



Full wwPDB EM Validation Report ⓘ

Mar 9, 2024 – 09:59 AM EST

PDB ID : 6O2O
EMDB ID : EMD-0610
Title : CDTb Double Heptamer Short Form Modeled from Cryo-EM Map Reconstructed using C1 Symmetry
Authors : Lacy, D.B.; Sheedlo, M.J.; Anderson, D.M.
Deposited on : 2019-02-24
Resolution : 4.53 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:

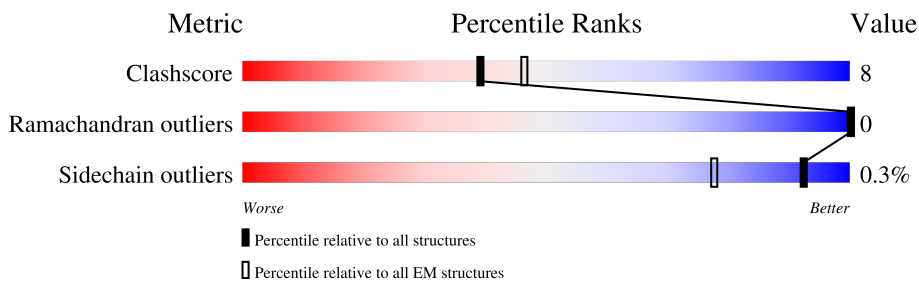
EMDB validation analysis : 0.0.1.dev70
MolProbity : 4.02b-467
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.36

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 4.53 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.



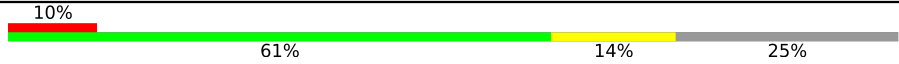
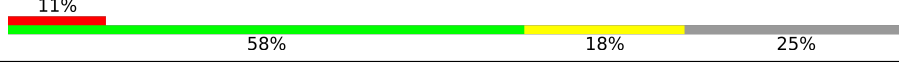



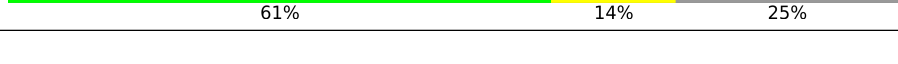
Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826

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

Mol	Chain	Length	Quality of chain
1	A	876	
1	B	876	
1	C	876	
1	D	876	
1	E	876	
1	F	876	
1	G	876	
1	H	876	

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Mol	Chain	Length	Quality of chain
1	I	876	
1	J	876	
1	K	876	
1	L	876	
1	M	876	
1	Z	876	

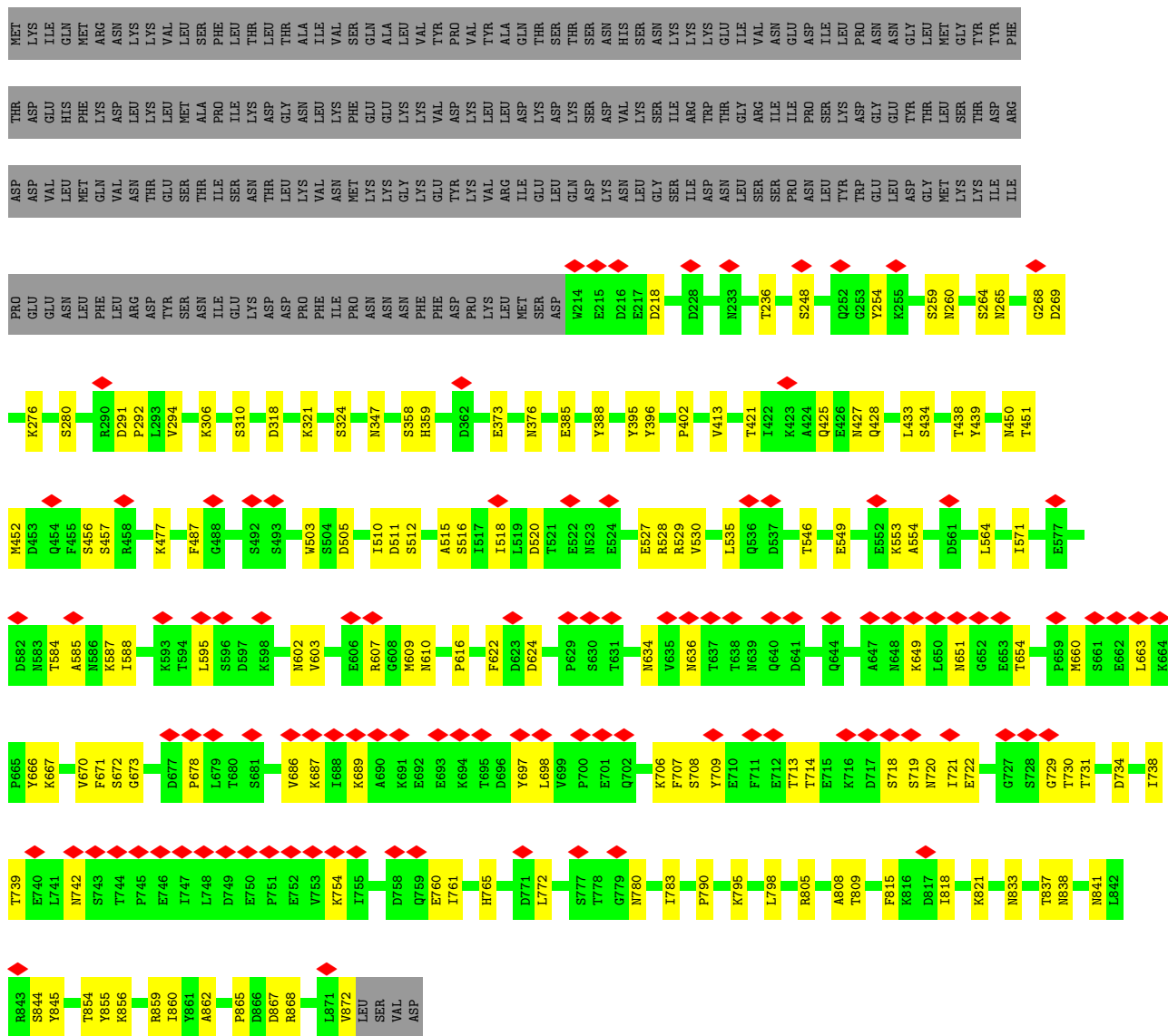
2 Entry composition [i](#)

There is only 1 type of molecule in this entry. The entry contains 72637 atoms, of which 0 are hydrogens and 0 are deuteriums.

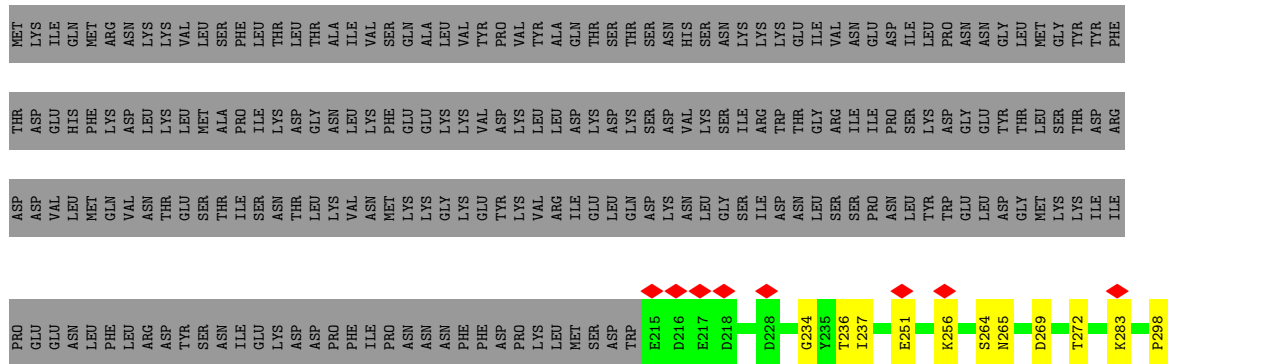
In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

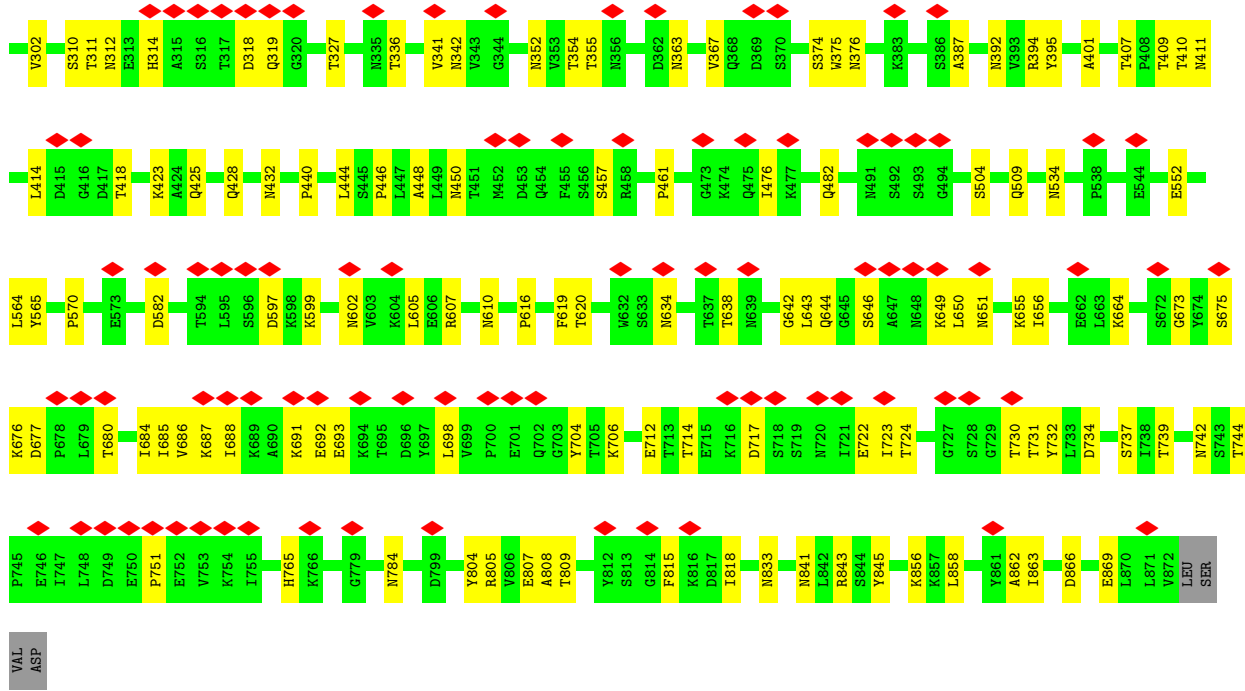
- Molecule 1 is a protein called ADP-ribosyltransferase binding component.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	A	659	5196	3254	844	1088	10	0	0
1	B	659	5196	3254	844	1088	10	0	0
1	C	658	5182	3243	842	1087	10	0	0
1	D	659	5196	3254	844	1088	10	0	0
1	E	658	5182	3243	842	1087	10	0	0
1	F	659	5196	3254	844	1088	10	0	0
1	G	658	5182	3243	842	1087	10	0	0
1	H	659	5196	3254	844	1088	10	0	0
1	I	658	5182	3243	842	1087	10	0	0
1	J	659	5196	3254	844	1088	10	0	0
1	K	658	5182	3243	842	1087	10	0	0
1	L	659	5196	3254	844	1088	10	0	0
1	M	658	5182	3243	842	1087	10	0	0
1	Z	657	5173	3238	841	1084	10	0	0

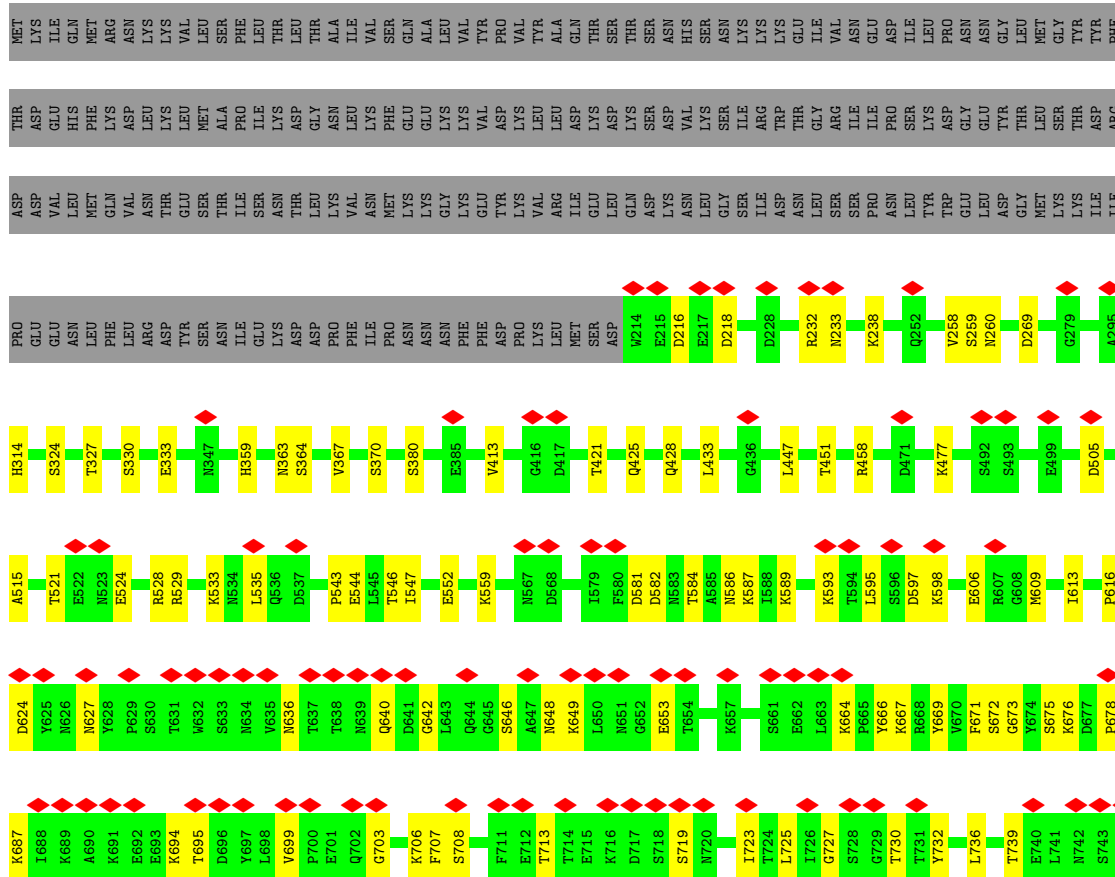


● Molecule 1: ADP-ribosyltransferase binding component





• Molecule 1: ADP-ribosyltransferase binding component





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MET LYS ILE GLN MET ARG ASN LYS LYS VAL LEU MET LEU PHE SER PHE LEU THR THR ASP THR ALA THR ILE VAL SER GLN LEU VAL TYR PRO ASP F815 TYR ALA ARG GLN THR SER ASP ASN HIS SER ASN VAL LYS LYS TRP LYS LEU ILE VAL R859 I860 D867 V872 LEU SER VAL ASP

THR ASP GLU HIS PHE LYS ASP LEU MET LEU MET LEU ALA PRO ILE LEU THR ASP THR ASP ASN ALA THR ILE VAL PHE GLN LEU VAL TYR PRO ASP F815 TYR ALA ARG GLN THR SER ASP ASN HIS SER ASN VAL LYS LYS TRP LYS LEU ILE VAL R859 I860 D867 V872 LEU SER VAL ASP

ASP ASP VAL LEU MET GLM VAL ASP THR THR LEU MET LEU MET LEU ILE SER ASN THR THR ASP THR LYS LYS VAL ASN MET PHE GLN LEU VAL TYR PRO ASP F815 TYR ALA ARG GLN THR SER ASP ASN HIS SER ASN VAL LYS LYS TRP LYS LEU ILE VAL R859 I860 D867 V872 LEU SER VAL ASP

PRO GLU ASN ANS LEU PHE LEU ARG ASP TYR SER SER ILE GLU ASN THR ASP THR ASP ASN ALA THR ILE VAL PHE GLN LEU VAL TYR PRO ASP F815 TYR ALA ARG GLN THR SER ASP ASN HIS SER ASN VAL LYS LYS TRP LYS LEU ILE VAL R859 I860 D867 V872 LEU SER VAL ASP

I299 V300 G301 V302 E305 K306 L307 N312 E313 H314 A315 S316 T317 D318 Q319 G320 K321 T327 N335 T336 A337 S340 V341 N342 V343 G344 Y345 Q346 T354 T355 S358 D362 N363 S374 V375 N376 T377 G378 S380 K383 A387 Y388 I389 R394 G399 T400

A401 T410 M411 L412 V413 G416 D417 T418 Q425 E426 M431 M432 P440 K441 K442 G443 L449 Q454 F455 S456 S457 T460 P461 T462 D465 L470 K474 L478 E479 V483 F487 M491 S492 S493 E499 G500 N501 S504 I513 S514 A515

L519 T531 A532 K533 N534 D537 P538 E539 D540 K541 L545 G556 K560 D561 G562 L563 L564 E577 D582 N583 T584 K587 D590 S591 L592 K593 T594 L595 S596 D597 K598 E606 R607 G608 M609 R610 K614 T615 P616 N621 F622 N634 D641 G642 L643 Q644

G645 S646 A647 N648 K649 L650 N651 G652 E653 L656 E662 S675 K676 D677 P678 L679 T680 L684 I685 V686 K687 L688 K689 A690 E692 E693 K694 D696 L698 V699 P700 E701 G702 G703 Y704 T705 T714 D717 S718 S719 N720 I721 E722 I723 T724 L725 T730 T731 Y732 L733

S737 I738 I739 N742 D749 E750 F751 E752 W754 I755 T757 D758 Q759 H765 G779 N780 L798 A808 T809 Y812 F815 I818 K821 R826 N827 Y828 D831 P832 N833 D834 P835 K836 T837 N838 R843 S844 Y845 E850 I863 E869 L870

