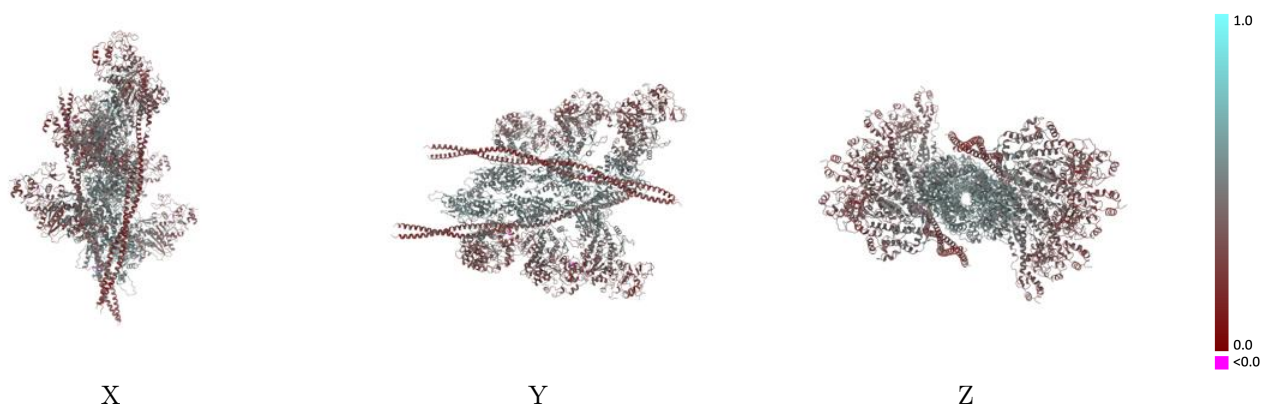
This section contains information regarding the fit between EMDB map EMD-39905 and PDB model 8ZBM. Per-residue inclusion information can be found in [section 3](#) on [page 6](#).

9.1 Map-model overlay [i](#)



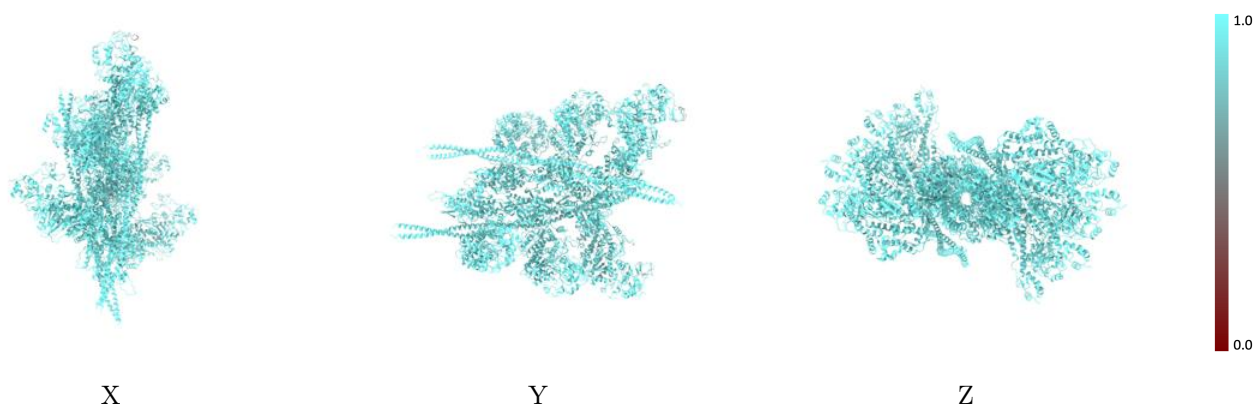
The images above show the 3D surface view of the map at the recommended contour level 0.003 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



