Full wwPDB EM Validation Report ⓘ

Nov 9, 2026 – 07:24 PM JST

PDB ID	:	25DE / pdb_000025de
EMDB ID	:	EMD-80026
Title	:	RB43 intact state capsid side vertex
Authors	:	Zhang, Y.; Ayala, R.; Moiseenko, A.V.
Deposited on	:	2026-03-30
Resolution	:	3.52 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:

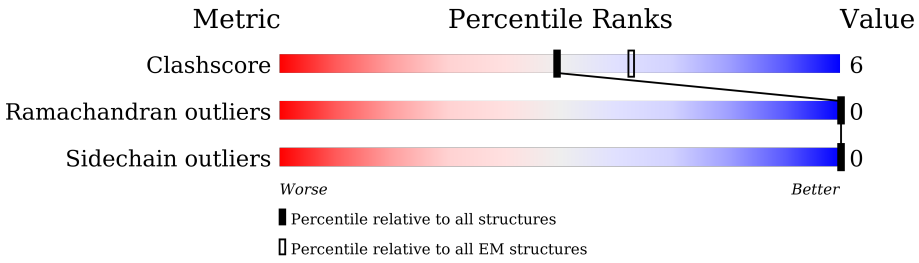
EMDB validation analysis	:	0.0.1.dev133
MolProbity	:	4-5-2 with Phenix2.2
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics	:	202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.51

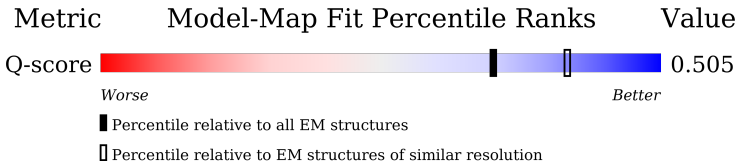
1 Overall quality at a glance (i)

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

The reported resolution of this entry is 3.52 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	13017 (3.02 - 4.02)

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 <=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	440	78% 12% 10%
1	B	440	80% 10% 10%
1	C	440	77% 13% 10%
1	D	440	78% 12% 10%

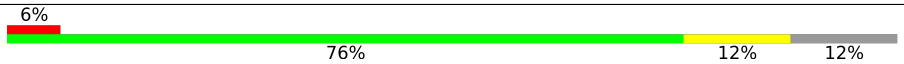
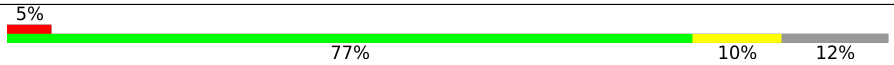
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Mol	Chain	Length	Quality of chain
1	E	440	77% 13% 10%
2	F	524	76% 11% 12%
2	G	524	78% 9% 12%
2	H	524	75% 13% 12%
2	I	524	76% 12% 12%
2	J	524	75% 12% 12%
2	K	524	76% 12% 12%
2	L	524	77% 10% 12%
2	M	524	79% 9% 12%
2	N	524	80% 8% 12%
2	O	524	79% 9% 12%
2	P	524	77% 10% 12%
2	Q	524	77% 10% 12%
2	R	524	77% 10% 12%
2	S	524	74% 13% 12%
2	T	524	78% 10% 12%
2	U	524	79% 8% 12%
2	V	524	77% 11% 12%
2	W	524	76% 11% 12%
2	X	524	76% 11% 12%
2	Y	524	76% 12% 12%
2	Z	524	17% 75% 12% 12%
2	a	524	24% 74% 14% 12%
2	b	524	12% 74% 13% 12%
2	c	524	75% 12% 12%

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Mol	Chain	Length	Quality of chain
2	d	524	
2	e	524	
2	f	524	
2	g	524	
2	h	524	
2	i	524	

2 Entry composition (i)

There are 2 unique types of molecules in this entry. The entry contains 118925 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 Capsid vertex protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	396	Total 3067	C 1929	N 503	O 622	S 13	0	0
1	B	396	Total 3067	C 1929	N 503	O 622	S 13	0	0
1	C	396	Total 3067	C 1929	N 503	O 622	S 13	0	0
1	D	396	Total 3067	C 1929	N 503	O 622	S 13	0	0
1	E	396	Total 3067	C 1929	N 503	O 622	S 13	0	0