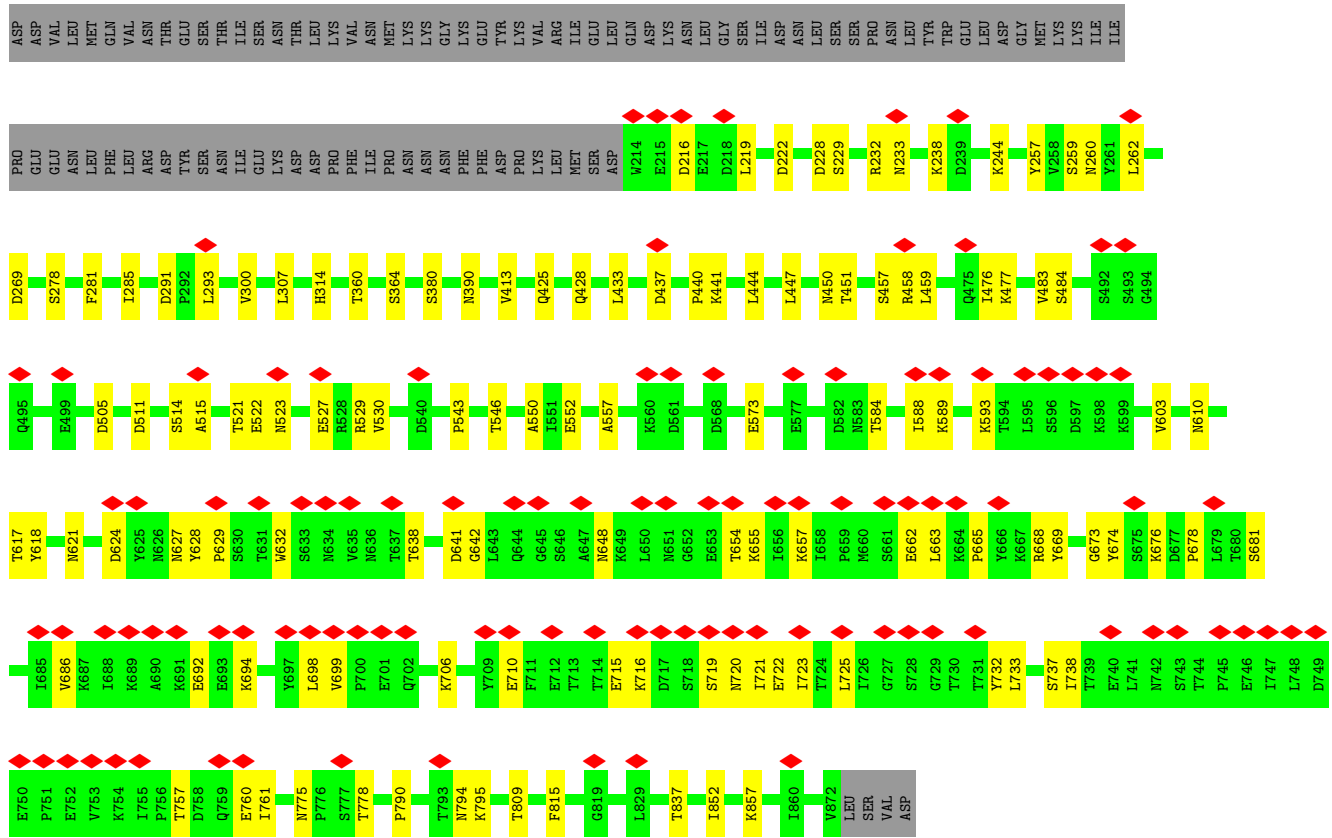
L871 V872 LEU SER VAL ASP

• Molecule 1: ADP-ribosyltransferase binding component

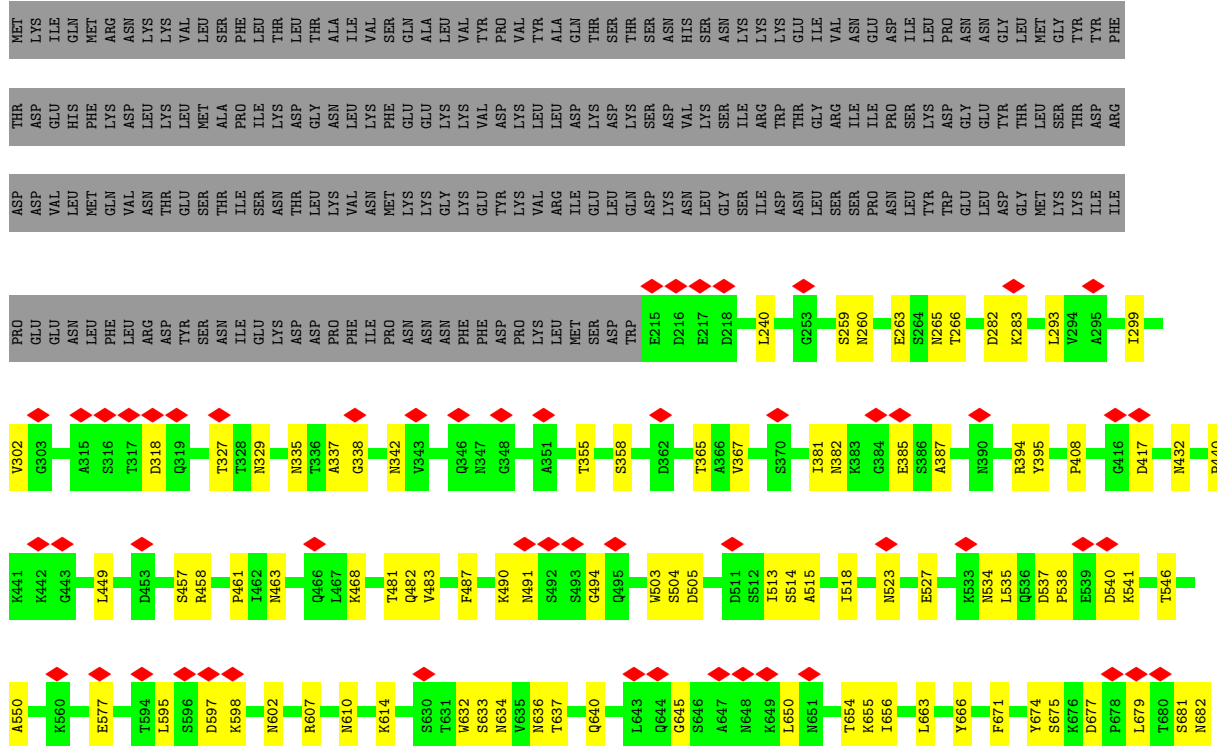


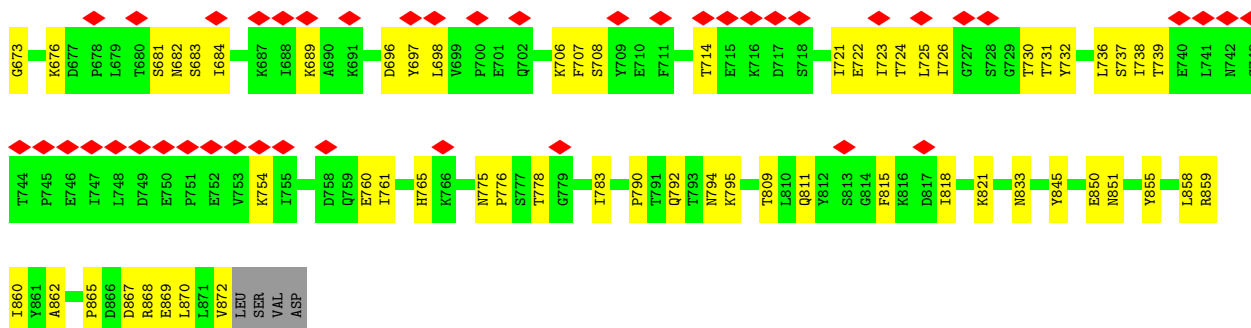
MET LYS ILE GLN MET ARG ASN LYS LYS VAL LEU MET LEU MET LEU ALA PRO ILE LEU THR THR ASP THR ALA THR ILE VAL SER GLN LEU VAL TYR PRO ASP F815 TYR ALA ARG GLN THR SER ASP ASN HIS SER ASN VAL LYS LYS TRP LYS LEU ILE VAL R859 I860 D867 V872 LEU SER VAL ASP

THR ASP GLU HIS PHE LYS ASP LEU MET LEU MET LEU ALA PRO ILE LEU THR ASP THR ASP ASN ALA THR ILE VAL PHE GLN LEU VAL TYR PRO ASP F815 TYR ALA ARG GLN THR SER ASP ASN HIS SER ASN VAL LYS LYS TRP LYS LEU ILE VAL R859 I860 D867 V872 LEU SER VAL ASP

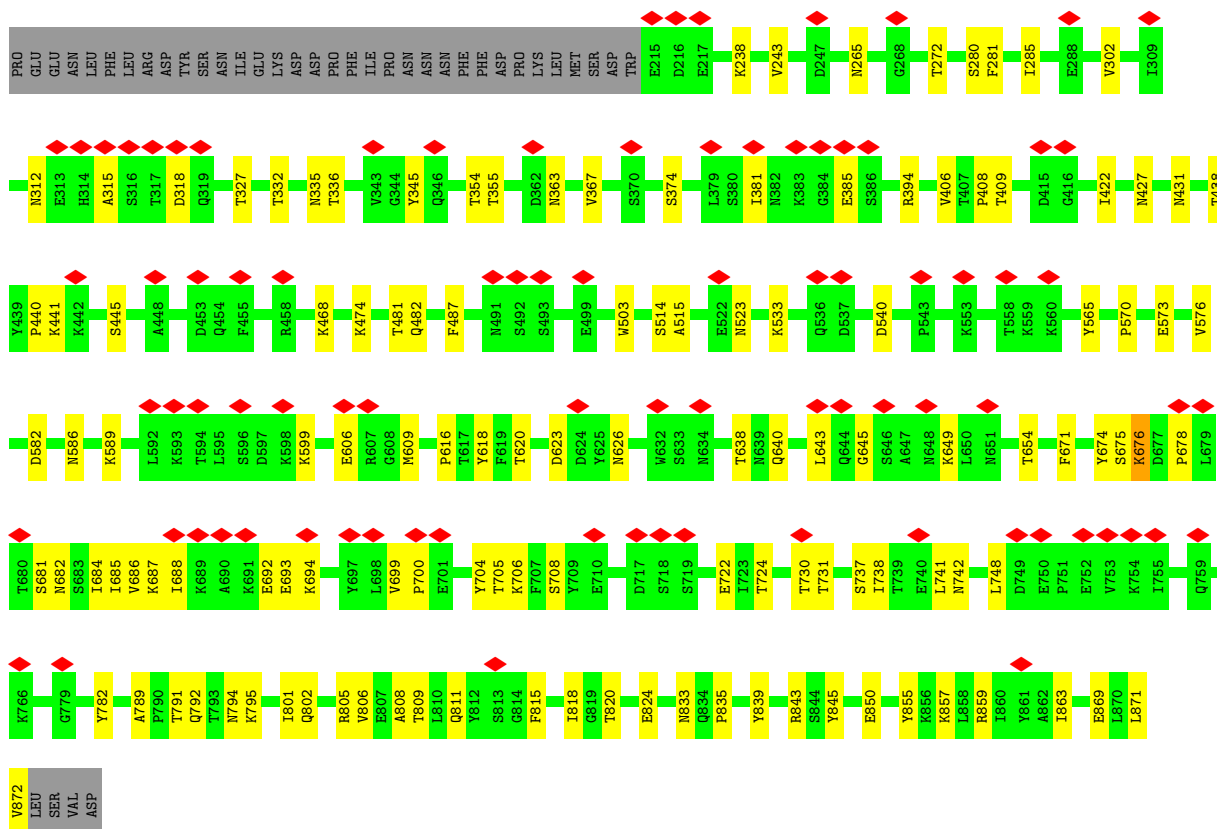
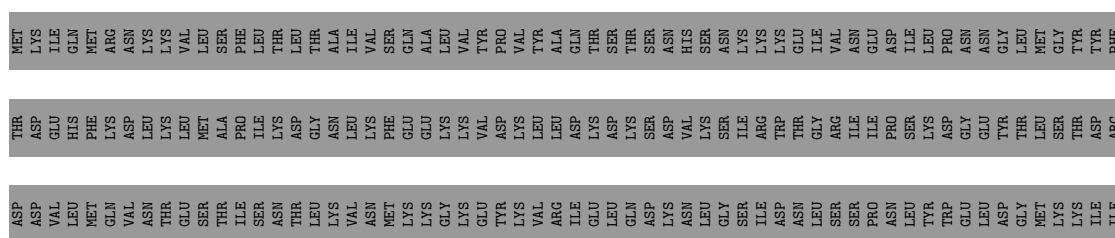


● Molecule 1: ADP-ribosyltransferase binding component



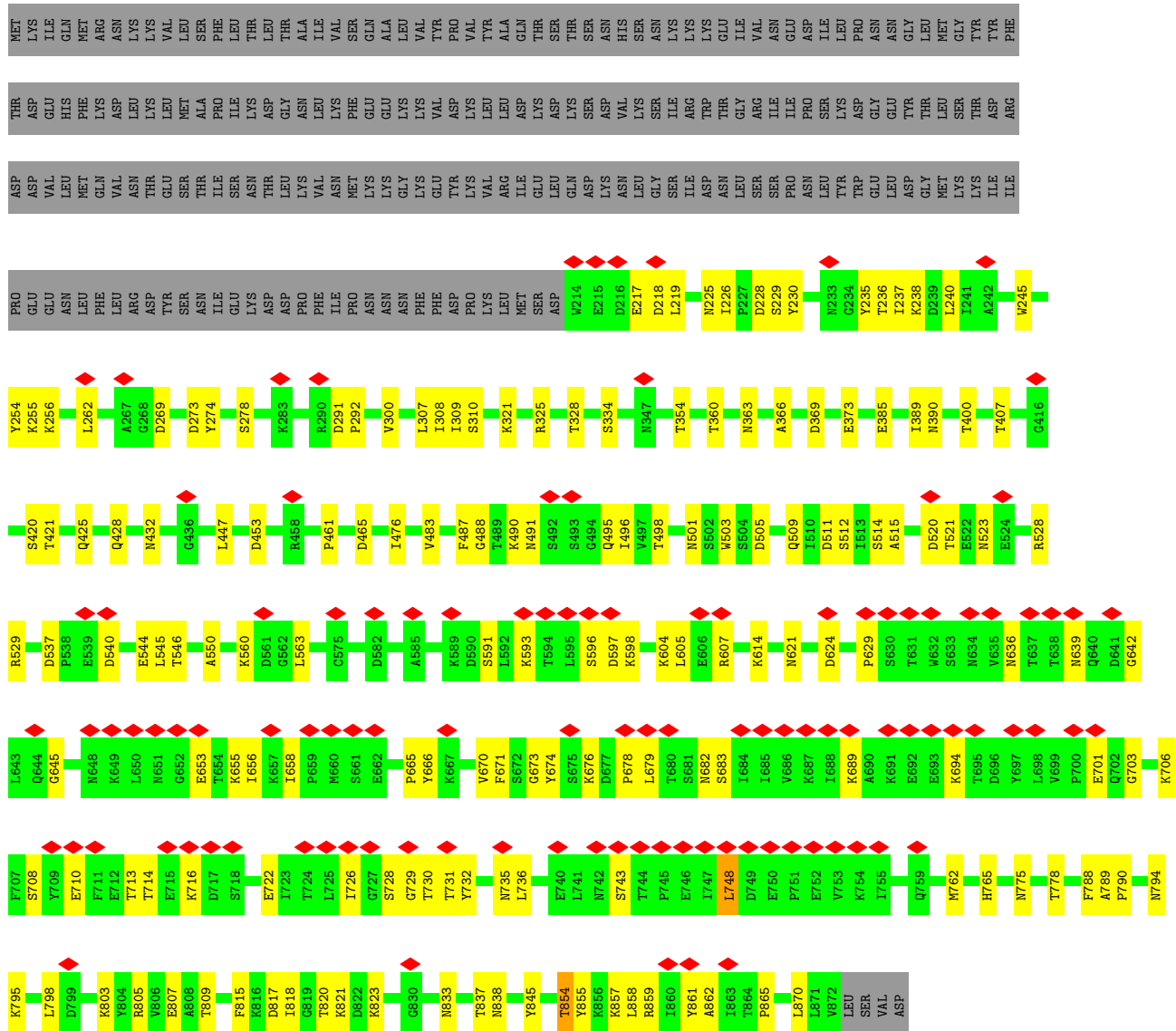


• Molecule 1: ADP-ribosyltransferase binding component

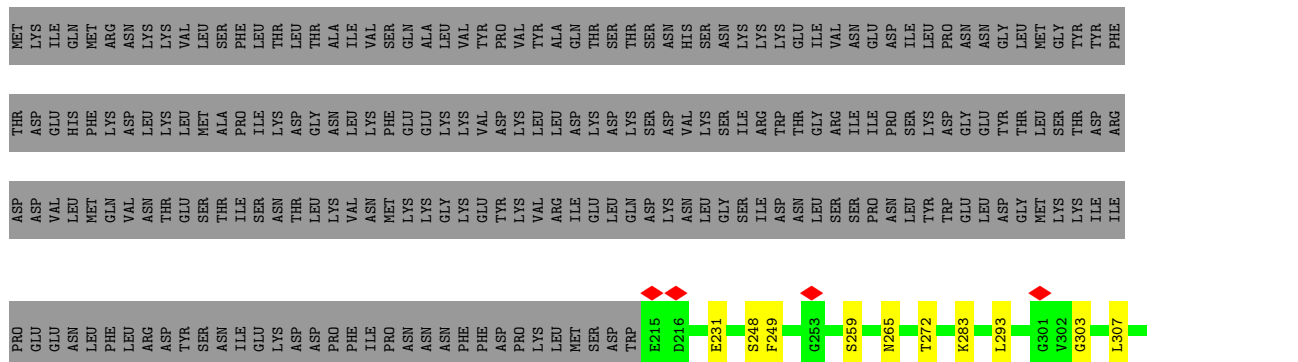


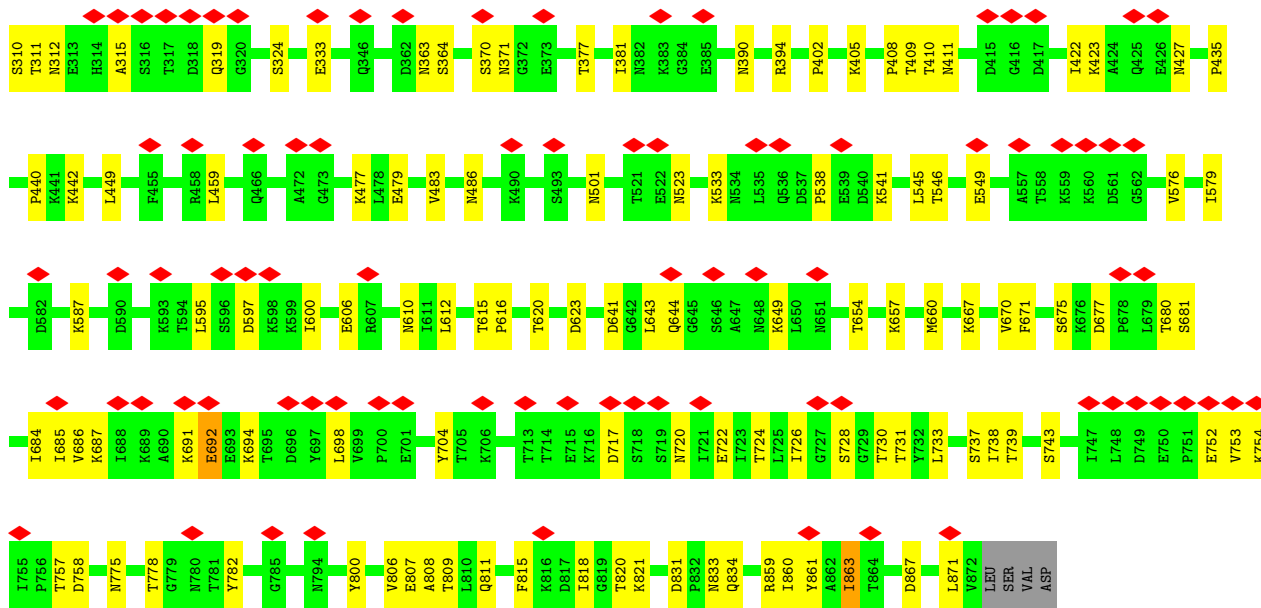
• Molecule 1: ADP-ribosyltransferase binding component



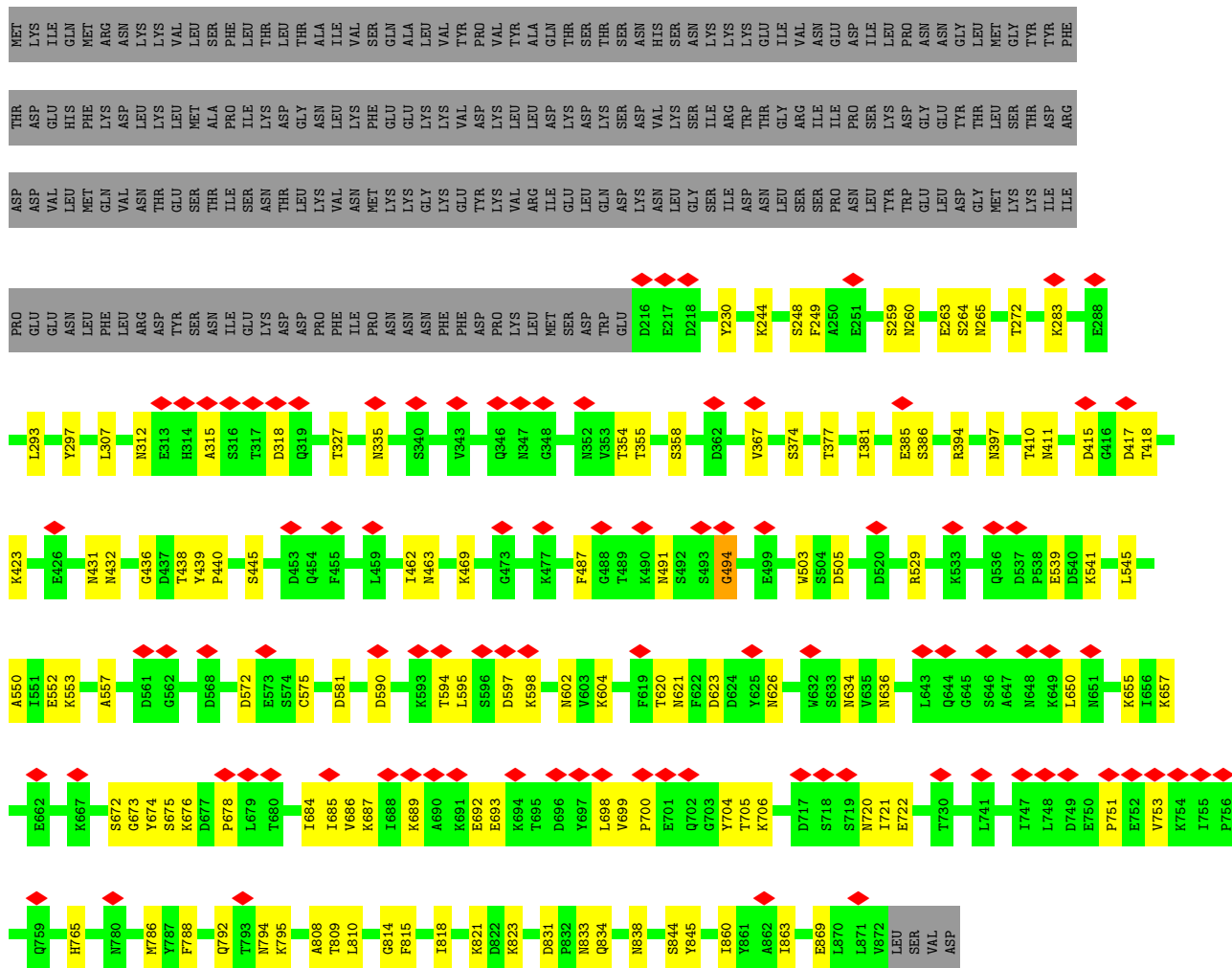


- Molecule 1: ADP-ribosyltransferase binding component





● Molecule 1: ADP-ribosyltransferase binding component



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	12306	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	110.1	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.168	Depositor
Minimum map value	-0.078	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.013	Depositor
Recommended contour level	0.0545	Depositor
Map size (Å)	362.5, 362.5, 362.5	wwPDB
Map dimensions	250, 250, 250	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.45, 1.45, 1.45	Depositor

5 Model quality

5.1 Standard geometry

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	A	0.34	0/5294	0.59	2/7187 (0.0%)
1	B	0.34	0/5294	0.60	2/7187 (0.0%)
1	C	0.33	0/5278	0.59	2/7164 (0.0%)
1	D	0.34	0/5294	0.58	1/7187 (0.0%)
1	E	0.33	0/5278	0.58	0/7164
1	F	0.35	0/5294	0.59	1/7187 (0.0%)
1	G	0.33	0/5278	0.60	2/7164 (0.0%)
1	H	0.34	0/5294	0.60	3/7187 (0.0%)
1	I	0.33	0/5278	0.58	1/7164 (0.0%)
1	J	0.36	0/5294	0.60	3/7187 (0.0%)
1	K	0.34	0/5278	0.58	1/7164 (0.0%)
1	L	0.34	0/5294	0.59	1/7187 (0.0%)
1	M	0.32	0/5278	0.59	2/7164 (0.0%)
1	Z	0.33	0/5269	0.57	0/7152
All	All	0.34	0/73995	0.59	21/100445 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	C	0	3
1	E	0	1
1	G	0	2
1	I	0	2
1	K	0	1
1	M	0	3
1	Z	0	2
All	All	0	14

There are no bond length outliers.