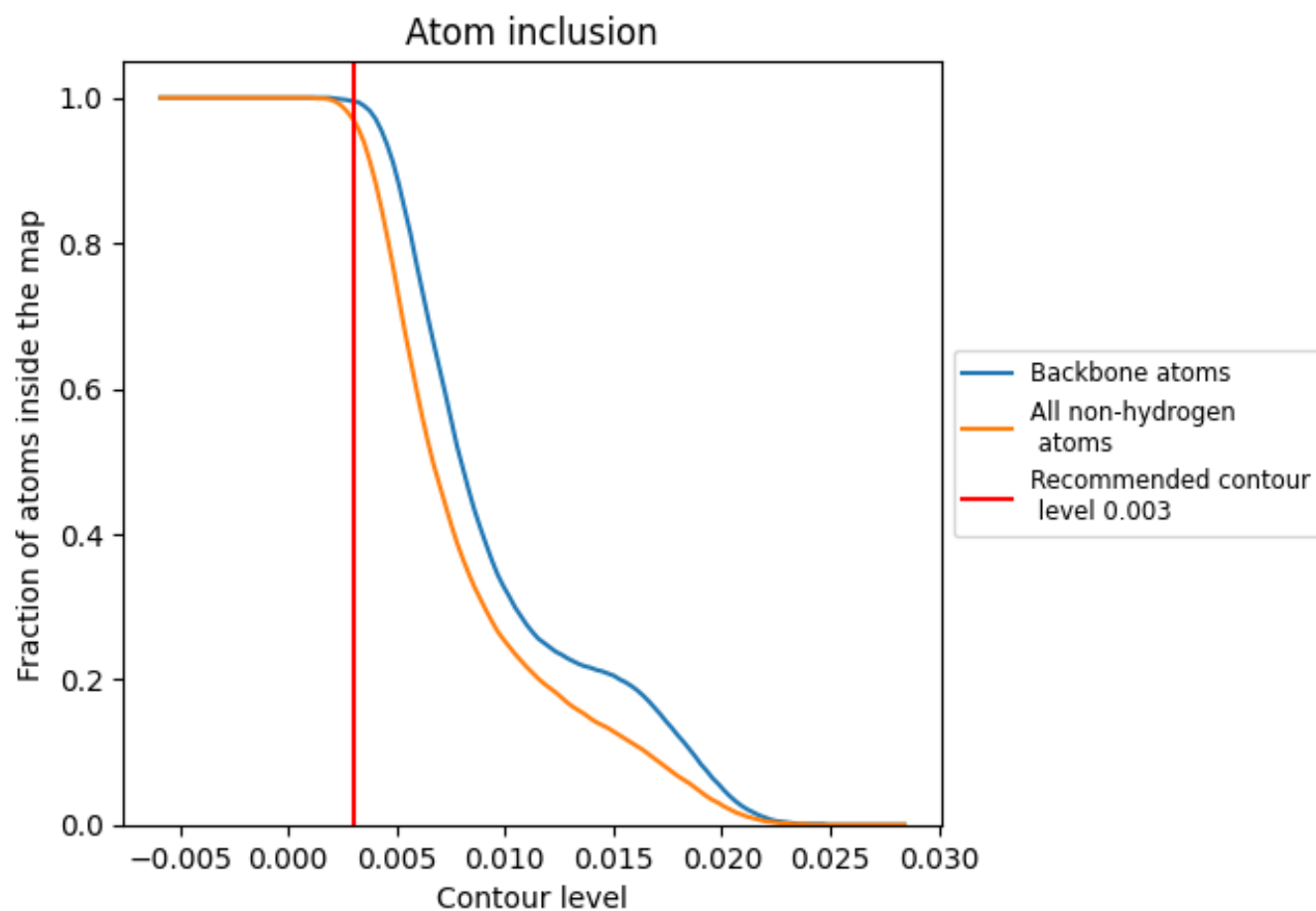
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.003).

9.4 Atom inclusion [i](#)



At the recommended contour level, 100% of all backbone atoms, 97% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary

The table lists the average atom inclusion at the recommended contour level (0.003) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9700	 0.4180
A	 0.9600	 0.3860
B	 0.9800	 0.2430
C	 0.9790	 0.2510
D	 0.9580	 0.3840
E	 0.9970	 0.5410
F	 0.9820	 0.2370
G	 0.9760	 0.2400
H	 0.9970	 0.5380
J	 0.9590	 0.3860
K	 0.9470	 0.3780
L	 0.9570	 0.3880
N	 0.9530	 0.3820
O	 0.9990	 0.5420
P	 0.9980	 0.5360
Q	 0.9980	 0.5430
R	 0.9980	 0.5390