All (21) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	H	698	LEU	CA-CB-CG	7.55	132.67	115.30
1	A	698	LEU	CA-CB-CG	7.53	132.62	115.30
1	F	698	LEU	CA-CB-CG	7.51	132.58	115.30
1	J	698	LEU	CA-CB-CG	7.50	132.55	115.30
1	K	643	LEU	CA-CB-CG	7.11	131.65	115.30
1	C	643	LEU	CA-CB-CG	7.06	131.54	115.30
1	G	240	LEU	CA-CB-CG	6.80	130.93	115.30
1	M	643	LEU	CA-CB-CG	6.27	129.73	115.30
1	C	444	LEU	C-N-CA	6.25	137.33	121.70
1	I	643	LEU	CA-CB-CG	5.90	128.86	115.30
1	A	447	LEU	CA-CB-CG	5.89	128.85	115.30
1	H	852	ILE	CG1-CB-CG2	-5.76	98.73	111.40
1	J	240	LEU	CA-CB-CG	5.75	128.51	115.30
1	B	698	LEU	CA-CB-CG	5.66	128.32	115.30
1	M	871	LEU	CA-CB-CG	5.65	128.30	115.30
1	D	852	ILE	CG1-CB-CG2	-5.61	99.07	111.40
1	L	748	LEU	CA-CB-CG	5.58	128.13	115.30
1	H	239	ASP	CB-CG-OD1	5.45	123.20	118.30
1	G	871	LEU	CA-CB-CG	5.41	127.75	115.30
1	J	650	LEU	CA-CB-CG	5.39	127.71	115.30
1	B	663	LEU	C-N-CA	5.19	134.68	121.70

There are no chirality outliers.

All (14) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	C	620	THR	Peptide
1	C	862	ALA	Peptide
1	C	863	ILE	Peptide
1	E	863	ILE	Peptide
1	G	494	GLY	Peptide
1	G	863	ILE	Peptide
1	I	620	THR	Peptide
1	I	863	ILE	Peptide
1	K	863	ILE	Peptide
1	M	620	THR	Peptide
1	M	692	GLU	Peptide
1	M	863	ILE	Peptide
1	Z	494	GLY	Peptide
1	Z	863	ILE	Peptide

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	5196	0	5028	71	0
1	B	5196	0	5028	94	0
1	C	5182	0	5018	83	0
1	D	5196	0	5028	76	0
1	E	5182	0	5018	80	0
1	F	5196	0	5028	78	0
1	G	5182	0	5018	88	0
1	H	5196	0	5028	69	0
1	I	5182	0	5018	83	0
1	J	5196	0	5028	96	0
1	K	5182	0	5018	73	0
1	L	5196	0	5028	107	0
1	M	5182	0	5018	75	0
1	Z	5173	0	5012	81	0
All	All	72637	0	70316	1117	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 8.

All (1117) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Z:675:SER:O	1:Z:704:TYR:HA	1.66	0.96
1:E:675:SER:O	1:E:704:TYR:HA	1.68	0.94
1:G:675:SER:O	1:G:704:TYR:HA	1.69	0.92
1:E:808:ALA:O	1:E:815:PHE:HA	1.73	0.89
1:B:673:GLY:O	1:B:706:LYS:HA	1.73	0.89
1:D:673:GLY:O	1:D:706:LYS:HA	1.75	0.86
1:G:685:ILE:O	1:G:692:GLU:HA	1.77	0.85
1:J:656:ILE:O	1:J:722:GLU:HA	1.76	0.84
1:C:808:ALA:O	1:C:815:PHE:HA	1.78	0.83
1:C:675:SER:O	1:C:704:TYR:HA	1.78	0.82
1:A:653:GLU:HA	1:A:725:LEU:O	1.81	0.81
1:G:808:ALA:O	1:G:815:PHE:HA	1.84	0.77
1:A:673:GLY:O	1:A:706:LYS:HA	1.84	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:809:THR:HA	1:H:815:PHE:H	1.52	0.74
1:E:685:ILE:O	1:E:692:GLU:HA	1.88	0.73
1:Z:792:GLN:HE22	1:Z:795:LYS:HE2	1.55	0.72
1:J:657:LYS:HA	1:J:721:ILE:O	1.88	0.72
1:Z:685:ILE:O	1:Z:692:GLU:HA	1.90	0.72
1:E:684:ILE:HA	1:E:693:GLU:O	1.89	0.71
1:M:675:SER:O	1:M:704:TYR:HA	1.91	0.70
1:B:671:PHE:O	1:B:708:SER:HA	1.92	0.69
1:J:792:GLN:H	1:J:795:LYS:HD2	1.58	0.69
1:M:808:ALA:O	1:M:815:PHE:HA	1.93	0.68
1:I:792:GLN:HG2	1:I:794:ASN:H	1.57	0.68
1:M:809:THR:HA	1:M:815:PHE:H	1.60	0.67
1:K:809:THR:HA	1:K:815:PHE:H	1.59	0.67
1:C:809:THR:HA	1:C:815:PHE:H	1.58	0.67
1:E:809:THR:HA	1:E:815:PHE:H	1.60	0.67
1:D:672:SER:HA	1:D:707:PHE:O	1.95	0.66
1:D:671:PHE:O	1:D:708:SER:HA	1.95	0.66
1:D:678:PRO:HD2	1:D:699:VAL:HG21	1.77	0.66
1:J:676:LYS:HG2	1:J:730:THR:HG21	1.78	0.66
1:H:340:SER:HG	1:H:354:THR:HG1	1.40	0.65
1:I:534:ASN:HB2	1:I:607:ARG:HE	1.61	0.65
1:A:677:ASP:HB2	1:A:702:GLN:HB3	1.77	0.65
1:G:684:ILE:HA	1:G:693:GLU:O	1.96	0.65
1:I:809:THR:HA	1:I:815:PHE:H	1.62	0.65
1:J:655:LYS:HA	1:J:723:ILE:O	1.95	0.65
1:Z:786:MET:HG3	1:Z:788:PHE:HB2	1.78	0.65
1:E:641:ASP:HB3	1:E:644:GLN:HB3	1.78	0.64
1:F:790:PRO:HA	1:F:837:THR:HG21	1.79	0.64
1:L:807:GLU:HG2	1:L:817:ASP:HA	1.79	0.64
1:C:634:ASN:HD22	1:C:651:ASN:HB2	1.62	0.64
1:F:648:ASN:HB2	1:F:732:TYR:HB3	1.80	0.64
1:C:597:ASP:OD2	1:C:602:ASN:ND2	2.31	0.64
1:J:860:ILE:HD12	1:J:867:ASP:HB3	1.79	0.64
1:L:673:GLY:O	1:L:706:LYS:HA	1.98	0.64
1:B:318:ASP:HB2	1:B:376:ASN:HB3	1.79	0.64
1:F:262:LEU:HD12	1:H:240:LEU:HD13	1.78	0.64
1:M:265:ASN:HB3	1:M:272:THR:HA	1.80	0.64
1:L:809:THR:HG21	1:L:854:THR:HG23	1.79	0.64
1:Z:394:ARG:HG3	1:Z:440:PRO:HD2	1.80	0.64
1:Z:809:THR:HA	1:Z:815:PHE:H	1.62	0.64
1:D:653:GLU:HA	1:D:725:LEU:O	1.97	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:409:THR:HA	1:K:422:ILE:O	1.98	0.63
1:E:765:HIS:ND1	1:E:869:GLU:OE2	2.31	0.63
1:H:649:LYS:HA	1:H:730:THR:HA	1.79	0.63
1:L:701:GLU:HG3	1:L:703:GLY:H	1.64	0.63
1:I:265:ASN:HB3	1:I:272:THR:HA	1.81	0.63
1:A:654:THR:O	1:A:724:THR:HA	1.98	0.63
1:E:689:LYS:HB2	1:E:714:THR:HG23	1.79	0.63
1:C:656:ILE:O	1:C:722:GLU:HA	1.99	0.62
1:J:653:GLU:HA	1:J:725:LEU:O	1.99	0.62
1:I:686:VAL:HB	1:I:722:GLU:HB3	1.80	0.62
1:A:862:ALA:HB3	1:A:865:PRO:HD2	1.82	0.62
1:C:677:ASP:HB3	1:C:731:THR:HG22	1.81	0.62
1:C:685:ILE:O	1:C:692:GLU:HA	1.99	0.62
1:E:677:ASP:HB2	1:E:731:THR:HG23	1.81	0.62
1:M:677:ASP:HB3	1:M:731:THR:HG22	1.82	0.62
1:I:808:ALA:O	1:I:815:PHE:HA	1.98	0.62
1:L:809:THR:HA	1:L:815:PHE:H	1.64	0.62
1:M:312:ASN:HB2	1:M:315:ALA:HB2	1.80	0.62
1:A:687:LYS:HD2	1:A:721:ILE:HD13	1.82	0.61
1:G:381:ILE:HG23	1:G:385:GLU:HB2	1.82	0.61
1:A:453:ASP:HA	1:B:456:SER:HB2	1.82	0.61
1:M:675:SER:HA	1:M:733:LEU:HD22	1.82	0.61
1:A:701:GLU:HG3	1:A:703:GLY:H	1.65	0.61
1:I:792:GLN:HE22	1:I:795:LYS:HE3	1.64	0.61
1:M:686:VAL:HB	1:M:722:GLU:HB3	1.83	0.61
1:Z:684:ILE:HA	1:Z:693:GLU:O	2.00	0.61
1:C:784:ASN:HB3	1:C:843:ARG:HH21	1.66	0.61
1:L:671:PHE:O	1:L:708:SER:HA	2.01	0.61
1:L:798:LEU:HB3	1:L:838:ASN:HD21	1.66	0.61
1:B:672:SER:HA	1:B:707:PHE:O	2.01	0.60
1:C:534:ASN:HB2	1:C:607:ARG:HH21	1.66	0.60
1:M:671:PHE:HA	1:M:737:SER:O	2.01	0.60
1:Z:674:TYR:HA	1:Z:705:THR:O	2.01	0.60
1:F:360:THR:HG22	1:H:336:THR:HG22	1.84	0.60
1:B:321:LYS:HG2	1:B:373:GLU:HG2	1.83	0.60
1:C:686:VAL:HA	1:C:692:GLU:HG2	1.84	0.60
1:H:259:SER:OG	1:H:260:ASN:N	2.35	0.60
1:L:775:ASN:ND2	1:L:778:THR:OG1	2.35	0.60
1:B:425:GLN:OE1	1:B:428:GLN:NE2	2.34	0.59
1:C:312:ASN:ND2	1:C:319:GLN:O	2.35	0.59
1:D:642:GLY:O	1:D:732:TYR:OH	2.20	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:665:PRO:HG3	1:F:716:LYS:HG2	1.84	0.59
1:Z:765:HIS:ND1	1:Z:869:GLU:OE2	2.35	0.59
1:C:686:VAL:HB	1:C:722:GLU:HB3	1.83	0.59
1:H:623:ASP:HB2	1:H:641:ASP:HA	1.84	0.59
1:K:674:TYR:HA	1:K:705:THR:O	2.02	0.59
1:D:809:THR:HA	1:D:815:PHE:H	1.68	0.59
1:E:374:SER:OG	1:E:375:TRP:N	2.35	0.59
1:F:269:ASP:OD1	1:F:269:ASP:N	2.35	0.59
1:M:782:TYR:OH	1:M:811:GLN:NE2	2.36	0.59
1:C:387:ALA:O	1:C:461:PRO:HA	2.02	0.59
1:D:582:ASP:O	1:D:586:ASN:HB2	2.03	0.59
1:I:672:SER:HG	1:I:737:SER:HG	1.51	0.59
1:L:237:ILE:HD13	1:L:278:SER:HA	1.85	0.59
1:L:653:GLU:HB3	1:L:726:ILE:HD12	1.84	0.59
1:C:642:GLY:O	1:C:644:GLN:NE2	2.36	0.59
1:D:546:THR:OG1	1:D:547:ILE:N	2.36	0.59
1:J:682:ASN:ND2	1:J:696:ASP:OD1	2.36	0.59
1:I:722:GLU:OE2	1:I:724:THR:OG1	2.19	0.59
1:K:808:ALA:O	1:K:815:PHE:HA	2.02	0.59
1:D:648:ASN:HB2	1:D:732:TYR:HB2	1.83	0.59
1:M:806:VAL:HG23	1:M:818:ILE:HB	1.85	0.59
1:B:634:ASN:HB3	1:B:654:THR:HG22	1.85	0.58
1:I:466:GLN:HA	1:I:469:LYS:HE2	1.84	0.58
1:J:314:HIS:HB3	1:J:380:SER:HB2	1.85	0.58
1:H:291:ASP:OD1	1:H:291:ASP:N	2.35	0.58
1:K:345:TYR:OH	1:K:706:LYS:NZ	2.36	0.58
1:F:588:ILE:HD11	1:F:603:VAL:HG11	1.85	0.58
1:F:719:SER:OG	1:F:720:ASN:N	2.35	0.58
1:L:673:GLY:HA3	1:L:736:LEU:HD12	1.83	0.58
1:D:667:LYS:HE2	1:D:669:TYR:HE1	1.69	0.58
1:C:649:LYS:HB2	1:C:730:THR:HG22	1.85	0.58
1:F:259:SER:OG	1:F:260:ASN:N	2.36	0.58
1:L:521:THR:HG23	1:L:523:ASN:H	1.69	0.58
1:C:691:LYS:HB2	1:C:693:GLU:HG3	1.84	0.58
1:D:425:GLN:OE1	1:D:428:GLN:NE2	2.37	0.58
1:H:236:THR:HG21	1:H:254:TYR:HB3	1.85	0.58
1:A:577:GLU:HB3	1:A:614:LYS:HB3	1.85	0.57
1:C:298:PRO:HD3	1:C:401:ALA:HB3	1.86	0.57
1:C:805:ARG:NH1	1:C:807:GLU:OE2	2.36	0.57
1:G:686:VAL:HB	1:G:722:GLU:HB3	1.85	0.57
1:H:621:ASN:ND2	1:H:624:ASP:O	2.33	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:686:VAL:HA	1:E:692:GLU:HG3	1.86	0.57
1:L:308:ILE:HD12	1:L:390:ASN:HD21	1.70	0.57
1:Z:259:SER:OG	1:Z:260:ASN:N	2.36	0.57
1:Z:810:LEU:H	1:Z:814:GLY:HA2	1.67	0.57
1:K:265:ASN:HB3	1:K:272:THR:HA	1.85	0.57
1:K:706:LYS:NZ	1:K:708:SER:OG	2.37	0.57
1:C:428:GLN:NE2	1:C:448:ALA:O	2.37	0.57
1:G:577:GLU:HB3	1:G:614:LYS:HB3	1.86	0.57
1:G:597:ASP:OD2	1:G:602:ASN:ND2	2.37	0.57
1:I:687:LYS:HZ2	1:I:689:LYS:H	1.52	0.57
1:F:668:ARG:NH2	1:F:710:GLU:OE1	2.36	0.57
1:B:666:TYR:N	1:B:713:THR:OG1	2.37	0.57
1:C:265:ASN:HB3	1:C:272:THR:HA	1.86	0.57
1:D:587:LYS:HD3	1:D:606:GLU:HG3	1.87	0.57
1:I:338:GLY:HA3	1:I:355:THR:HG22	1.85	0.57
1:M:680:THR:HA	1:M:698:LEU:HA	1.85	0.57
1:B:790:PRO:HA	1:B:837:THR:HG21	1.86	0.57
1:H:653:GLU:HG2	1:H:726:ILE:HG22	1.87	0.57
1:H:790:PRO:O	1:H:795:LYS:NZ	2.38	0.57
1:I:370:SER:HB2	1:I:748:LEU:HD21	1.87	0.57
1:K:824:GLU:HB2	1:K:839:TYR:O	2.05	0.57
1:L:229:SER:HB2	1:L:235:TYR:HB3	1.87	0.57
1:D:682:ASN:ND2	1:D:695:THR:O	2.38	0.57
1:I:492:SER:O	1:I:495:GLN:NE2	2.38	0.57
1:Z:751:PRO:HD2	1:Z:753:VAL:HG12	1.87	0.56
1:Z:792:GLN:HG2	1:Z:794:ASN:H	1.70	0.56
1:C:410:THR:OG1	1:C:411:ASN:N	2.38	0.56
1:E:649:LYS:HB2	1:E:730:THR:HG22	1.88	0.56
1:L:425:GLN:OE1	1:L:428:GLN:NE2	2.38	0.56
1:D:333:GLU:OE2	1:D:359:HIS:NE2	2.38	0.56
1:H:425:GLN:NE2	1:H:451:THR:OG1	2.39	0.56
1:J:533:LYS:NZ	1:J:540:ASP:O	2.38	0.56
1:E:321:LYS:NZ	1:E:380:SER:OG	2.39	0.56
1:F:589:LYS:O	1:F:593:LYS:NZ	2.39	0.56
1:A:259:SER:OG	1:A:260:ASN:N	2.38	0.56
1:C:432:ASN:ND2	1:E:504:SER:O	2.36	0.56
1:J:818:ILE:HG21	1:J:845:TYR:HB3	1.88	0.56
1:K:332:THR:OG1	1:K:335:ASN:ND2	2.38	0.56
1:A:790:PRO:O	1:A:795:LYS:NZ	2.36	0.56
1:A:520:ASP:OD2	1:A:614:LYS:NZ	2.38	0.56
1:A:673:GLY:HA3	1:A:736:LEU:HD12	1.87	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:676:LYS:NZ	1:J:732:TYR:O	2.35	0.56
1:L:857:LYS:HE3	1:L:859:ARG:HH12	1.71	0.56
1:C:336:THR:O	1:C:742:ASN:ND2	2.35	0.55
1:Z:818:ILE:HG21	1:Z:845:TYR:HB3	1.88	0.55
1:B:396:TYR:HB3	1:B:438:THR:HG22	1.88	0.55
1:D:269:ASP:OD1	1:D:269:ASP:N	2.37	0.55
1:F:514:SER:OG	1:F:515:ALA:N	2.39	0.55
1:J:682:ASN:HD22	1:J:696:ASP:HA	1.71	0.55
1:Z:312:ASN:HB2	1:Z:315:ALA:HB2	1.87	0.55
1:C:841:ASN:HD21	1:Z:833:ASN:HD22	1.54	0.55
1:E:387:ALA:O	1:E:461:PRO:HA	2.05	0.55
1:J:858:LEU:HB3	1:J:870:LEU:HB3	1.87	0.55
1:K:782:TYR:OH	1:K:811:GLN:NE2	2.39	0.55
1:L:682:ASN:HB3	1:L:694:LYS:HD2	1.88	0.55
1:Z:265:ASN:HB3	1:Z:272:THR:HA	1.87	0.55
1:B:512:SER:O	1:B:607:ARG:NH2	2.39	0.55
1:C:409:THR:HA	1:C:423:LYS:HA	1.87	0.55
1:F:638:THR:HB	1:F:648:ASN:HD21	1.72	0.55
1:G:636:ASN:O	1:G:640:GLN:NE2	2.39	0.55
1:K:582:ASP:OD2	1:K:586:ASN:ND2	2.40	0.55
1:B:860:ILE:HB	1:B:867:ASP:HB3	1.88	0.55
1:H:511:ASP:OD1	1:H:529:ARG:NH1	2.40	0.55
1:J:269:ASP:OD1	1:J:269:ASP:N	2.36	0.55
1:J:293:LEU:HD11	1:J:543:PRO:HG2	1.88	0.55
1:J:390:ASN:HB3	1:J:450:ASN:HB3	1.87	0.55
1:L:858:LEU:HB3	1:L:870:LEU:HB3	1.88	0.55
1:M:408:PRO:HA	1:M:483:VAL:HG12	1.88	0.55
1:M:775:ASN:ND2	1:M:778:THR:OG1	2.40	0.55
1:D:259:SER:OG	1:D:260:ASN:N	2.40	0.55
1:K:318:ASP:N	1:K:318:ASP:OD1	2.40	0.55
1:J:259:SER:OG	1:J:260:ASN:N	2.40	0.55
1:J:520:ASP:OD2	1:J:614:LYS:NZ	2.36	0.55
1:E:701:GLU:HG2	1:E:703:GLY:H	1.71	0.55
1:E:675:SER:HA	1:E:733:LEU:HD22	1.89	0.55
1:I:505:ASP:OD1	1:I:505:ASP:N	2.40	0.55
1:J:811:GLN:HG2	1:J:850:GLU:H	1.72	0.55
1:L:428:GLN:HB2	1:L:447:LEU:HD21	1.89	0.55
1:M:657:LYS:HG3	1:M:722:GLU:HB2	1.89	0.55
1:M:753:VAL:HG23	1:M:754:LYS:HG2	1.88	0.55
1:C:374:SER:OG	1:C:375:TRP:N	2.40	0.54
1:F:775:ASN:ND2	1:F:778:THR:OG1	2.40	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:649:LYS:HB2	1:K:730:THR:HG22	1.88	0.54
1:L:639:ASN:ND2	1:L:645:GLY:O	2.40	0.54
1:Z:620:THR:HG22	1:Z:626:ASN:HA	1.88	0.54
1:A:514:SER:OG	1:A:515:ALA:N	2.40	0.54
1:H:269:ASP:OD1	1:H:269:ASP:N	2.38	0.54
1:E:269:ASP:OD1	1:E:269:ASP:N	2.40	0.54
1:G:860:ILE:HG13	1:G:869:GLU:HG3	1.88	0.54
1:H:299:ILE:HD13	1:H:527:GLU:HB3	1.90	0.54
1:H:522:GLU:OE1	1:H:614:LYS:NZ	2.37	0.54
1:I:336:THR:O	1:I:742:ASN:ND2	2.37	0.54
1:B:841:ASN:ND2	1:B:844:SER:OG	2.40	0.54
1:E:275:GLU:HG2	1:E:281:PHE:HB3	1.89	0.54
1:J:328:THR:HB	1:J:366:ALA:HB3	1.90	0.54
1:L:790:PRO:O	1:L:795:LYS:NZ	2.33	0.54
1:B:291:ASP:OD1	1:B:291:ASP:N	2.39	0.54
1:F:511:ASP:OD1	1:F:529:ARG:NH1	2.40	0.54
1:L:593:LYS:HA	1:L:598:LYS:HE3	1.88	0.54
1:G:299:ILE:HD13	1:G:527:GLU:HB3	1.90	0.54
1:B:528:ARG:NH1	1:B:554:ALA:O	2.40	0.54
1:Z:297:TYR:OH	1:Z:529:ARG:NE	2.38	0.54
1:Z:397:ASN:HB3	1:Z:436:GLY:H	1.72	0.54
1:B:636:ASN:ND2	1:B:731:THR:OG1	2.40	0.54
1:B:809:THR:HA	1:B:815:PHE:H	1.73	0.54
1:I:616:PRO:HA	1:I:739:THR:HG22	1.90	0.54
1:F:425:GLN:OE1	1:F:428:GLN:NE2	2.41	0.54
1:K:684:ILE:HG12	1:K:694:LYS:HD2	1.88	0.54
1:L:291:ASP:N	1:L:291:ASP:OD1	2.41	0.54
1:B:413:VAL:HG23	1:B:477:LYS:HB2	1.90	0.54
1:D:640:GLN:NE2	1:D:648:ASN:OD1	2.39	0.54
1:G:674:TYR:HA	1:G:705:THR:O	2.08	0.54
1:B:294:VAL:HG12	1:B:530:VAL:HG22	1.91	0.53
1:I:318:ASP:OD1	1:I:318:ASP:N	2.39	0.53
1:K:654:THR:O	1:K:724:THR:HA	2.09	0.53
1:K:765:HIS:ND1	1:K:869:GLU:OE2	2.40	0.53
1:A:534:ASN:HD21	1:A:536:GLN:HB2	1.73	0.53
1:A:675:SER:OG	1:A:703:GLY:O	2.25	0.53
1:K:638:THR:H	1:K:640:GLN:HE21	1.56	0.53
1:M:523:ASN:OD1	1:M:523:ASN:N	2.39	0.53
1:G:636:ASN:HD22	1:G:650:LEU:HD23	1.72	0.53
1:K:312:ASN:HB2	1:K:315:ALA:HB2	1.90	0.53
1:L:520:ASP:OD2	1:L:614:LYS:NZ	2.41	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:505:ASP:OD1	1:A:505:ASP:N	2.41	0.53
1:B:687:LYS:HD2	1:B:721:ILE:HD13	1.91	0.53
1:C:616:PRO:HA	1:C:739:THR:HG23	1.90	0.53
1:I:818:ILE:HG21	1:I:845:TYR:HB3	1.89	0.53
1:J:684:ILE:HG22	1:J:724:THR:HB	1.91	0.53
1:C:649:LYS:NZ	1:C:650:LEU:O	2.38	0.53
1:D:622:PHE:HB3	1:D:640:GLN:HB3	1.91	0.53
1:E:577:GLU:HB2	1:E:614:LYS:HB3	1.90	0.53
1:F:552:GLU:HG2	1:F:557:ALA:HB3	1.91	0.53
1:K:857:LYS:HB3	1:K:859:ARG:HH12	1.72	0.53
1:A:686:VAL:HB	1:A:722:GLU:HB3	1.91	0.53
1:B:269:ASP:N	1:B:269:ASP:OD1	2.41	0.53
1:E:610:ASN:N	1:E:610:ASN:OD1	2.41	0.53
1:K:374:SER:OG	1:K:748:LEU:O	2.23	0.53
1:M:410:THR:OG1	1:M:411:ASN:N	2.41	0.53
1:F:629:PRO:HG3	1:F:662:GLU:HG2	1.89	0.53
1:H:790:PRO:HA	1:H:837:THR:HG21	1.89	0.53
1:K:685:ILE:O	1:K:692:GLU:HA	2.08	0.53
1:Z:672:SER:HB3	1:Z:706:LYS:HE2	1.91	0.53
1:A:671:PHE:O	1:A:708:SER:HA	2.09	0.53
1:B:451:THR:OG1	1:B:457:SER:O	2.26	0.53
1:M:310:SER:OG	1:M:311:THR:N	2.42	0.53
1:A:214:TRP:N	1:A:217:GLU:OE1	2.42	0.53
1:E:456:SER:OG	1:E:457:SER:N	2.42	0.53
1:L:488:GLY:HA2	1:L:498:THR:HG22	1.91	0.53
1:L:670:VAL:HG23	1:L:710:GLU:HB3	1.90	0.53
1:A:521:THR:OG1	1:A:522:GLU:N	2.42	0.52
1:B:859:ARG:HA	1:B:868:ARG:HA	1.91	0.52
1:D:421:THR:HG21	1:F:447:LEU:HD12	1.91	0.52
1:D:687:LYS:NZ	1:D:719:SER:OG	2.40	0.52
1:K:645:GLY:O	1:K:704:TYR:OH	2.26	0.52
1:Z:581:ASP:N	1:Z:581:ASP:OD1	2.41	0.52
1:C:687:LYS:HZ3	1:C:688:ILE:H	1.57	0.52
1:C:833:ASN:HB2	1:E:844:SER:HB3	1.91	0.52
1:G:791:THR:HA	1:G:795:LYS:HD2	1.92	0.52
1:E:425:GLN:NE2	1:E:455:PHE:O	2.39	0.52
1:E:514:SER:OG	1:E:515:ALA:N	2.42	0.52
1:I:595:LEU:HG	1:I:597:ASP:H	1.73	0.52
1:L:269:ASP:N	1:L:269:ASP:OD1	2.38	0.52
1:Z:335:ASN:ND2	1:Z:358:SER:O	2.42	0.52
1:G:513:ILE:HG23	1:G:607:ARG:HH12	1.73	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:595:LEU:O	1:G:598:LYS:NZ	2.42	0.52
1:G:671:PHE:O	1:G:708:SER:HA	2.10	0.52
1:B:798:LEU:HB3	1:B:838:ASN:HD21	1.74	0.52
1:C:450:ASN:ND2	1:C:457:SER:OG	2.42	0.52
1:I:671:PHE:HA	1:I:737:SER:O	2.09	0.52
1:L:325:ARG:NH1	1:L:369:ASP:OD2	2.40	0.52
1:L:420:SER:OG	1:L:421:THR:N	2.42	0.52
1:Z:410:THR:OG1	1:Z:411:ASN:N	2.43	0.52
1:D:589:LYS:O	1:D:593:LYS:NZ	2.42	0.52
1:G:327:THR:HG22	1:G:367:VAL:HA	1.92	0.52
1:M:422:ILE:HG21	1:M:449:LEU:HD21	1.90	0.52
1:Z:374:SER:O	1:Z:377:THR:OG1	2.25	0.52
1:H:580:PHE:HB2	1:H:585:ALA:HB2	1.92	0.52
1:I:457:SER:OG	1:I:458:ARG:N	2.43	0.52
1:A:521:THR:HG23	1:A:524:GLU:H	1.74	0.52
1:B:347:ASN:OD1	1:E:454:GLN:NE2	2.42	0.52
1:B:546:THR:HB	1:B:549:GLU:HG2	1.92	0.52
1:F:291:ASP:OD1	1:F:291:ASP:N	2.40	0.52
1:J:754:LYS:HD3	1:L:665:PRO:HG2	1.91	0.52
1:K:620:THR:HG22	1:K:626:ASN:HA	1.91	0.52
1:M:231:GLU:OE2	1:M:259:SER:OG	2.28	0.52
1:E:410:THR:OG1	1:E:411:ASN:N	2.42	0.52
1:M:657:LYS:HG2	1:M:720:ASN:HB3	1.91	0.52
1:M:807:GLU:OE1	1:M:859:ARG:NH1	2.43	0.52
1:D:533:LYS:HD3	1:D:544:GLU:HB3	1.92	0.52
1:E:749:ASP:OD1	1:E:749:ASP:N	2.42	0.52
1:F:390:ASN:HB3	1:F:450:ASN:HB3	1.92	0.52
1:H:397:ASN:HB2	1:H:433:LEU:HD21	1.91	0.52
1:I:687:LYS:HZ1	1:I:689:LYS:HB3	1.75	0.52
1:M:722:GLU:OE2	1:M:724:THR:OG1	2.27	0.52
1:C:269:ASP:OD1	1:C:269:ASP:N	2.42	0.51
1:J:616:PRO:HB3	1:J:739:THR:HG22	1.90	0.51
1:B:622:PHE:HD2	1:B:734:ASP:HA	1.75	0.51
1:B:660:MET:SD	1:B:714:THR:OG1	2.63	0.51
1:B:687:LYS:HE2	1:B:713:THR:HA	1.91	0.51
1:C:354:THR:OG1	1:C:355:THR:N	2.44	0.51
1:A:765:HIS:HB3	1:A:795:LYS:HD3	1.92	0.51
1:B:402:PRO:HB3	1:B:434:SER:HA	1.92	0.51
1:B:686:VAL:HB	1:B:722:GLU:HB3	1.93	0.51
1:G:259:SER:OG	1:G:260:ASN:N	2.44	0.51
1:G:655:LYS:HA	1:G:723:ILE:O	2.10	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:689:LYS:HD3	1:G:714:THR:HG22	1.91	0.51
1:G:792:GLN:HG2	1:G:794:ASN:H	1.75	0.51
1:J:504:SER:O	1:L:432:ASN:ND2	2.39	0.51
1:L:328:THR:HB	1:L:366:ALA:HB3	1.92	0.51
1:J:297:TYR:H	1:J:400:THR:HG1	1.57	0.51
1:E:687:LYS:HG3	1:E:689:LYS:H	1.75	0.51
1:G:538:PRO:O	1:G:541:LYS:NZ	2.44	0.51
1:I:638:THR:OG1	1:I:646:SER:O	2.25	0.51
1:A:240:LEU:HD23	1:L:262:LEU:HD12	1.92	0.51
1:B:511:ASP:OD1	1:B:529:ARG:NH1	2.43	0.51
1:B:602:ASN:N	1:B:602:ASN:OD1	2.42	0.51
1:H:393:VAL:O	1:H:447:LEU:HB3	2.11	0.51
1:J:790:PRO:O	1:J:795:LYS:NZ	2.35	0.51
1:M:649:LYS:HB2	1:M:730:THR:HA	1.91	0.51
1:A:798:LEU:HB3	1:A:838:ASN:HD21	1.75	0.51
1:C:680:THR:HG22	1:C:698:LEU:HD13	1.91	0.51
1:E:389:ILE:HG22	1:E:460:ILE:HB	1.93	0.51
1:J:582:ASP:O	1:J:586:ASN:HB2	2.11	0.51
1:J:641:ASP:N	1:J:641:ASP:OD1	2.44	0.51
1:K:789:ALA:HB1	1:K:795:LYS:HD3	1.93	0.51
1:M:660:MET:HG2	1:M:717:ASP:H	1.75	0.51
1:B:520:ASP:OD2	1:B:742:ASN:ND2	2.42	0.51
1:C:504:SER:O	1:Z:432:ASN:ND2	2.41	0.51
1:J:621:ASN:ND2	1:J:624:ASP:O	2.44	0.51
1:K:833:ASN:OD1	1:K:833:ASN:N	2.43	0.51
1:M:691:LYS:NZ	1:M:692:GLU:OE1	2.44	0.51
1:A:511:ASP:OD1	1:A:529:ARG:NH1	2.43	0.51
1:B:518:ILE:HG12	1:B:527:GLU:HG3	1.92	0.51
1:D:798:LEU:O	1:D:823:LYS:NZ	2.44	0.51
1:L:805:ARG:HB2	1:L:820:THR:HG22	1.93	0.51
1:C:638:THR:OG1	1:C:646:SER:O	2.28	0.51
1:G:329:ASN:HD22	1:G:365:THR:HG22	1.76	0.51
1:H:737:SER:OG	1:H:738:ILE:N	2.44	0.51
1:M:370:SER:OG	1:M:371:ASN:N	2.42	0.51
1:H:675:SER:OG	1:H:703:GLY:O	2.28	0.50
1:L:678:PRO:HB3	1:L:730:THR:HG22	1.93	0.50
1:F:617:THR:O	1:F:627:ASN:ND2	2.44	0.50
1:G:753:VAL:HG23	1:G:754:LYS:HD3	1.93	0.50
1:A:425:GLN:NE2	1:A:451:THR:OG1	2.44	0.50
1:F:293:LEU:HD11	1:F:543:PRO:HG2	1.93	0.50
1:J:670:VAL:O	1:J:738:ILE:HA	2.11	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:809:THR:HG22	1:D:815:PHE:HB2	1.94	0.50
1:D:818:ILE:HG21	1:D:847:THR:HG22	1.93	0.50
1:B:856:LYS:HG2	1:B:872:VAL:HG12	1.92	0.50
1:G:633:SER:HB2	1:G:654:THR:HG23	1.93	0.50
1:H:805:ARG:HB2	1:H:820:THR:HG22	1.93	0.50
1:I:676:LYS:HZ1	1:I:732:TYR:HD2	1.60	0.50
1:M:248:SER:OG	1:M:249:PHE:N	2.44	0.50
1:Z:431:ASN:N	1:Z:431:ASN:OD1	2.45	0.50
1:B:259:SER:OG	1:B:260:ASN:N	2.45	0.50
1:E:337:ALA:HA	1:E:742:ASN:HD21	1.77	0.50
1:E:828:TYR:HB3	1:E:834:GLN:HE21	1.76	0.50
1:J:618:TYR:HB3	1:J:628:TYR:HE1	1.77	0.50
1:L:321:LYS:HG2	1:L:373:GLU:HG2	1.94	0.50
1:B:515:ALA:HB1	1:B:609:MET:HB2	1.92	0.50
1:B:765:HIS:HB3	1:B:795:LYS:HD3	1.93	0.50
1:H:669:TYR:HD1	1:H:740:GLU:HA	1.76	0.50
1:J:660:MET:SD	1:J:714:THR:OG1	2.70	0.50
1:L:512:SER:O	1:L:607:ARG:NH2	2.39	0.50
1:M:595:LEU:HG	1:M:597:ASP:H	1.77	0.50
1:Z:386:SER:HA	1:Z:462:ILE:O	2.12	0.50
1:C:582:ASP:N	1:C:582:ASP:OD1	2.40	0.50
1:Z:678:PRO:HA	1:Z:699:VAL:HB	1.94	0.50
1:J:218:ASP:N	1:J:218:ASP:OD1	2.43	0.50
1:M:409:THR:HA	1:M:423:LYS:HA	1.93	0.50
1:E:641:ASP:O	1:E:645:GLY:N	2.44	0.49
1:D:218:ASP:OD1	1:D:218:ASP:N	2.45	0.49
1:I:291:ASP:HB3	1:I:294:VAL:HG22	1.93	0.49
1:I:597:ASP:OD2	1:I:602:ASN:ND2	2.46	0.49
1:I:634:ASN:HD22	1:I:651:ASN:HB2	1.77	0.49
1:J:672:SER:HA	1:J:707:PHE:O	2.12	0.49
1:B:808:ALA:HB2	1:B:856:LYS:HE2	1.93	0.49
1:C:509:GLN:HG3	1:Z:283:LYS:HB2	1.95	0.49
1:D:425:GLN:NE2	1:D:451:THR:OG1	2.45	0.49
1:E:259:SER:OG	1:E:260:ASN:N	2.44	0.49
1:G:337:ALA:HA	1:G:742:ASN:HD21	1.76	0.49
1:G:518:ILE:HG13	1:G:527:GLU:HG3	1.94	0.49
1:H:450:ASN:N	1:H:450:ASN:OD1	2.45	0.49
1:L:300:VAL:HG21	1:L:483:VAL:HG11	1.95	0.49
1:D:258:VAL:HG23	1:D:543:PRO:HG3	1.94	0.49
1:K:843:ARG:HH22	1:K:850:GLU:HG2	1.77	0.49
1:L:309:ILE:HG22	1:L:389:ILE:HG22	1.95	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Z:248:SER:OG	1:Z:249:PHE:N	2.46	0.49
1:A:229:SER:HB2	1:A:235:TYR:HB3	1.93	0.49
1:A:596:SER:OG	1:A:597:ASP:N	2.46	0.49
1:E:532:ALA:O	1:E:607:ARG:NH2	2.46	0.49
1:E:701:GLU:OE2	1:E:705:THR:OG1	2.30	0.49
1:A:636:ASN:ND2	1:A:731:THR:OG1	2.45	0.49
1:A:683:SER:OG	1:A:695:THR:OG1	2.30	0.49
1:E:341:VAL:O	1:E:342:ASN:ND2	2.46	0.49
1:E:798:LEU:HB3	1:E:838:ASN:HD21	1.77	0.49
1:F:618:TYR:HD2	1:F:738:ILE:HD11	1.77	0.49
1:H:330:SER:OG	1:H:364:SER:OG	2.30	0.49
1:I:269:ASP:N	1:I:269:ASP:OD1	2.43	0.49
1:B:805:ARG:HB3	1:B:859:ARG:HB2	1.93	0.49
1:E:377:THR:HB	1:E:751:PRO:HA	1.94	0.49
1:E:577:GLU:HG3	1:E:739:THR:HG21	1.94	0.49
1:G:772:LEU:HD22	1:G:781:THR:HG22	1.95	0.49
1:B:421:THR:HG21	1:D:447:LEU:HD12	1.95	0.49
1:I:410:THR:OG1	1:I:411:ASN:N	2.46	0.49
1:L:803:LYS:HB2	1:L:861:TYR:HB2	1.94	0.49
1:J:672:SER:O	1:J:736:LEU:HA	2.13	0.49
1:L:854:THR:OG1	1:L:855:TYR:N	2.45	0.49
1:A:283:LYS:HB2	1:L:509:GLN:HG3	1.95	0.49
1:A:858:LEU:HB3	1:A:870:LEU:HB3	1.94	0.49
1:F:809:THR:HA	1:F:815:PHE:H	1.76	0.49
1:I:303:GLY:HA2	1:I:363:ASN:HD21	1.78	0.49
1:I:537:ASP:N	1:I:537:ASP:OD1	2.44	0.49
1:J:420:SER:OG	1:J:421:THR:N	2.46	0.49
1:J:489:THR:OG1	1:J:490:LYS:N	2.46	0.49
1:J:519:LEU:HA	1:J:613:ILE:HG13	1.94	0.49
1:B:264:SER:OG	1:B:265:ASN:ND2	2.46	0.48
1:B:291:ASP:OD2	1:B:553:LYS:NZ	2.38	0.48
1:B:318:ASP:OD2	1:B:376:ASN:ND2	2.42	0.48
1:H:585:ALA:HA	1:H:588:ILE:HD12	1.94	0.48
1:H:596:SER:OG	1:H:597:ASP:N	2.46	0.48
1:K:792:GLN:HG2	1:K:794:ASN:H	1.77	0.48
1:A:533:LYS:NZ	1:A:540:ASP:O	2.41	0.48
1:C:676:LYS:HZ1	1:C:732:TYR:HD2	1.61	0.48
1:F:437:ASP:OD2	1:F:441:LYS:NZ	2.44	0.48
1:H:665:PRO:HG3	1:H:716:LYS:HG2	1.93	0.48
1:J:534:ASN:HD21	1:J:536:GLN:HB3	1.77	0.48
1:J:860:ILE:HD11	1:J:869:GLU:HG3	1.93	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:381:ILE:HG23	1:K:385:GLU:HB2	1.95	0.48
1:E:843:ARG:HH12	1:E:850:GLU:HG2	1.79	0.48
1:H:654:THR:O	1:H:724:THR:HA	2.13	0.48
1:J:833:ASN:OD1	1:J:833:ASN:N	2.46	0.48
1:K:327:THR:HG22	1:K:367:VAL:HA	1.94	0.48
1:L:679:LEU:H	1:L:729:GLY:HA3	1.78	0.48
1:G:682:ASN:HD22	1:G:694:LYS:HD3	1.78	0.48
1:I:276:LYS:HE3	1:I:292:PRO:HA	1.95	0.48
1:I:687:LYS:NZ	1:I:689:LYS:H	2.11	0.48
1:Z:657:LYS:HD3	1:Z:720:ASN:HD22	1.78	0.48
1:C:638:THR:OG1	1:C:638:THR:O	2.32	0.48
1:L:560:LYS:N	1:L:563:LEU:O	2.47	0.48
1:C:283:LYS:HG3	1:E:513:ILE:HD11	1.96	0.48
1:F:216:ASP:HB3	1:F:228:ASP:HB2	1.96	0.48
1:G:338:GLY:HA3	1:G:355:THR:H	1.79	0.48
1:H:363:ASN:OD1	1:H:363:ASN:N	2.45	0.48
1:B:516:SER:OG	1:B:610:ASN:OD1	2.31	0.48
1:B:649:LYS:HA	1:B:730:THR:HA	1.96	0.48
1:L:230:TYR:OH	1:L:273:ASP:OD2	2.32	0.48
1:L:385:GLU:HG3	1:L:461:PRO:HB3	1.95	0.48
1:D:649:LYS:HA	1:D:730:THR:HA	1.95	0.48
1:H:633:SER:OG	1:H:655:LYS:N	2.44	0.48
1:L:218:ASP:OD1	1:L:218:ASP:N	2.39	0.48
1:Z:636:ASN:HD22	1:Z:650:LEU:HB3	1.78	0.48
1:C:376:ASN:HB3	1:C:751:PRO:HB3	1.95	0.48
1:G:537:ASP:OD2	1:G:540:ASP:N	2.46	0.48
1:H:579:ILE:HD12	1:H:612:LEU:HD22	1.96	0.48
1:H:859:ARG:HG3	1:H:868:ARG:HG2	1.94	0.48
1:J:463:ASN:ND2	1:L:310:SER:OG	2.40	0.48
1:K:354:THR:OG1	1:K:355:THR:N	2.46	0.48
1:K:686:VAL:HB	1:K:722:GLU:HB3	1.96	0.48
1:L:788:PHE:HE1	1:L:870:LEU:HD22	1.79	0.48
1:M:283:LYS:NZ	1:Z:263:GLU:OE2	2.42	0.48
1:G:679:LEU:HD13	1:G:729:GLY:HA3	1.96	0.48
1:I:807:GLU:HB2	1:I:857:LYS:HB2	1.95	0.48
1:L:400:THR:HG22	1:L:528:ARG:HH11	1.79	0.48
1:M:265:ASN:OD1	1:M:265:ASN:N	2.47	0.48
1:M:587:LYS:HD3	1:M:606:GLU:HG3	1.96	0.48
1:Z:595:LEU:O	1:Z:598:LYS:NZ	2.36	0.48
1:F:737:SER:OG	1:F:738:ILE:N	2.47	0.47
1:G:265:ASN:OD1	1:G:265:ASN:N	2.47	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M:667:LYS:HD3	1:M:743:SER:HA	1.96	0.47
1:A:678:PRO:HB3	1:A:730:THR:HG22	1.97	0.47
1:D:860:ILE:HB	1:D:867:ASP:HB3	1.96	0.47
1:D:314:HIS:HB3	1:D:380:SER:HB3	1.96	0.47
1:F:527:GLU:OE2	1:F:529:ARG:NH2	2.42	0.47
1:L:833:ASN:OD1	1:L:833:ASN:N	2.42	0.47
1:M:293:LEU:HD23	1:M:545:LEU:HD11	1.95	0.47
1:Z:415:ASP:OD2	1:Z:469:LYS:NZ	2.42	0.47
1:B:624:ASP:N	1:B:624:ASP:OD2	2.47	0.47
1:D:646:SER:HB3	1:D:676:LYS:HE2	1.97	0.47
1:E:298:PRO:HA	1:E:399:GLY:HA3	1.95	0.47
1:E:307:LEU:HD23	1:E:327:THR:HG21	1.97	0.47
1:F:546:THR:O	1:F:550:ALA:N	2.46	0.47
1:F:676:LYS:HB3	1:F:678:PRO:HD3	1.95	0.47
1:G:394:ARG:HG3	1:G:440:PRO:HD2	1.95	0.47
1:J:236:THR:HG21	1:J:254:TYR:HB3	1.96	0.47
1:J:638:THR:O	1:J:648:ASN:ND2	2.48	0.47
1:K:406:VAL:HG12	1:K:408:PRO:HD3	1.97	0.47
1:L:217:GLU:HA	1:L:226:ILE:HG23	1.96	0.47
1:A:221:THR:OG1	1:A:261:TYR:O	2.32	0.47
1:C:236:THR:OG1	1:C:237:ILE:N	2.47	0.47
1:D:511:ASP:OD1	1:D:529:ARG:NH1	2.47	0.47
1:H:673:GLY:O	1:H:706:LYS:HA	2.14	0.47
1:I:417:ASP:OD1	1:I:417:ASP:N	2.46	0.47
1:J:450:ASN:OD1	1:J:450:ASN:N	2.45	0.47
1:K:336:THR:OG1	1:K:742:ASN:OD1	2.30	0.47
1:A:328:THR:HB	1:A:366:ALA:HB3	1.96	0.47
1:A:579:ILE:HB	1:A:612:LEU:HB3	1.95	0.47
1:H:818:ILE:HG21	1:H:845:TYR:HB3	1.95	0.47
1:A:794:ASN:OD1	1:A:794:ASN:N	2.44	0.47
1:B:862:ALA:HB3	1:B:865:PRO:HD2	1.97	0.47
1:C:552:GLU:HB2	1:C:564:LEU:HD22	1.97	0.47
1:C:673:GLY:O	1:C:706:LYS:HA	2.15	0.47
1:D:673:GLY:HA3	1:D:736:LEU:HD12	1.97	0.47
1:E:656:ILE:O	1:E:722:GLU:HA	2.15	0.47
1:F:676:LYS:HB2	1:F:733:LEU:HD21	1.97	0.47
1:H:579:ILE:HB	1:H:612:LEU:HB3	1.95	0.47
1:I:621:ASN:ND2	1:I:623:ASP:OD2	2.48	0.47
1:J:862:ALA:HB3	1:J:865:PRO:HD2	1.97	0.47
1:L:546:THR:O	1:L:550:ALA:N	2.48	0.47
1:L:642:GLY:O	1:L:732:TYR:OH	2.27	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:790:PRO:HA	1:L:837:THR:HG21	1.96	0.47
1:M:303:GLY:HA2	1:M:363:ASN:HD21	1.79	0.47
1:M:641:ASP:HB3	1:M:644:GLN:HB2	1.94	0.47
1:Z:293:LEU:HD13	1:Z:545:LEU:HD11	1.96	0.47
1:Z:685:ILE:O	1:Z:692:GLU:CA	2.62	0.47
1:C:310:SER:OG	1:C:311:THR:N	2.48	0.47
1:G:505:ASP:OD1	1:G:505:ASP:N	2.46	0.47
1:L:545:LEU:HD21	1:L:605:LEU:HD23	1.96	0.47
1:D:627:ASN:OD1	1:D:627:ASN:N	2.48	0.47
1:L:666:TYR:N	1:L:713:THR:OG1	2.47	0.47
1:L:674:TYR:HD2	1:L:735:ASN:HB2	1.80	0.47
1:M:684:ILE:HG12	1:M:694:LYS:HG2	1.97	0.47
1:B:689:LYS:HD2	1:B:714:THR:HA	1.96	0.47
1:C:394:ARG:HG3	1:C:440:PRO:HD2	1.97	0.47
1:D:363:ASN:OD1	1:D:363:ASN:N	2.44	0.47
1:A:334:SER:OG	1:A:360:THR:OG1	2.33	0.46
1:E:247:ASP:OD1	1:E:247:ASP:N	2.48	0.46
1:H:260:ASN:HD22	1:H:263:GLU:HG2	1.80	0.46
1:I:362:ASP:OD1	1:I:362:ASP:N	2.47	0.46
1:C:808:ALA:HB2	1:C:856:LYS:HG3	1.97	0.46
1:G:382:ASN:H	1:G:385:GLU:HG3	1.79	0.46
1:I:311:THR:OG1	1:I:312:ASN:N	2.47	0.46
1:I:622:PHE:HB2	1:I:640:GLN:HG2	1.98	0.46
1:L:226:ILE:HG22	1:L:228:ASP:H	1.81	0.46
1:Z:860:ILE:HD11	1:Z:869:GLU:HB2	1.96	0.46
1:A:571:ILE:HG23	1:A:576:VAL:HG11	1.98	0.46
1:B:236:THR:HG21	1:B:254:TYR:HB3	1.98	0.46
1:D:790:PRO:HA	1:D:837:THR:HG21	1.97	0.46
1:H:565:TYR:HD1	1:H:570:PRO:HA	1.80	0.46
1:I:653:GLU:HA	1:I:725:LEU:O	2.15	0.46
1:I:767:ILE:HD12	1:I:790:PRO:HB2	1.97	0.46
1:K:606:GLU:N	1:K:609:MET:SD	2.87	0.46
1:K:638:THR:O	1:K:638:THR:OG1	2.33	0.46
1:A:656:ILE:O	1:A:722:GLU:HA	2.14	0.46
1:A:818:ILE:HD11	1:A:846:PHE:HB2	1.96	0.46
1:C:234:GLY:HA3	1:C:256:LYS:HE3	1.97	0.46
1:G:514:SER:OG	1:G:515:ALA:O	2.34	0.46
1:J:377:THR:OG1	1:J:378:GLY:N	2.49	0.46
1:Z:491:ASN:ND2	1:Z:494:GLY:O	2.49	0.46
1:A:463:ASN:ND2	1:B:310:SER:OG	2.48	0.46
1:B:760:GLU:HG2	1:B:761:ILE:H	1.79	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:610:ASN:N	1:G:610:ASN:OD1	2.48	0.46
1:I:310:SER:HB2	1:I:322:THR:HG22	1.97	0.46
1:J:596:SER:OG	1:J:597:ASP:N	2.48	0.46
1:K:427:ASN:OD1	1:K:427:ASN:N	2.48	0.46
1:L:334:SER:OG	1:L:360:THR:OG1	2.33	0.46
1:C:818:ILE:HG21	1:C:845:TYR:HB3	1.97	0.46
1:F:521:THR:OG1	1:F:522:GLU:N	2.49	0.46
1:H:238:LYS:HE2	1:H:254:TYR:CZ	2.51	0.46
1:L:743:SER:O	1:L:743:SER:OG	2.32	0.46
1:A:616:PRO:HB3	1:A:739:THR:HG22	1.97	0.46
1:F:314:HIS:HB3	1:F:380:SER:HB2	1.98	0.46
1:F:621:ASN:ND2	1:F:624:ASP:O	2.46	0.46
1:F:632:TRP:NE1	1:F:654:THR:OG1	2.45	0.46
1:H:505:ASP:OD1	1:H:505:ASP:N	2.39	0.46
1:I:577:GLU:HB3	1:I:614:LYS:HB3	1.97	0.46
1:K:806:VAL:HG23	1:K:818:ILE:HB	1.98	0.46
1:L:818:ILE:HG21	1:L:845:TYR:HB3	1.98	0.46
1:A:641:ASP:OD1	1:A:641:ASP:N	2.44	0.46
1:D:675:SER:OG	1:D:703:GLY:O	2.30	0.46
1:E:335:ASN:ND2	1:E:358:SER:O	2.39	0.46
1:E:432:ASN:ND2	1:G:504:SER:O	2.36	0.46
1:F:641:ASP:OD1	1:F:641:ASP:N	2.44	0.46
1:G:795:LYS:HD3	1:G:798:LEU:HD11	1.98	0.46
1:I:274:TYR:O	1:I:278:SER:CB	2.64	0.46
1:I:828:TYR:CZ	1:I:829:LEU:HD23	2.51	0.46
1:L:307:LEU:HD11	1:L:476:ILE:HD11	1.98	0.46
1:B:395:TYR:HB2	1:B:439:TYR:HB3	1.98	0.46
1:F:229:SER:OG	1:F:244:LYS:NZ	2.32	0.46
1:F:618:TYR:OH	1:F:662:GLU:O	2.34	0.46
1:G:318:ASP:OD1	1:G:318:ASP:N	2.48	0.46
1:H:328:THR:HB	1:H:366:ALA:HB3	1.97	0.46
1:H:346:GLN:HB3	1:H:350:THR:HG21	1.98	0.46
1:L:238:LYS:HE3	1:L:238:LYS:HB2	1.82	0.46
1:L:689:LYS:HD2	1:L:714:THR:HA	1.96	0.46
1:M:394:ARG:HG3	1:M:440:PRO:HD2	1.98	0.46
1:C:314:HIS:O	1:C:319:GLN:NE2	2.49	0.46
1:C:687:LYS:HZ3	1:C:688:ILE:N	2.14	0.46
1:E:298:PRO:HD3	1:E:401:ALA:HB3	1.98	0.46
1:E:354:THR:OG1	1:E:355:THR:N	2.49	0.46
1:G:490:LYS:NZ	1:G:491:ASN:O	2.49	0.46
1:J:619:PHE:HD1	1:J:737:SER:HB2	1.79	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:794:ASN:N	1:J:794:ASN:OD1	2.49	0.46
1:Z:318:ASP:OD1	1:Z:318:ASP:N	2.46	0.46
1:B:671:PHE:HD2	1:B:709:TYR:HB2	1.81	0.45
1:C:407:THR:O	1:C:407:THR:OG1	2.34	0.45
1:I:465:ASP:OD2	1:I:465:ASP:N	2.48	0.45
1:I:632:TRP:HA	1:I:656:ILE:HD11	1.98	0.45
1:K:676:LYS:HE3	1:K:731:THR:HA	1.97	0.45
1:M:685:ILE:O	1:M:692:GLU:HA	2.16	0.45
1:E:389:ILE:HB	1:E:462:ILE:HD11	1.96	0.45
1:F:794:ASN:OD1	1:F:794:ASN:N	2.49	0.45
1:G:481:THR:OG1	1:G:482:GLN:N	2.49	0.45
1:G:546:THR:O	1:G:550:ALA:N	2.49	0.45
1:I:327:THR:HG22	1:I:367:VAL:HG12	1.99	0.45
1:J:245:TRP:CD1	1:J:256:LYS:HG3	2.52	0.45
1:J:574:SER:HG	1:J:575:CYS:HG	1.50	0.45
1:K:618:TYR:HD2	1:K:738:ILE:HD11	1.81	0.45
1:L:537:ASP:OD2	1:L:540:ASP:N	2.49	0.45
1:M:390:ASN:HD22	1:M:459:LEU:HD21	1.81	0.45
1:B:427:ASN:ND2	1:B:456:SER:OG	2.50	0.45
1:C:714:THR:OG1	1:C:717:ASP:OD2	2.33	0.45
1:D:825:MET:HB3	1:D:836:LYS:HD3	1.97	0.45
1:F:521:THR:OG1	1:F:522:GLU:OE1	2.34	0.45
1:F:584:THR:HG21	1:F:610:ASN:H	1.81	0.45
1:G:645:GLY:O	1:G:704:TYR:OH	2.31	0.45
1:I:417:ASP:OD2	1:I:466:GLN:NE2	2.44	0.45
1:I:687:LYS:HD2	1:I:721:ILE:HD11	1.99	0.45
1:M:833:ASN:HB2	1:Z:844:SER:HB2	1.96	0.45
1:A:627:ASN:OD1	1:A:627:ASN:N	2.50	0.45
1:B:718:SER:O	1:B:718:SER:OG	2.33	0.45
1:E:265:ASN:HB3	1:E:272:THR:HA	1.97	0.45
1:F:678:PRO:HD2	1:F:699:VAL:HG21	1.98	0.45
1:G:408:PRO:HA	1:G:483:VAL:HG12	1.97	0.45
1:H:670:VAL:O	1:H:738:ILE:HA	2.16	0.45
1:J:521:THR:HG23	1:J:523:ASN:H	1.81	0.45
1:K:684:ILE:HA	1:K:693:GLU:O	2.17	0.45
1:L:862:ALA:HB3	1:L:865:PRO:HD2	1.98	0.45
1:Z:686:VAL:HB	1:Z:722:GLU:HB3	1.99	0.45
1:A:297:TYR:H	1:A:400:THR:HG1	1.64	0.45
1:A:314:HIS:HB3	1:A:380:SER:HB3	1.99	0.45
1:A:684:ILE:HG23	1:A:694:LYS:HB3	1.98	0.45
1:B:280:SER:O	1:B:280:SER:OG	2.32	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:216:ASP:OD2	1:D:216:ASP:N	2.43	0.45
1:D:649:LYS:HG2	1:D:676:LYS:HZ1	1.81	0.45
1:E:680:THR:HG22	1:E:698:LEU:HD13	1.98	0.45
1:F:281:PHE:HE2	1:F:285:ILE:HG13	1.81	0.45
1:G:432:ASN:ND2	1:I:504:SER:O	2.40	0.45
1:I:265:ASN:N	1:I:265:ASN:OD1	2.50	0.45
1:I:856:LYS:HE2	1:I:856:LYS:HB2	1.78	0.45
1:J:681:SER:HB2	1:J:697:TYR:HB2	1.99	0.45
1:K:681:SER:OG	1:K:682:ASN:N	2.50	0.45
1:Z:831:ASP:HB2	1:Z:834:GLN:HB2	1.96	0.45
1:B:616:PRO:HB3	1:B:739:THR:HG22	1.99	0.45
1:C:264:SER:O	1:C:272:THR:OG1	2.29	0.45
1:C:363:ASN:OD1	1:C:363:ASN:N	2.49	0.45
1:F:440:PRO:HB2	1:F:444:LEU:HD12	1.99	0.45
1:F:484:SER:OG	1:H:431:ASN:ND2	2.49	0.45
1:G:417:ASP:OD1	1:G:417:ASP:N	2.50	0.45
1:H:488:GLY:HA2	1:H:498:THR:HG22	1.99	0.45
1:I:336:THR:OG1	1:I:742:ASN:OD1	2.29	0.45
1:M:616:PRO:HA	1:M:739:THR:HB	1.99	0.45
1:B:450:ASN:OD1	1:B:450:ASN:N	2.50	0.45
1:C:655:LYS:HA	1:C:723:ILE:O	2.16	0.45
1:F:425:GLN:NE2	1:F:451:THR:OG1	2.50	0.45
1:G:666:TYR:HD1	1:G:744:THR:HG23	1.82	0.45
1:H:468:LYS:HA	1:H:468:LYS:HD3	1.73	0.45
1:I:685:ILE:O	1:I:692:GLU:HA	2.16	0.45
1:J:636:ASN:ND2	1:J:731:THR:OG1	2.49	0.45
1:L:274:TYR:O	1:L:278:SER:OG	2.32	0.45
1:Z:657:LYS:HE2	1:Z:720:ASN:HB2	1.99	0.45
1:B:358:SER:OG	1:B:359:HIS:N	2.50	0.45
1:C:318:ASP:OD1	1:C:318:ASP:N	2.49	0.45
1:C:684:ILE:HB	1:C:724:THR:HB	1.99	0.45
1:J:689:LYS:HD2	1:J:714:THR:HA	1.99	0.45
1:K:623:ASP:N	1:K:623:ASP:OD1	2.47	0.45
1:D:584:THR:HG22	1:D:609:MET:HG2	1.99	0.45
1:D:636:ASN:OD1	1:D:636:ASN:N	2.48	0.45
1:E:818:ILE:HG21	1:E:845:TYR:HB3	1.98	0.45
1:G:514:SER:OG	1:G:515:ALA:N	2.50	0.45
1:G:650:LEU:H	1:G:650:LEU:HG	1.70	0.45
1:G:792:GLN:HE22	1:G:795:LYS:HE3	1.80	0.45
1:L:798:LEU:O	1:L:823:LYS:NZ	2.47	0.45
1:M:579:ILE:HD12	1:M:612:LEU:HD23	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:514:SER:OG	1:D:515:ALA:N	2.50	0.45
1:D:775:ASN:O	1:D:778:THR:OG1	2.33	0.45
1:H:858:LEU:HB3	1:H:870:LEU:HB3	1.98	0.45
1:J:760:GLU:HG2	1:J:761:ILE:H	1.82	0.45
1:M:377:THR:OG1	1:M:752:GLU:OE1	2.30	0.45
1:Z:572:ASP:H	1:Z:575:CYS:HB2	1.81	0.45
1:Z:634:ASN:N	1:Z:634:ASN:OD1	2.50	0.45
1:D:330:SER:OG	1:D:364:SER:OG	2.33	0.44
1:F:232:ARG:HG3	1:F:233:ASN:H	1.82	0.44
1:G:282:ASP:OD1	1:G:283:LYS:N	2.51	0.44
1:G:640:GLN:OE1	1:G:732:TYR:OH	2.31	0.44
1:H:795:LYS:HD2	1:H:798:LEU:HD11	1.99	0.44
1:H:809:THR:OG1	1:H:854:THR:OG1	2.33	0.44
1:J:274:TYR:O	1:J:278:SER:OG	2.27	0.44
1:J:385:GLU:HG3	1:J:461:PRO:HB3	1.99	0.44
1:J:859:ARG:HG3	1:J:868:ARG:HG3	1.99	0.44
1:L:655:LYS:NZ	1:L:722:GLU:OE2	2.40	0.44
1:L:794:ASN:OD1	1:L:794:ASN:N	2.48	0.44
1:Z:505:ASP:OD1	1:Z:505:ASP:N	2.49	0.44
1:Z:539:GLU:O	1:Z:541:LYS:NZ	2.40	0.44
1:A:841:ASN:HD21	1:B:833:ASN:HB2	1.82	0.44
1:D:505:ASP:N	1:D:505:ASP:OD1	2.46	0.44
1:D:801:ILE:O	1:D:823:LYS:NZ	2.44	0.44
1:F:795:LYS:HB2	1:F:795:LYS:HE3	1.86	0.44
1:G:302:VAL:HG22	1:G:395:TYR:HD1	1.83	0.44
1:G:342:ASN:O	1:G:708:SER:OG	2.35	0.44
1:G:633:SER:OG	1:G:655:LYS:O	2.33	0.44
1:I:414:LEU:HD13	1:I:476:ILE:HG12	1.99	0.44
1:K:445:SER:OG	1:M:411:ASN:ND2	2.50	0.44
1:M:610:ASN:OD1	1:M:610:ASN:N	2.49	0.44
1:Z:597:ASP:OD2	1:Z:602:ASN:ND2	2.50	0.44
1:B:595:LEU:HD11	1:B:603:VAL:HG23	1.99	0.44
1:D:595:LEU:O	1:D:598:LYS:NZ	2.42	0.44
1:J:765:HIS:O	1:J:765:HIS:ND1	2.50	0.44
1:M:402:PRO:HB3	1:M:435:PRO:HD3	1.98	0.44
1:Z:621:ASN:ND2	1:Z:623:ASP:OD2	2.50	0.44
1:B:584:THR:HG21	1:B:610:ASN:H	1.81	0.44
1:B:818:ILE:HG21	1:B:845:TYR:HB3	1.98	0.44
1:C:414:LEU:HD13	1:C:476:ILE:HG13	2.00	0.44
1:H:614:LYS:HD2	1:H:614:LYS:HA	1.83	0.44
1:J:593:LYS:HG3	1:J:594:THR:HG23	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:481:THR:OG1	1:K:482:GLN:N	2.51	0.44
1:Z:264:SER:O	1:Z:272:THR:OG1	2.32	0.44
1:Z:552:GLU:HA	1:Z:557:ALA:HB3	1.98	0.44
1:Z:687:LYS:HZ1	1:Z:689:LYS:HB2	1.82	0.44
1:C:302:VAL:HG22	1:C:395:TYR:HD1	1.83	0.44
1:D:621:ASN:ND2	1:D:624:ASP:O	2.50	0.44
1:E:719:SER:OG	1:E:720:ASN:N	2.51	0.44
1:H:674:TYR:HA	1:H:706:LYS:HA	1.99	0.44
1:I:638:THR:OG1	1:I:638:THR:O	2.35	0.44
1:I:672:SER:OG	1:I:737:SER:OG	2.26	0.44
1:I:734:ASP:OD1	1:I:734:ASP:N	2.49	0.44
1:J:683:SER:HA	1:J:724:THR:O	2.16	0.44
1:K:281:PHE:HE2	1:K:285:ILE:HG13	1.83	0.44
1:A:637:THR:O	1:A:637:THR:OG1	2.33	0.44
1:B:859:ARG:HH11	1:B:868:ARG:HG3	1.82	0.44
1:F:573:GLU:O	1:F:674:TYR:OH	2.36	0.44
1:G:387:ALA:O	1:G:461:PRO:HA	2.18	0.44
1:G:687:LYS:HG3	1:G:690:ALA:H	1.82	0.44
1:K:576:VAL:HA	1:K:616:PRO:HD3	1.99	0.44
1:K:805:ARG:HB2	1:K:820:THR:HG22	1.99	0.44
1:K:855:TYR:HA	1:K:872:VAL:HG13	1.98	0.44
1:L:636:ASN:OD1	1:L:636:ASN:N	2.50	0.44
1:M:670:VAL:O	1:M:738:ILE:HA	2.17	0.44
1:Z:354:THR:OG1	1:Z:355:THR:N	2.50	0.44
1:Z:604:LYS:HD2	1:Z:604:LYS:HA	1.76	0.44
1:A:246:GLU:OE1	1:A:248:SER:OG	2.36	0.44
1:K:700:PRO:HD2	1:K:705:THR:HG21	1.99	0.44
1:F:364:SER:HB3	1:H:332:THR:HG22	2.00	0.44
1:G:868:ARG:HD3	1:G:871:LEU:HD23	1.99	0.44
1:H:573:GLU:O	1:H:674:TYR:OH	2.36	0.44
1:K:678:PRO:HA	1:K:699:VAL:HB	1.98	0.44
1:B:666:TYR:H	1:B:713:THR:HG1	1.64	0.44
1:E:413:VAL:HG22	1:E:418:THR:HG22	2.00	0.44
1:F:757:THR:OG1	1:H:666:TYR:OH	2.31	0.44
1:I:856:LYS:O	1:I:871:LEU:HA	2.18	0.44
1:J:574:SER:OG	1:J:575:CYS:SG	2.66	0.44
1:K:431:ASN:OD1	1:K:431:ASN:N	2.48	0.44
1:K:565:TYR:CZ	1:K:570:PRO:HB3	2.53	0.44
1:Z:590:ASP:OD1	1:Z:590:ASP:N	2.50	0.44
1:F:857:LYS:HA	1:F:857:LYS:HD2	1.80	0.43
1:L:683:SER:O	1:L:683:SER:OG	2.34	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:616:PRO:HB3	1:D:739:THR:HG22	2.01	0.43
1:E:265:ASN:OD1	1:E:265:ASN:N	2.49	0.43
1:K:238:LYS:HE2	1:K:243:VAL:HG21	2.00	0.43
1:C:482:GLN:HG2	1:Z:439:TYR:HE1	1.83	0.43
1:C:656:ILE:HD13	1:C:656:ILE:HA	1.89	0.43
1:G:457:SER:OG	1:G:458:ARG:N	2.49	0.43
1:J:291:ASP:N	1:J:291:ASP:OD1	2.48	0.43
1:J:663:LEU:HD12	1:J:669:TYR:HE2	1.83	0.43
1:L:238:LYS:HE2	1:L:254:TYR:CZ	2.53	0.43
1:M:546:THR:OG1	1:M:549:GLU:OE2	2.33	0.43
1:F:278:SER:OG	1:F:278:SER:O	2.36	0.43
1:G:260:ASN:HD22	1:G:263:GLU:HB2	1.83	0.43
1:H:334:SER:OG	1:H:360:THR:OG1	2.30	0.43
1:L:491:ASN:HD22	1:L:495:GLN:H	1.65	0.43
1:L:505:ASP:OD1	1:L:505:ASP:N	2.48	0.43
1:L:636:ASN:ND2	1:L:731:THR:OG1	2.51	0.43
1:L:789:ALA:HB1	1:L:795:LYS:HZ2	1.82	0.43
1:Z:821:LYS:HB2	1:Z:845:TYR:CZ	2.53	0.43
1:A:821:LYS:HA	1:A:821:LYS:HD3	1.87	0.43
1:C:392:ASN:HB3	1:C:446:PRO:HB2	2.00	0.43
1:D:324:SER:OG	1:D:370:SER:OG	2.26	0.43
1:E:653:GLU:HA	1:E:725:LEU:O	2.18	0.43
1:B:306:LYS:HB3	1:B:306:LYS:HE3	1.81	0.43
1:C:327:THR:HG22	1:C:367:VAL:HA	2.00	0.43
1:C:734:ASP:OD1	1:C:734:ASP:N	2.46	0.43
1:F:219:LEU:HD13	1:F:222:ASP:HA	2.00	0.43
1:F:523:ASN:OD1	1:F:523:ASN:N	2.52	0.43
1:I:307:LEU:O	1:I:324:SER:HA	2.18	0.43
1:I:391:ALA:HB3	1:I:449:LEU:HB3	1.99	0.43
1:J:821:LYS:HB2	1:J:845:TYR:CZ	2.54	0.43
1:K:438:THR:HG23	1:K:441:LYS:HA	2.01	0.43
1:B:585:ALA:HA	1:B:588:ILE:HG22	2.00	0.43
1:D:666:TYR:N	1:D:713:THR:OG1	2.50	0.43
1:E:302:VAL:O	1:E:363:ASN:ND2	2.38	0.43
1:E:442:LYS:HB2	1:E:442:LYS:HE3	1.73	0.43
1:E:449:LEU:HD23	1:E:449:LEU:HA	1.85	0.43
1:L:487:PHE:CZ	1:L:501:ASN:HB3	2.54	0.43
1:Z:808:ALA:O	1:Z:815:PHE:HA	2.19	0.43
1:F:657:LYS:HB2	1:F:720:ASN:ND2	2.34	0.43
1:I:676:LYS:NZ	1:I:732:TYR:O	2.44	0.43
1:I:808:ALA:HA	1:I:856:LYS:HG3	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:809:THR:HA	1:J:815:PHE:H	1.83	0.43
1:K:468:LYS:HB3	1:K:468:LYS:HE3	1.81	0.43
1:M:315:ALA:HB1	1:M:319:GLN:HB3	2.01	0.43
1:M:831:ASP:HB3	1:M:834:GLN:HB2	2.01	0.43
1:M:860:ILE:N	1:M:867:ASP:O	2.49	0.43
1:B:651:ASN:OD1	1:B:729:GLY:N	2.51	0.43
1:C:342:ASN:OD1	1:C:342:ASN:N	2.51	0.43
1:C:664:LYS:HD2	1:C:664:LYS:HA	1.83	0.43
1:D:458:ARG:HH21	1:F:459:LEU:HD13	1.83	0.43
1:E:684:ILE:HG12	1:E:694:LYS:HB3	2.00	0.43
1:J:505:ASP:OD1	1:J:505:ASP:N	2.50	0.43
1:L:679:LEU:HD12	1:L:728:SER:HB2	2.00	0.43
1:A:687:LYS:HE2	1:A:713:THR:HA	2.01	0.43
1:B:678:PRO:HG2	1:B:697:TYR:HE2	1.84	0.43
1:C:804:TYR:HD1	1:C:858:LEU:HD11	1.84	0.43
1:F:514:SER:OG	1:F:530:VAL:N	2.52	0.43
1:F:665:PRO:HB2	1:F:715:GLU:HA	1.99	0.43
1:M:820:THR:HG21	1:M:861:TYR:CE2	2.54	0.43
1:A:464:TYR:OH	1:A:468:LYS:NZ	2.52	0.42
1:B:505:ASP:OD1	1:B:505:ASP:N	2.44	0.42
1:D:783:ILE:HG12	1:D:851:ASN:HB2	2.00	0.42
1:E:431:ASN:OD1	1:E:431:ASN:N	2.45	0.42
1:E:584:THR:HG22	1:E:609:MET:HB2	2.01	0.42
1:E:621:ASN:OD1	1:E:622:PHE:N	2.52	0.42
1:F:681:SER:HB3	1:F:725:LEU:HD11	2.00	0.42
1:G:677:ASP:HB3	1:G:731:THR:HG22	2.01	0.42
1:H:678:PRO:HB3	1:H:730:THR:HG22	1.99	0.42
1:J:227:PRO:HA	1:J:230:TYR:HB2	2.01	0.42
1:J:318:ASP:HB2	1:J:376:ASN:HB3	2.01	0.42
1:L:665:PRO:HD3	1:L:716:LYS:HE2	2.01	0.42
1:M:486:ASN:ND2	1:M:501:ASN:O	2.39	0.42
1:M:538:PRO:O	1:M:541:LYS:NZ	2.39	0.42
1:Z:687:LYS:HD3	1:Z:721:ILE:HD12	2.00	0.42
1:B:268:GLY:HA3	1:B:510:ILE:HG12	2.01	0.42
1:B:670:VAL:O	1:B:738:ILE:HA	2.19	0.42
1:C:341:VAL:HG23	1:C:352:ASN:HD21	1.84	0.42
1:D:664:LYS:HB2	1:D:667:LYS:HZ1	1.84	0.42
1:F:457:SER:OG	1:F:458:ARG:N	2.52	0.42
1:G:335:ASN:ND2	1:G:358:SER:O	2.41	0.42
1:G:342:ASN:N	1:G:342:ASN:OD1	2.52	0.42
1:I:813:SER:O	1:I:813:SER:OG	2.35	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:288:GLU:OE1	1:J:556:GLY:N	2.45	0.42
1:J:514:SER:HA	1:J:531:THR:HA	2.01	0.42
1:J:653:GLU:HB3	1:J:726:ILE:HD12	2.01	0.42
1:L:245:TRP:CD1	1:L:256:LYS:HD3	2.53	0.42
1:L:596:SER:OG	1:L:597:ASP:N	2.52	0.42
1:C:418:THR:HG22	1:Z:445:SER:HB2	2.00	0.42
1:G:468:LYS:HD2	1:G:468:LYS:HA	1.84	0.42
1:I:671:PHE:HB2	1:I:738:ILE:HG22	2.01	0.42
1:J:432:ASN:OD1	1:J:432:ASN:N	2.50	0.42
1:J:518:ILE:HB	1:J:612:LEU:HD23	2.01	0.42
1:J:624:ASP:N	1:J:624:ASP:OD1	2.50	0.42
1:J:855:TYR:HA	1:J:872:VAL:HG11	2.01	0.42
1:K:533:LYS:HE2	1:K:540:ASP:HB3	2.01	0.42
1:L:236:THR:OG1	1:L:255:LYS:O	2.37	0.42
1:M:757:THR:OG1	1:M:758:ASP:N	2.53	0.42
1:Z:594:THR:OG1	1:Z:595:LEU:N	2.52	0.42
1:A:619:PHE:HD1	1:A:737:SER:HB2	1.84	0.42
1:B:451:THR:OG1	1:B:452:MET:N	2.52	0.42
1:B:667:LYS:HE3	1:B:742:ASN:HA	2.01	0.42
1:C:687:LYS:HA	1:C:687:LYS:HD2	1.84	0.42
1:F:505:ASP:OD1	1:F:505:ASP:N	2.37	0.42
1:G:810:LEU:H	1:G:814:GLY:HA2	1.84	0.42
1:G:818:ILE:HG21	1:G:845:TYR:HB3	2.00	0.42
1:L:511:ASP:OD1	1:L:529:ARG:NH1	2.52	0.42
1:B:218:ASP:OD1	1:B:218:ASP:N	2.45	0.42
1:B:535:LEU:HD23	1:B:535:LEU:HA	1.88	0.42
1:E:236:THR:OG1	1:E:237:ILE:N	2.53	0.42
1:E:582:ASP:N	1:E:582:ASP:OD1	2.51	0.42
1:G:855:TYR:HA	1:G:872:VAL:HG23	2.00	0.42
1:M:405:LYS:HA	1:M:405:LYS:HD3	1.75	0.42
1:Z:833:ASN:N	1:Z:833:ASN:OD1	2.49	0.42
1:C:712:GLU:HB2	1:C:744:THR:HG21	2.00	0.42
1:D:681:SER:HA	1:D:727:GLY:HA3	2.02	0.42
1:D:790:PRO:O	1:D:795:LYS:NZ	2.49	0.42
1:G:681:SER:OG	1:G:697:TYR:O	2.30	0.42
1:J:321:LYS:HB3	1:J:321:LYS:HE2	1.74	0.42
1:L:407:THR:O	1:L:407:THR:OG1	2.35	0.42
1:Z:438:THR:OG1	1:Z:440:PRO:O	2.26	0.42
1:Z:463:ASN:OD1	1:Z:463:ASN:N	2.46	0.42
1:A:672:SER:HA	1:A:707:PHE:O	2.19	0.42
1:B:587:LYS:HE3	1:B:587:LYS:HB2	1.90	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:754:LYS:HZ3	1:D:666:TYR:HB2	1.84	0.42
1:D:684:ILE:HG12	1:D:694:LYS:HD3	2.02	0.42
1:G:634:ASN:HD21	1:G:650:LEU:HD13	1.84	0.42
1:J:383:LYS:HE2	1:J:383:LYS:HB3	1.88	0.42
1:J:514:SER:OG	1:J:515:ALA:N	2.51	0.42
1:K:336:THR:OG1	1:K:741:LEU:O	2.38	0.42
1:D:833:ASN:OD1	1:D:833:ASN:N	2.47	0.42
1:J:262:LEU:HD12	1:L:240:LEU:HD13	2.02	0.42
1:J:783:ILE:HG12	1:J:851:ASN:HB2	2.02	0.42
1:K:474:LYS:HE3	1:K:474:LYS:HB2	1.87	0.42
1:K:514:SER:OG	1:K:515:ALA:O	2.37	0.42
1:L:291:ASP:HA	1:L:292:PRO:HD3	1.86	0.42
1:L:591:SER:O	1:L:591:SER:OG	2.34	0.42
1:Z:265:ASN:OD1	1:Z:265:ASN:N	2.52	0.42
1:C:251:GLU:H	1:C:251:GLU:HG2	1.64	0.42
1:D:552:GLU:HG3	1:D:559:LYS:HE3	2.01	0.42
1:E:394:ARG:HG3	1:E:440:PRO:HD2	2.01	0.42
1:F:663:LEU:HD13	1:F:669:TYR:HE2	1.84	0.42
1:K:675:SER:O	1:K:704:TYR:HA	2.20	0.42
1:K:818:ILE:HG21	1:K:845:TYR:HB3	2.01	0.42
1:B:719:SER:OG	1:B:720:ASN:N	2.53	0.42
1:C:866:ASP:OD1	1:C:866:ASP:N	2.45	0.42
1:F:760:GLU:HG2	1:F:761:ILE:H	1.85	0.42
1:G:463:ASN:OD1	1:G:463:ASN:N	2.53	0.42
1:H:616:PRO:HA	1:H:739:THR:HG22	2.02	0.42
1:I:447:LEU:HD12	1:I:447:LEU:HA	1.89	0.42
1:I:754:LYS:HE2	1:I:754:LYS:HB2	1.90	0.42
1:M:681:SER:OG	1:M:726:ILE:O	2.25	0.42
1:C:619:PHE:HD1	1:C:737:SER:HB3	1.85	0.41
1:F:413:VAL:HG23	1:F:477:LYS:HB2	2.02	0.41
1:F:589:LYS:HE3	1:F:589:LYS:HB3	1.87	0.41
1:G:632:TRP:CG	1:G:656:ILE:HD11	2.55	0.41
1:H:245:TRP:CE2	1:H:256:LYS:HD3	2.55	0.41
1:H:249:PHE:HB3	1:H:254:TYR:HB2	2.02	0.41
1:H:559:LYS:HG2	1:H:564:LEU:HB3	2.02	0.41
1:J:390:ASN:N	1:J:390:ASN:OD1	2.52	0.41
1:J:397:ASN:HB2	1:J:433:LEU:HD21	2.02	0.41
1:J:673:GLY:O	1:J:706:LYS:HA	2.20	0.41
1:K:280:SER:O	1:K:280:SER:OG	2.33	0.41
1:L:363:ASN:N	1:L:363:ASN:OD1	2.52	0.41
1:L:855:TYR:HE2	1:L:857:LYS:HD3	1.85	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M:410:THR:OG1	1:M:479:GLU:O	2.31	0.41
1:Z:487:PHE:HB3	1:Z:503:TRP:CE2	2.55	0.41
1:C:610:ASN:OD1	1:C:610:ASN:N	2.53	0.41
1:D:232:ARG:HB3	1:D:233:ASN:H	1.77	0.41
1:D:685:ILE:HG12	1:D:723:ILE:HD12	2.01	0.41
1:F:390:ASN:OD1	1:F:390:ASN:N	2.50	0.41
1:F:720:ASN:HD21	1:F:722:GLU:HB3	1.85	0.41
1:G:687:LYS:HB3	1:G:690:ALA:HB3	2.02	0.41
1:H:417:ASP:HB3	1:J:308:ILE:HD11	2.02	0.41
1:K:589:LYS:HB2	1:K:589:LYS:HE3	1.93	0.41
1:K:687:LYS:HZ2	1:K:688:ILE:N	2.17	0.41
1:L:465:ASP:OD1	1:L:465:ASP:N	2.52	0.41
1:L:676:LYS:HD2	1:L:676:LYS:HA	1.86	0.41
1:M:533:LYS:HE2	1:M:533:LYS:HB3	1.92	0.41
1:Z:698:LEU:HD12	1:Z:700:PRO:HD3	2.03	0.41
1:A:587:LYS:O	1:A:591:SER:OG	2.37	0.41
1:C:425:GLN:NE2	1:C:428:GLN:OE1	2.43	0.41
1:D:327:THR:HG22	1:D:367:VAL:HG22	2.03	0.41
1:E:321:LYS:HD2	1:E:379:LEU:HA	2.02	0.41
1:E:616:PRO:HA	1:E:739:THR:HG23	2.03	0.41
1:E:634:ASN:OD1	1:E:634:ASN:N	2.52	0.41
1:F:673:GLY:O	1:F:706:LYS:HA	2.20	0.41
1:F:686:VAL:HA	1:F:692:GLU:HB2	2.02	0.41
1:I:262:LEU:HD23	1:I:262:LEU:HA	1.85	0.41
1:L:514:SER:OG	1:L:515:ALA:N	2.53	0.41
1:L:621:ASN:ND2	1:L:624:ASP:O	2.53	0.41
1:L:656:ILE:O	1:L:722:GLU:HA	2.19	0.41
1:M:680:THR:O	1:M:728:SER:OG	2.33	0.41
1:Z:417:ASP:OD1	1:Z:418:THR:N	2.53	0.41
1:Z:823:LYS:NZ	1:Z:838:ASN:OD1	2.40	0.41
1:B:248:SER:O	1:B:248:SER:OG	2.37	0.41
1:B:385:GLU:OE2	1:B:388:TYR:OH	2.31	0.41
1:F:721:ILE:HD12	1:F:721:ILE:HA	1.94	0.41
1:I:487:PHE:HB3	1:I:503:TRP:NE1	2.36	0.41
1:I:672:SER:HB2	1:I:706:LYS:HE2	2.02	0.41
1:J:792:GLN:HG3	1:J:795:LYS:HZ2	1.86	0.41
1:K:394:ARG:HG3	1:K:440:PRO:HD2	2.02	0.41
1:L:762:MET:O	1:L:765:HIS:NE2	2.54	0.41
1:Z:307:LEU:HD23	1:Z:327:THR:HG21	2.03	0.41
1:B:487:PHE:HB3	1:B:503:TRP:CE2	2.56	0.41
1:B:667:LYS:HD2	1:B:667:LYS:HA	1.67	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:300:VAL:HG13	1:E:483:VAL:HG11	2.01	0.41
1:E:487:PHE:CZ	1:E:501:ASN:HB3	2.55	0.41
1:H:720:ASN:OD1	1:H:720:ASN:N	2.50	0.41
1:I:833:ASN:OD1	1:I:833:ASN:N	2.53	0.41
1:C:765:HIS:ND1	1:C:869:GLU:OE2	2.53	0.41
1:D:428:GLN:HB2	1:D:447:LEU:HD21	2.01	0.41
1:G:637:THR:HA	1:G:640:GLN:HE21	1.83	0.41
1:G:806:VAL:HG13	1:G:818:ILE:HB	2.03	0.41
1:H:519:LEU:HD12	1:H:613:ILE:HD11	2.01	0.41
1:I:581:ASP:OD1	1:I:581:ASP:N	2.43	0.41
1:J:506:TYR:OH	1:L:496:ILE:N	2.43	0.41
1:K:302:VAL:O	1:K:363:ASN:ND2	2.53	0.41
1:M:427:ASN:O	1:Z:423:LYS:NZ	2.47	0.41
1:Z:327:THR:HG22	1:Z:367:VAL:HA	2.03	0.41
1:B:772:LEU:HB3	1:B:783:ILE:HG22	2.03	0.41
1:C:565:TYR:CZ	1:C:570:PRO:HB3	2.56	0.41
1:D:238:LYS:HE3	1:D:238:LYS:HB2	1.82	0.41
1:D:528:ARG:HA	1:D:528:ARG:HD3	1.95	0.41
1:E:870:LEU:HD12	1:E:870:LEU:HA	1.90	0.41
1:G:687:LYS:HZ1	1:G:689:LYS:H	1.67	0.41
1:I:551:ILE:HG21	1:I:571:ILE:HG21	2.03	0.41
1:I:699:VAL:HG21	1:I:731:THR:HG21	2.03	0.41
1:L:629:PRO:HG2	1:L:658:ILE:HG12	2.02	0.41
1:L:821:LYS:HD3	1:L:821:LYS:HA	1.92	0.41
1:M:411:ASN:HB3	1:M:479:GLU:HB3	2.02	0.41
1:M:654:THR:O	1:M:724:THR:HA	2.21	0.41
1:A:636:ASN:OD1	1:A:636:ASN:N	2.53	0.41
1:C:599:LYS:HB3	1:C:602:ASN:ND2	2.36	0.41
1:D:581:ASP:N	1:D:581:ASP:OD1	2.51	0.41
1:E:293:LEU:HD23	1:E:545:LEU:HD11	2.02	0.41
1:E:465:ASP:OD1	1:E:465:ASP:N	2.54	0.41
1:G:449:LEU:HD12	1:G:449:LEU:HA	1.92	0.41
1:G:487:PHE:HB3	1:G:503:TRP:CE2	2.56	0.41
1:G:535:LEU:HD23	1:G:535:LEU:HA	1.92	0.41
1:H:544:GLU:H	1:H:544:GLU:HG2	1.69	0.41
1:K:857:LYS:HG2	1:K:871:LEU:HG	2.01	0.41
1:Z:550:ALA:HA	1:Z:553:LYS:HB2	2.02	0.41
1:A:336:THR:HG1	1:A:358:SER:HG	1.59	0.41
1:A:514:SER:OG	1:A:530:VAL:N	2.54	0.41
1:B:276:LYS:HD2	1:B:292:PRO:HA	2.03	0.41
1:D:433:LEU:HD23	1:D:433:LEU:HA	1.82	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:826:ARG:O	1:E:836:LYS:HA	2.20	0.41
1:F:307:LEU:HD22	1:F:476:ILE:HG12	2.02	0.41
1:F:618:TYR:HB3	1:F:628:TYR:CE1	2.56	0.41
1:F:655:LYS:HA	1:F:723:ILE:O	2.19	0.41
1:G:534:ASN:N	1:G:607:ARG:HH21	2.19	0.41
1:H:825:MET:HB3	1:H:836:LYS:HD3	2.02	0.41
1:I:663:LEU:HD12	1:I:663:LEU:HA	1.86	0.41
1:I:855:TYR:HA	1:I:872:VAL:HG23	2.02	0.41
1:K:487:PHE:HB3	1:K:503:TRP:CE2	2.56	0.41
1:K:671:PHE:HA	1:K:737:SER:O	2.20	0.41
1:K:801:ILE:O	1:K:802:GLN:NE2	2.53	0.41
1:L:425:GLN:OE1	1:L:425:GLN:N	2.53	0.41
1:L:765:HIS:HB3	1:L:795:LYS:HD3	2.03	0.41
1:M:307:LEU:O	1:M:324:SER:HA	2.21	0.41
1:M:333:GLU:HG3	1:M:364:SER:HB2	2.02	0.41
1:M:381:ILE:HD13	1:M:381:ILE:HA	1.87	0.41
1:M:442:LYS:HB2	1:M:442:LYS:HE3	1.81	0.41
1:M:800:TYR:CZ	1:M:863:ILE:HD13	2.56	0.41
1:Z:230:TYR:HE1	1:Z:244:LYS:HE3	1.86	0.41
1:Z:381:ILE:HG23	1:Z:385:GLU:HB2	2.02	0.41
1:A:417:ASP:OD2	1:A:417:ASP:N	2.51	0.41
1:B:780:ASN:OD1	1:B:780:ASN:N	2.48	0.41
1:F:642:GLY:O	1:F:732:TYR:OH	2.39	0.41
1:J:671:PHE:O	1:J:708:SER:HA	2.21	0.41
1:L:544:GLU:HB2	1:L:604:LYS:HE3	2.02	0.41
1:M:364:SER:OG	1:M:477:LYS:NZ	2.40	0.41
1:A:342:ASN:HB3	1:L:354:THR:HG23	2.02	0.40
1:A:622:PHE:HB3	1:A:640:GLN:HB2	2.03	0.40
1:B:798:LEU:HD23	1:B:798:LEU:HA	1.91	0.40
1:E:514:SER:HA	1:E:531:THR:HA	2.02	0.40
1:I:382:ASN:H	1:I:385:GLU:HG3	1.85	0.40
1:J:229:SER:HG	1:J:244:LYS:HZ3	1.60	0.40
1:J:775:ASN:ND2	1:J:776:PRO:O	2.53	0.40
1:K:523:ASN:OD1	1:K:523:ASN:N	2.54	0.40
1:L:487:PHE:HB3	1:L:503:TRP:CE2	2.56	0.40
1:B:564:LEU:HD11	1:B:571:ILE:HB	2.02	0.40
1:D:533:LYS:HG2	1:D:535:LEU:HD22	2.04	0.40
1:E:251:GLU:H	1:E:251:GLU:HG2	1.67	0.40
1:F:238:LYS:HE3	1:F:238:LYS:HB2	1.89	0.40
1:G:656:ILE:HD13	1:G:656:ILE:HA	1.91	0.40
1:G:805:ARG:HH21	1:G:859:ARG:HG2	1.86	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:577:GLU:HG3	1:H:739:THR:HG21	2.02	0.40
1:I:409:THR:HA	1:I:423:LYS:HA	2.04	0.40
1:J:468:LYS:HA	1:J:468:LYS:HD2	1.90	0.40
1:J:649:LYS:HG2	1:J:730:THR:HG23	2.02	0.40
1:K:791:THR:HG21	1:K:835:PRO:HG2	2.04	0.40
1:L:219:LEU:HD22	1:L:225:ASN:H	1.85	0.40
1:M:576:VAL:HG13	1:M:615:THR:HA	2.03	0.40
1:Z:831:ASP:OD2	1:Z:834:GLN:NE2	2.44	0.40
1:A:371:ASN:O	1:B:324:SER:OG	2.31	0.40
1:A:649:LYS:HA	1:A:730:THR:HA	2.03	0.40
1:D:413:VAL:HG13	1:D:477:LYS:HB2	2.03	0.40
1:D:521:THR:HG23	1:D:524:GLU:H	1.86	0.40
1:D:597:ASP:N	1:D:597:ASP:OD1	2.53	0.40
1:I:386:SER:HA	1:I:462:ILE:O	2.22	0.40
1:I:649:LYS:HB2	1:I:730:THR:HA	2.02	0.40
1:K:573:GLU:OE1	1:K:599:LYS:NZ	2.54	0.40
1:M:600:ILE:HD12	1:M:600:ILE:HA	1.95	0.40
1:Z:655:LYS:HB2	1:Z:722:GLU:OE2	2.21	0.40
1:Z:687:LYS:HG3	1:Z:689:LYS:H	1.85	0.40
1:A:671:PHE:HB2	1:A:738:ILE:HG22	2.03	0.40
1:B:854:THR:HG22	1:B:855:TYR:H	1.86	0.40
1:C:605:LEU:HD23	1:C:605:LEU:HA	1.91	0.40
1:E:592:LEU:HD23	1:E:592:LEU:HA	1.89	0.40
1:F:300:VAL:HG23	1:F:483:VAL:HG11	2.04	0.40
1:G:266:THR:HG21	1:G:293:LEU:HD22	2.04	0.40
1:G:523:ASN:N	1:G:523:ASN:OD1	2.55	0.40
1:G:634:ASN:OD1	1:G:634:ASN:N	2.54	0.40
1:H:754:LYS:HE2	1:H:754:LYS:HB2	1.68	0.40
1:I:220:ASP:OD2	1:I:224:ASP:N	2.55	0.40
1:M:687:LYS:HA	1:M:687:LYS:HD2	1.96	0.40
1:Z:673:GLY:O	1:Z:706:LYS:HA	2.21	0.40
1:A:230:TYR:CD2	1:A:261:TYR:HB3	2.56	0.40
1:A:669:TYR:HB2	1:A:711:PHE:CE2	2.57	0.40
1:A:741:LEU:HD12	1:A:741:LEU:HA	1.93	0.40
1:B:821:LYS:HA	1:B:821:LYS:HD3	1.84	0.40
1:G:663:LEU:HD12	1:G:663:LEU:HA	1.94	0.40
1:J:581:ASP:N	1:J:581:ASP:OD1	2.45	0.40
1:L:490:LYS:HB2	1:L:490:LYS:HE3	1.91	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	A	657/876 (75%)	588 (90%)	69 (10%)	0	100	100
1	B	657/876 (75%)	592 (90%)	65 (10%)	0	100	100
1	C	656/876 (75%)	580 (88%)	76 (12%)	0	100	100
1	D	657/876 (75%)	576 (88%)	81 (12%)	0	100	100
1	E	656/876 (75%)	577 (88%)	79 (12%)	0	100	100
1	F	657/876 (75%)	578 (88%)	79 (12%)	0	100	100
1	G	656/876 (75%)	578 (88%)	78 (12%)	0	100	100
1	H	657/876 (75%)	592 (90%)	65 (10%)	0	100	100
1	I	656/876 (75%)	595 (91%)	61 (9%)	0	100	100
1	J	657/876 (75%)	584 (89%)	73 (11%)	0	100	100
1	K	656/876 (75%)	574 (88%)	82 (12%)	0	100	100
1	L	657/876 (75%)	581 (88%)	76 (12%)	0	100	100
1	M	656/876 (75%)	577 (88%)	79 (12%)	0	100	100
1	Z	655/876 (75%)	585 (89%)	70 (11%)	0	100	100
All	All	9190/12264 (75%)	8157 (89%)	1033 (11%)	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	A	585/790 (74%)	583 (100%)	2 (0%)	92	95
1	B	585/790 (74%)	584 (100%)	1 (0%)	93	96
1	C	584/790 (74%)	584 (100%)	0	100	100
1	D	585/790 (74%)	582 (100%)	3 (0%)	88	93
1	E	584/790 (74%)	579 (99%)	5 (1%)	78	87
1	F	585/790 (74%)	581 (99%)	4 (1%)	84	90
1	G	584/790 (74%)	584 (100%)	0	100	100
1	H	585/790 (74%)	582 (100%)	3 (0%)	88	93
1	I	584/790 (74%)	583 (100%)	1 (0%)	93	96
1	J	585/790 (74%)	583 (100%)	2 (0%)	92	95
1	K	584/790 (74%)	583 (100%)	1 (0%)	93	96
1	L	585/790 (74%)	582 (100%)	3 (0%)	88	93
1	M	584/790 (74%)	582 (100%)	2 (0%)	92	95
1	Z	583/790 (74%)	582 (100%)	1 (0%)	93	96
All	All	8182/11060 (74%)	8154 (100%)	28 (0%)	92	95

All (28) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	771	ASP
1	A	859	ARG
1	B	433	LEU
1	D	613	ILE
1	D	762	MET
1	D	859	ARG
1	E	465	ASP
1	E	478	LEU
1	E	610	ASN
1	E	821	LYS
1	E	831	ASP
1	F	257	TYR
1	F	433	LEU
1	F	694	LYS
1	F	852	ILE
1	H	257	TYR
1	H	291	ASP
1	H	433	LEU
1	I	350	THR

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Mol	Chain	Res	Type
1	J	638	THR
1	J	778	THR
1	K	676	LYS
1	L	453	ASP
1	L	748	LEU
1	L	854	THR
1	M	623	ASP
1	M	821	LYS
1	Z	676	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (97) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	636	ASN
1	A	682	ASN
1	A	735	ASN
1	A	759	GLN
1	A	775	ASN
1	A	841	ASN
1	B	265	ASN
1	B	347	ASN
1	B	427	ASN
1	B	636	ASN
1	B	648	ASN
1	B	838	ASN
1	B	841	ASN
1	C	312	ASN
1	C	352	ASN
1	C	432	ASN
1	C	450	ASN
1	C	486	ASN
1	C	491	ASN
1	C	501	ASN
1	C	634	ASN
1	C	644	GLN
1	C	841	ASN
1	D	252	GLN
1	D	501	ASN
1	D	621	ASN
1	D	651	ASN
1	D	682	ASN
1	D	841	ASN

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Mol	Chain	Res	Type
1	E	319	GLN
1	E	342	ASN
1	E	450	ASN
1	E	454	GLN
1	E	486	ASN
1	E	802	GLN
1	E	834	GLN
1	E	838	ASN
1	E	841	ASN
1	F	223	ASN
1	F	425	GLN
1	F	428	GLN
1	F	486	ASN
1	F	567	ASN
1	F	648	ASN
1	F	651	ASN
1	F	720	ASN
1	F	735	ASN
1	F	742	ASN
1	F	775	ASN
1	G	260	ASN
1	G	314	HIS
1	G	425	GLN
1	G	509	GLN
1	G	636	ASN
1	G	640	GLN
1	G	682	ASN
1	H	359	HIS
1	H	534	ASN
1	H	610	ASN
1	H	640	GLN
1	H	682	ASN
1	I	450	ASN
1	I	651	ASN
1	I	735	ASN
1	I	775	ASN
1	I	802	GLN
1	I	841	ASN
1	J	260	ASN
1	J	427	ASN
1	J	602	ASN
1	J	648	ASN

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Mol	Chain	Res	Type
1	J	682	ASN
1	J	811	GLN
1	K	335	ASN
1	K	432	ASN
1	K	450	ASN
1	K	640	GLN
1	K	644	GLN
1	K	735	ASN
1	K	802	GLN
1	K	811	GLN
1	L	491	ASN
1	L	621	ASN
1	L	636	ASN
1	L	775	ASN
1	L	838	ASN
1	M	390	ASN
1	M	411	ASN
1	M	432	ASN
1	M	682	ASN
1	M	775	ASN
1	M	811	GLN
1	M	841	ASN
1	M	851	ASN
1	Z	450	ASN
1	Z	735	ASN
1	Z	775	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 monosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

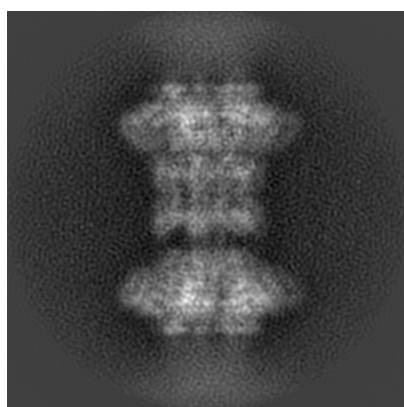
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-0610. These allow visual inspection of the internal detail of the map and identification of artifacts.

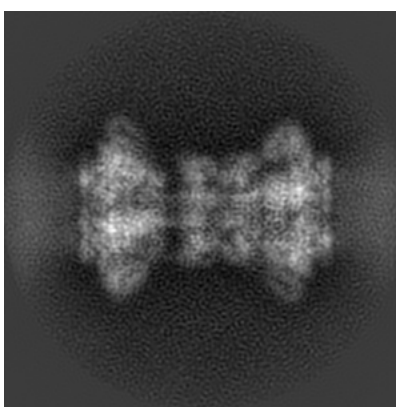
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

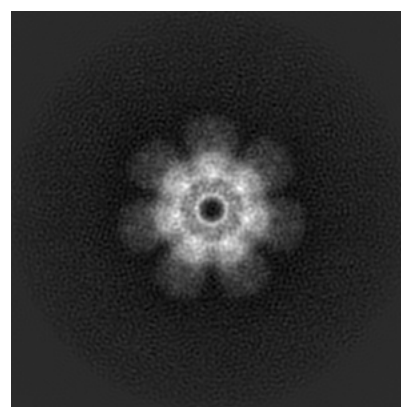
6.1.1 Primary map



X



Y

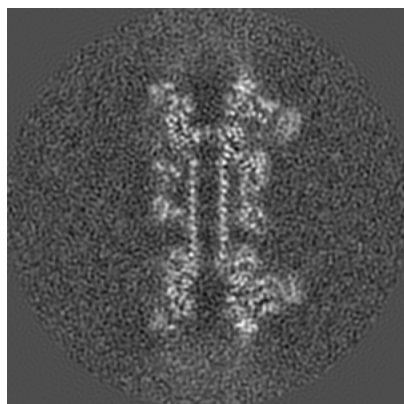


Z

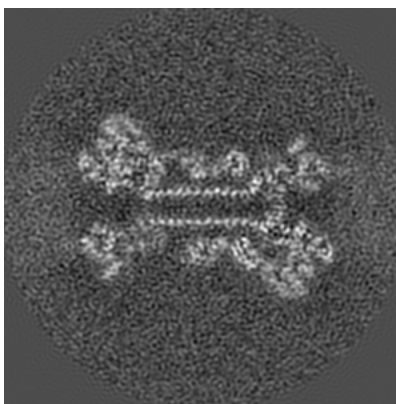
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

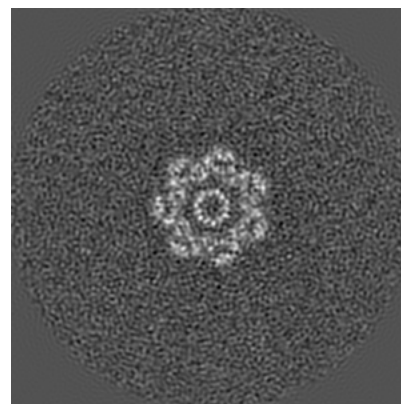
6.2.1 Primary map



X Index: 125



Y Index: 125

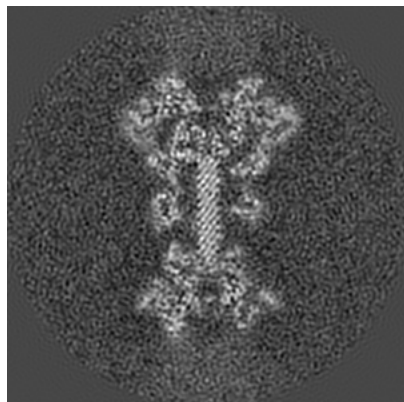


Z Index: 125

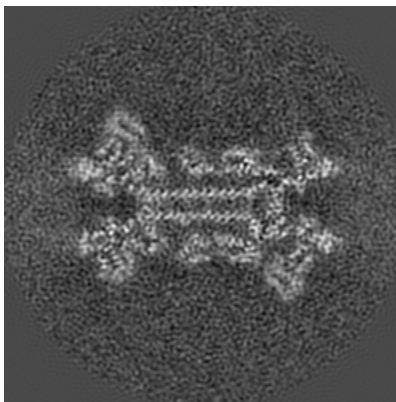
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

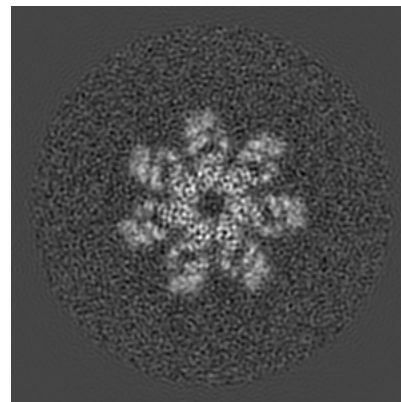
6.3.1 Primary map



X Index: 134



Y Index: 119

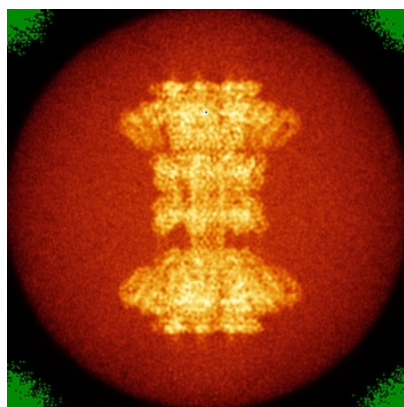


Z Index: 67

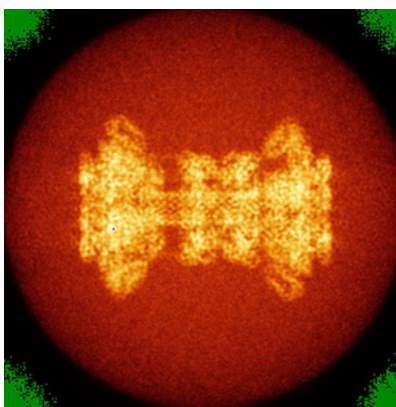
The images above show the largest variance slices of the map in three orthogonal directions.

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

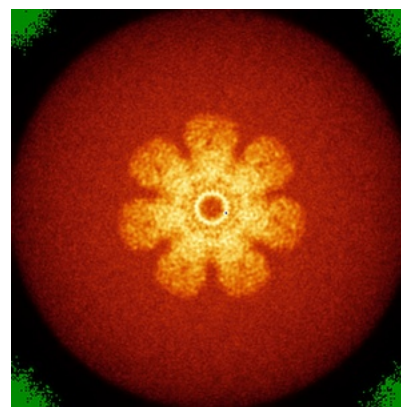
6.4.1 Primary map



X



Y

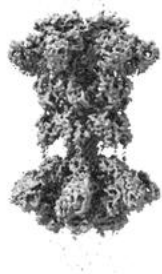


Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.0545. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

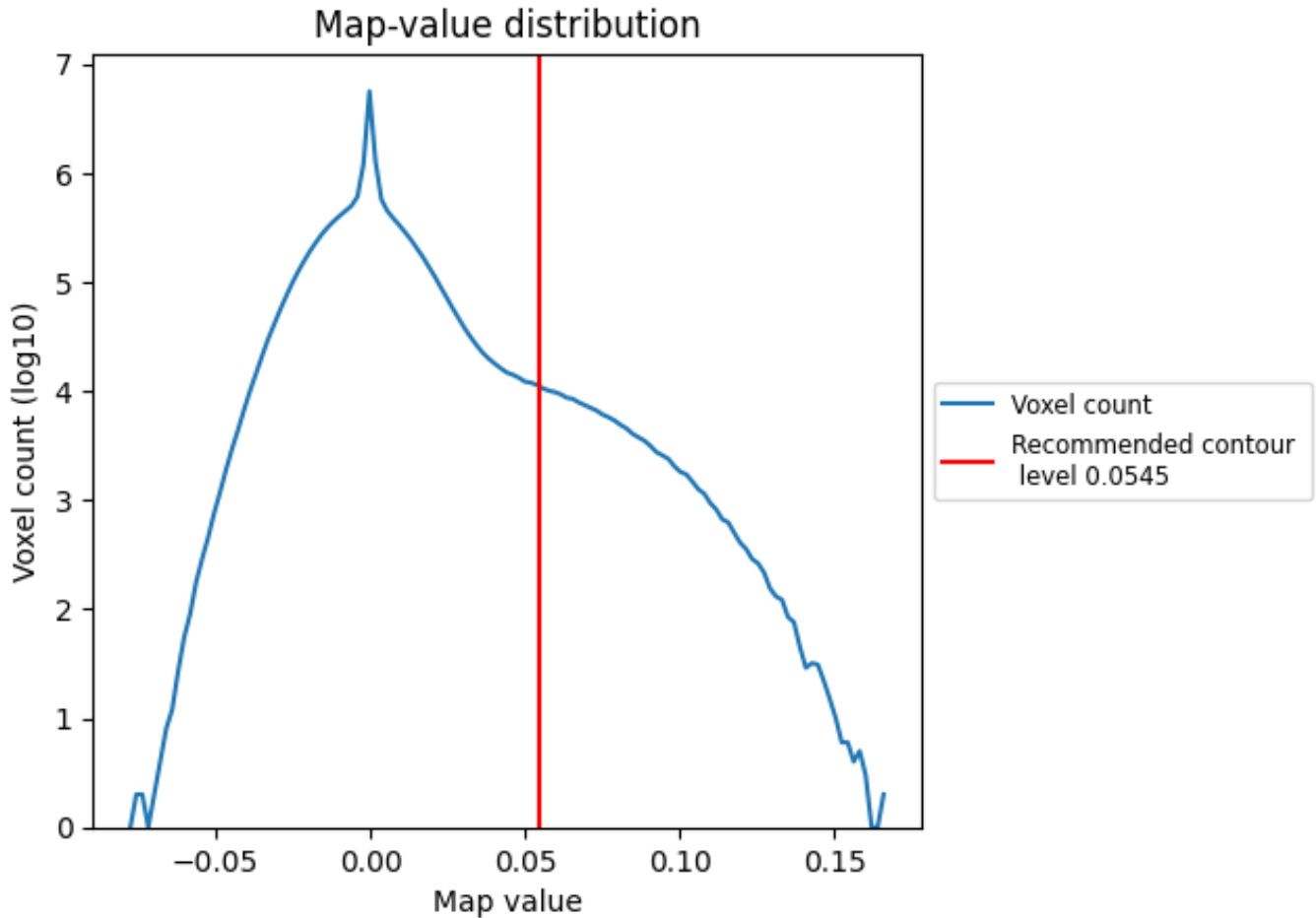
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

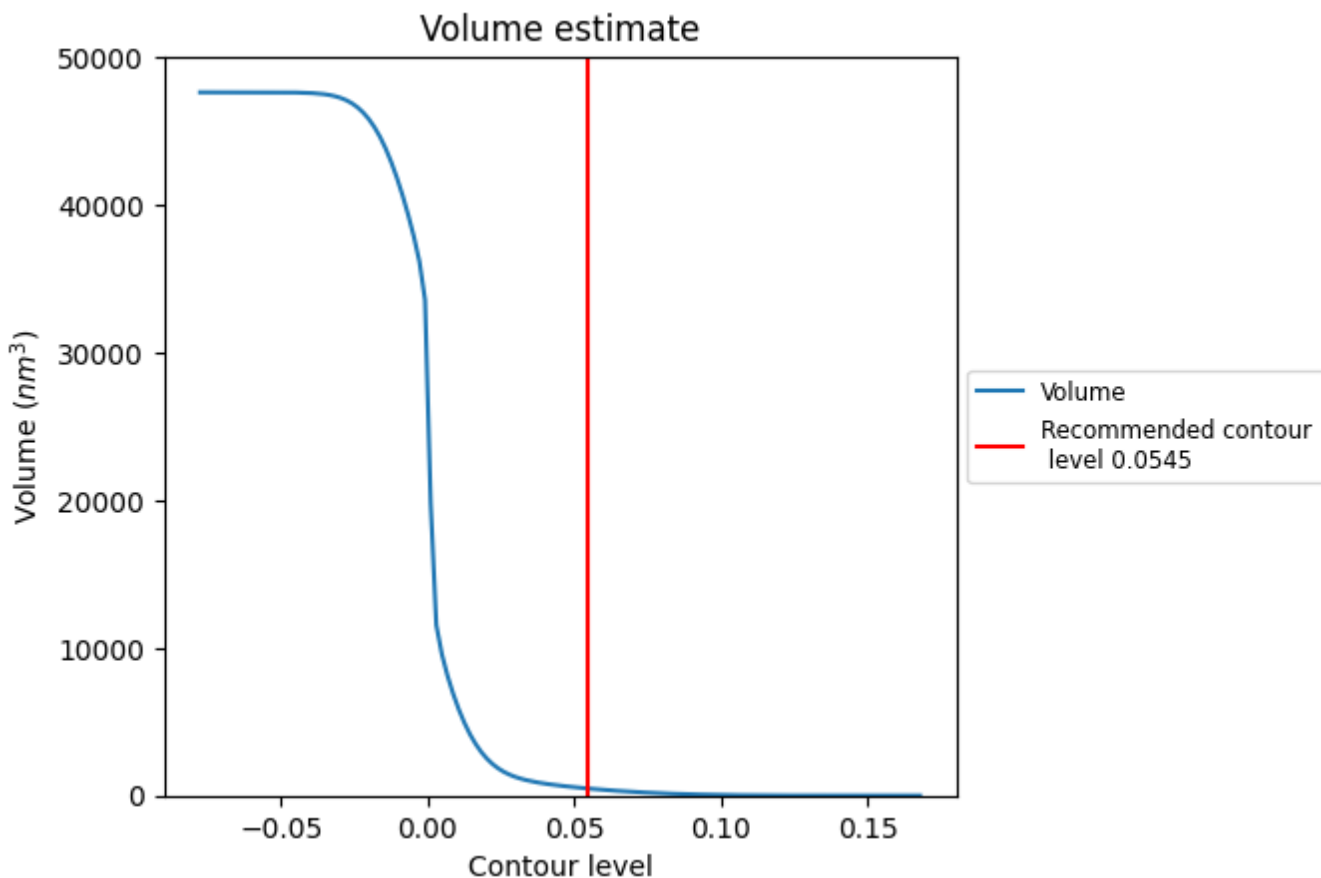
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

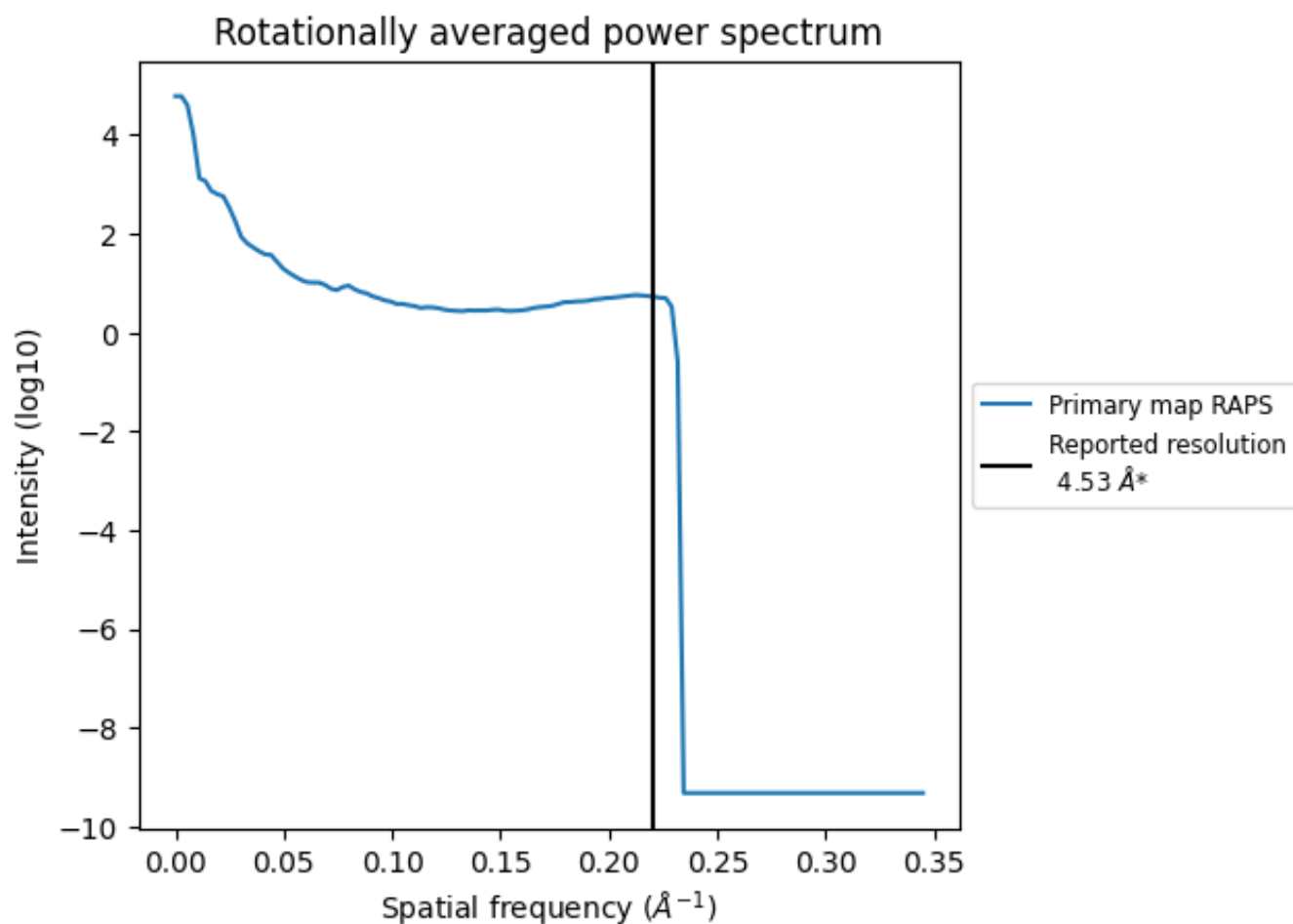
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 481 nm³; this corresponds to an approximate mass of 435 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 [\(i\)](#)

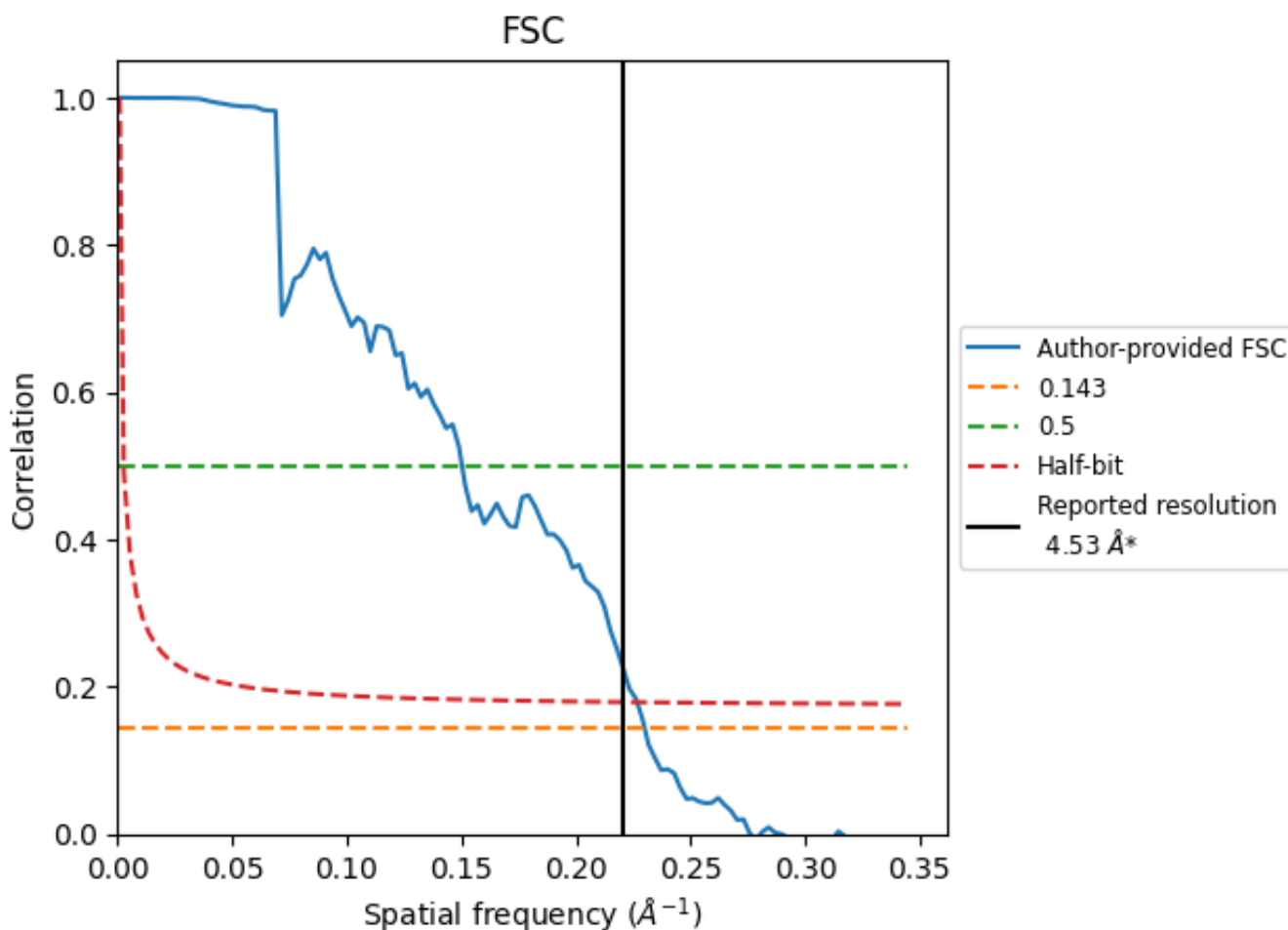


*Reported resolution corresponds to spatial frequency of 0.221 Å⁻¹

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 0.221 Å⁻¹

8.2 Resolution estimates [i](#)

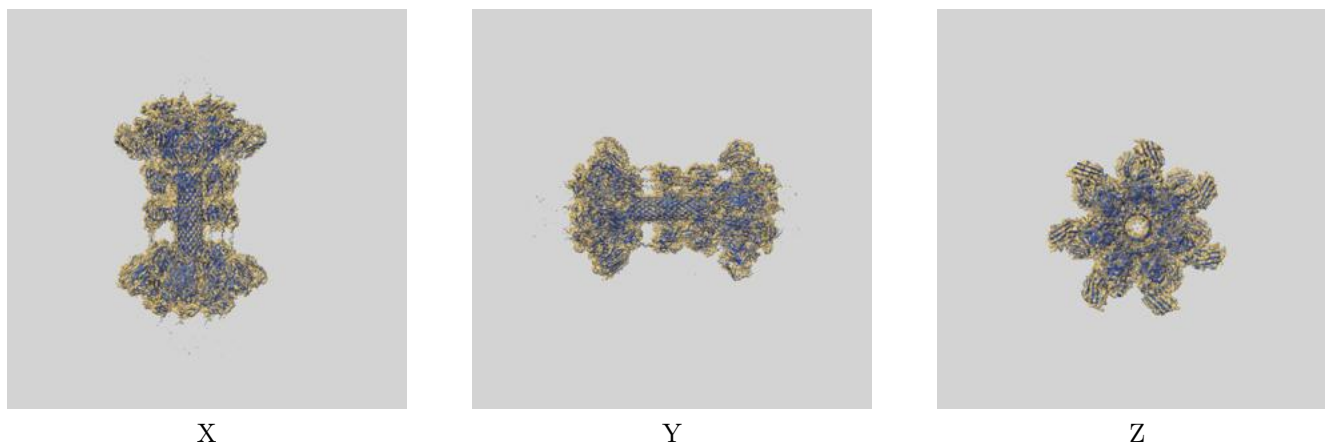
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.53	-	-
Author-provided FSC curve	4.35	6.65	4.41
Unmasked-calculated*	-	-	-

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

9 Map-model fit [i](#)

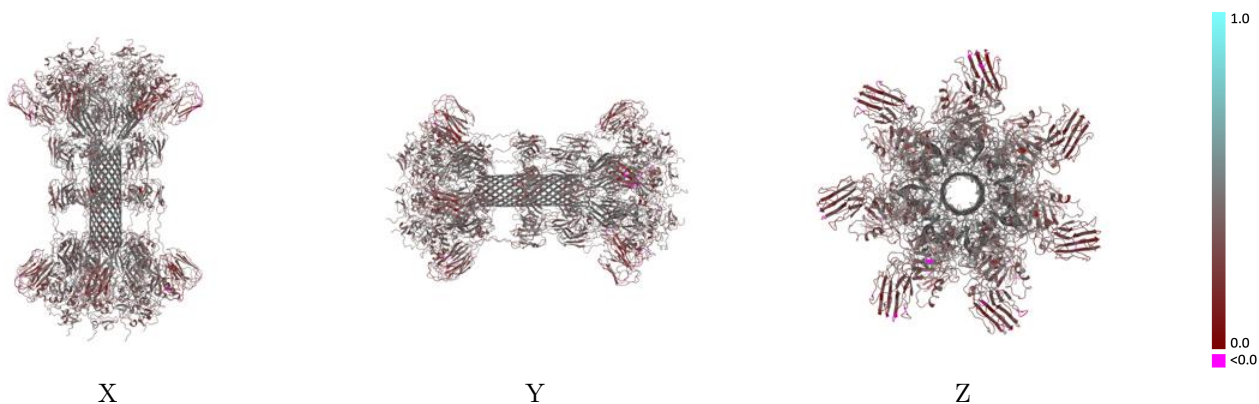
This section contains information regarding the fit between EMDB map EMD-0610 and PDB model 6O2O. Per-residue inclusion information can be found in section 3 on page 5.

9.1 Map-model overlay [i](#)



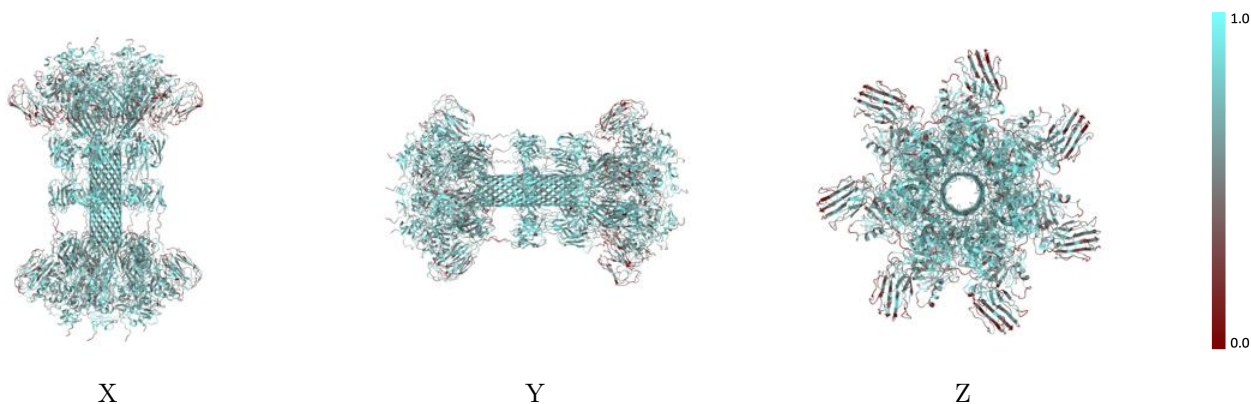
The images above show the 3D surface view of the map at the recommended contour level 0.0545 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



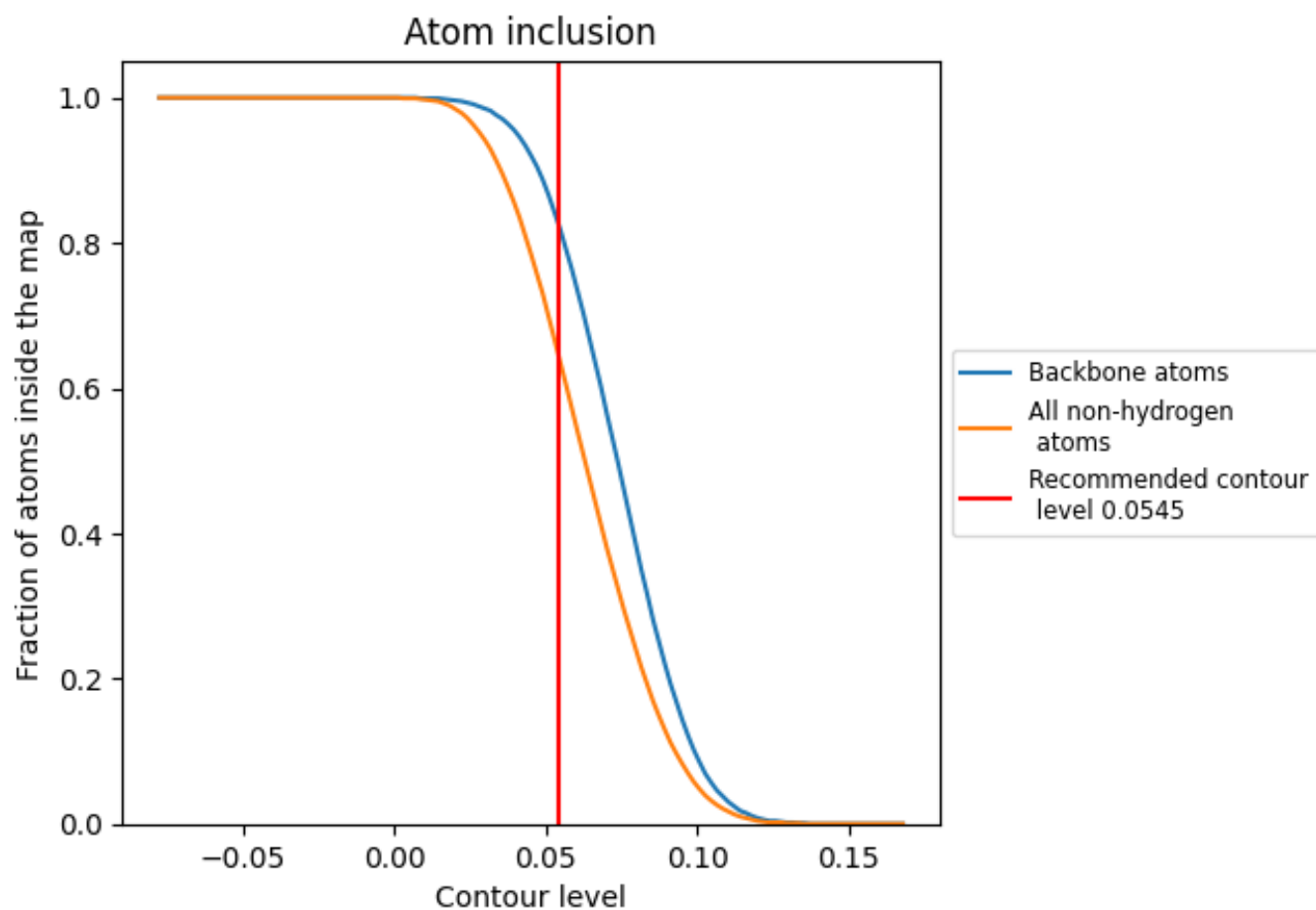
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.0545).































9.4 Atom inclusion [i](#)



At the recommended contour level, 82% of all backbone atoms, 64% 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 (0.0545) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.6420	 0.3770
A	 0.6310	 0.3860
B	 0.6350	 0.3810
C	 0.6410	 0.3670
D	 0.6350	 0.3810
E	 0.6500	 0.3750
F	 0.6440	 0.3830
G	 0.6360	 0.3720
H	 0.6340	 0.3810
I	 0.6430	 0.3710
J	 0.6480	 0.3880
K	 0.6540	 0.3740
L	 0.6410	 0.3780
M	 0.6500	 0.3700
Z	 0.6430	 0.3690