- Molecule 2 is a protein called Major capsid protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	F	459	Total 3453	C 2173	N 598	O 668	S 14	0	0
2	G	459	Total 3453	C 2173	N 598	O 668	S 14	0	0
2	H	459	Total 3453	C 2173	N 598	O 668	S 14	0	0
2	I	459	Total 3453	C 2173	N 598	O 668	S 14	0	0
2	J	459	Total 3453	C 2173	N 598	O 668	S 14	0	0
2	K	459	Total 3453	C 2173	N 598	O 668	S 14	0	0
2	L	459	Total 3453	C 2173	N 598	O 668	S 14	0	0
2	M	459	Total 3453	C 2173	N 598	O 668	S 14	0	0
2	N	459	Total 3453	C 2173	N 598	O 668	S 14	0	0
2	O	459	Total 3453	C 2173	N 598	O 668	S 14	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
2	P	459	Total	C	N	O	S	0	0
			3453	2173	598	668	14		
2	Q	459	Total	C	N	O	S	0	0
			3453	2173	598	668	14		
2	R	459	Total	C	N	O	S	0	0
			3453	2173	598	668	14		
2	S	459	Total	C	N	O	S	0	0
			3453	2173	598	668	14		
2	T	459	Total	C	N	O	S	0	0
			3453	2173	598	668	14		
2	U	459	Total	C	N	O	S	0	0
			3453	2173	598	668	14		
2	V	459	Total	C	N	O	S	0	0
			3453	2173	598	668	14		
2	W	459	Total	C	N	O	S	0	0
			3453	2173	598	668	14		
2	X	459	Total	C	N	O	S	0	0
			3453	2173	598	668	14		
2	Y	459	Total	C	N	O	S	0	0
			3453	2173	598	668	14		
2	Z	459	Total	C	N	O	S	0	0
			3453	2173	598	668	14		
2	a	459	Total	C	N	O	S	0	0
			3453	2173	598	668	14		
2	b	459	Total	C	N	O	S	0	0
			3453	2173	598	668	14		
2	c	459	Total	C	N	O	S	0	0
			3453	2173	598	668	14		
2	d	459	Total	C	N	O	S	0	0
			3453	2173	598	668	14		
2	e	459	Total	C	N	O	S	0	0
			3453	2173	598	668	14		
2	f	459	Total	C	N	O	S	0	0
			3453	2173	598	668	14		
2	g	459	Total	C	N	O	S	0	0
			3453	2173	598	668	14		
2	h	459	Total	C	N	O	S	0	0
			3453	2173	598	668	14		
2	i	459	Total	C	N	O	S	0	0
			3453	2173	598	668	14		

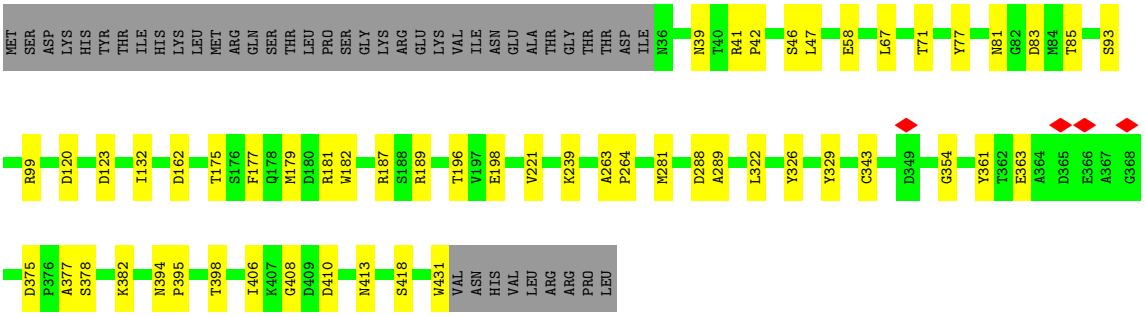
3 Residue-property plots (i)

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: Capsid vertex protein

Chain A:

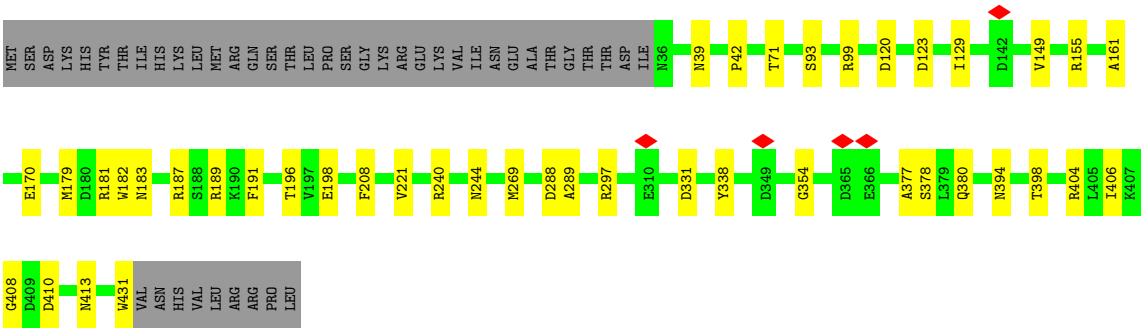




• Molecule 1: Capsid vertex protein

Chain B:



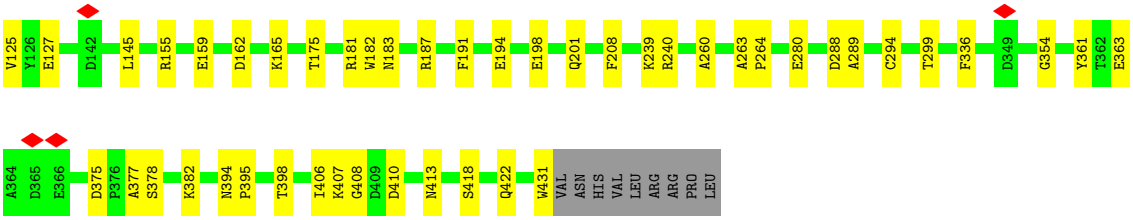


• Molecule 1: Capsid vertex protein

Chain C:

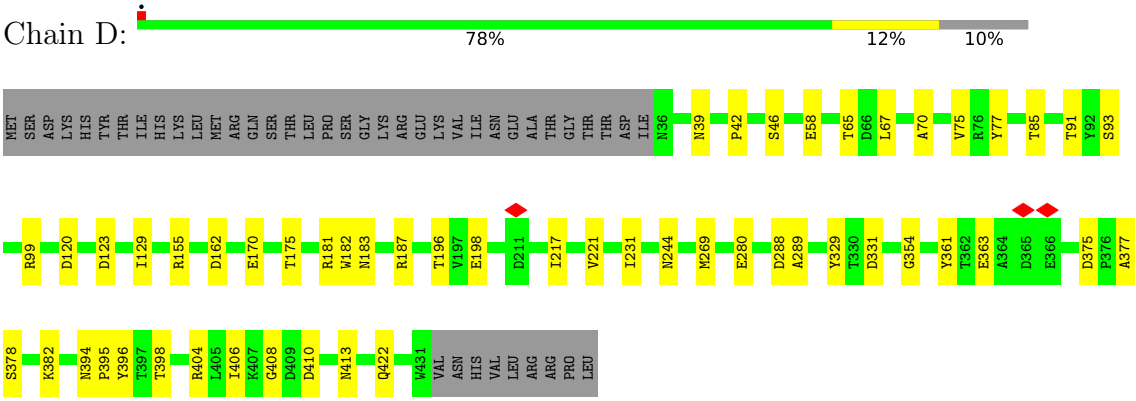






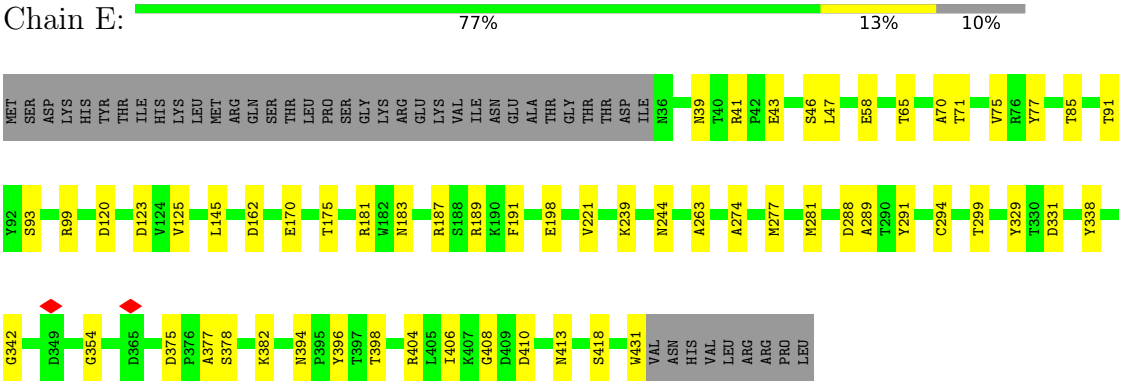
• Molecule 1: Capsid vertex protein

Chain D:



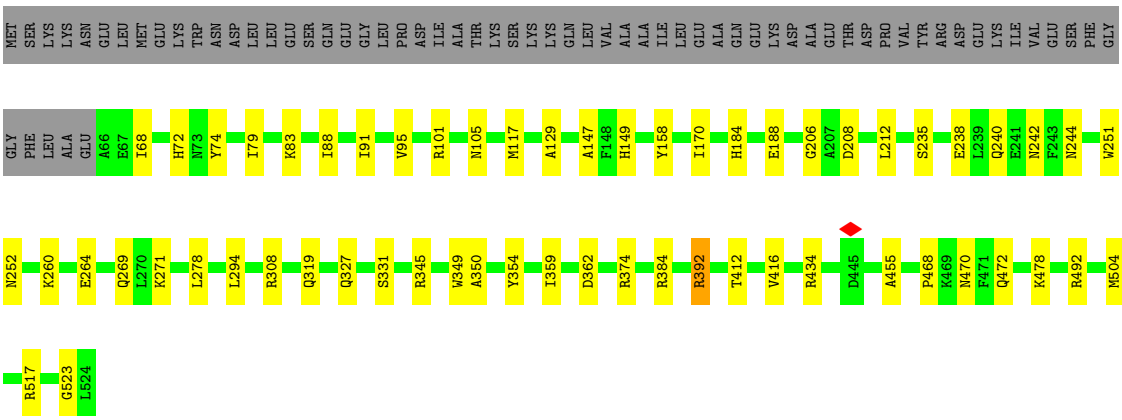
• Molecule 1: Capsid vertex protein

Chain E:



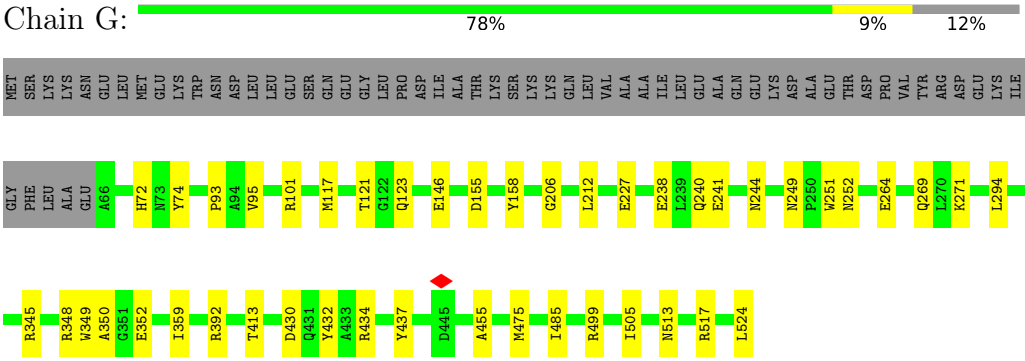
• Molecule 2: Major capsid protein

Chain F:



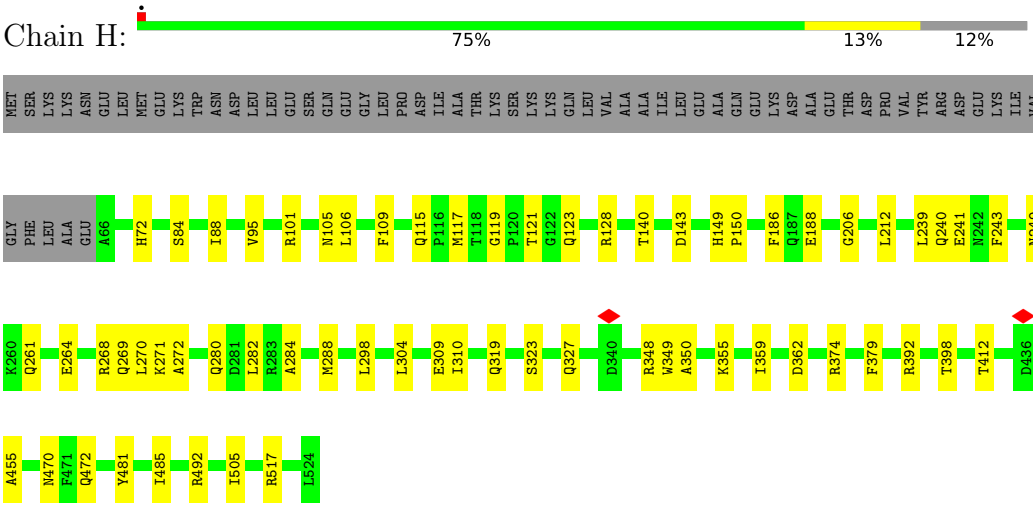
• Molecule 2: Major capsid protein

Chain G:



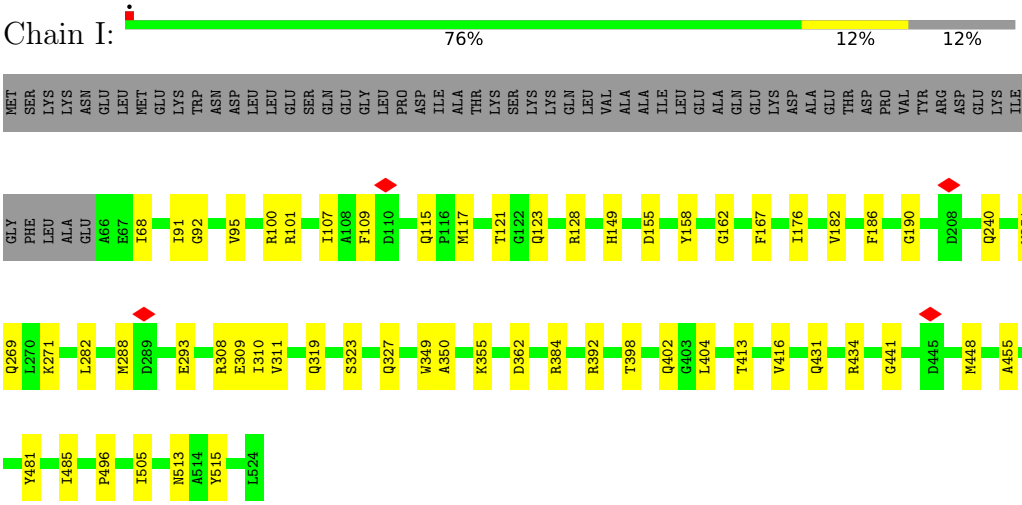
• Molecule 2: Major capsid protein

Chain H:



• Molecule 2: Major capsid protein

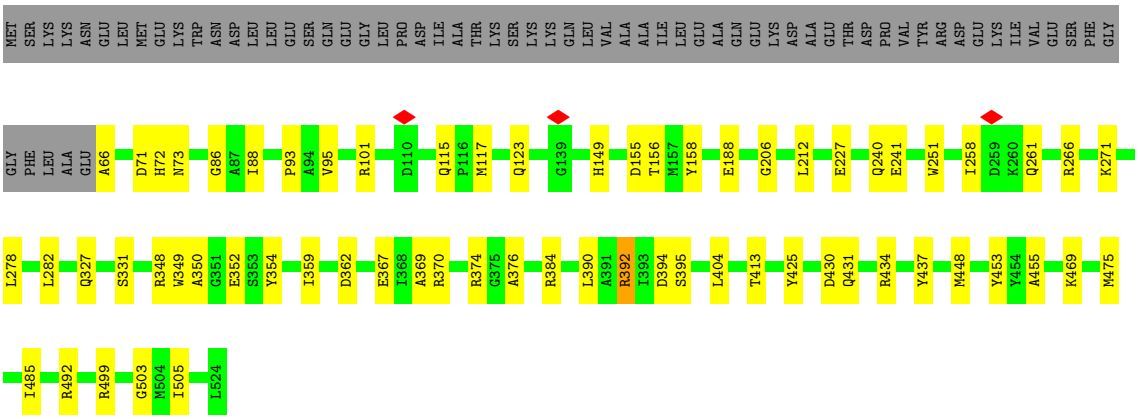
Chain I:



• Molecule 2: Major capsid protein

Chain J:

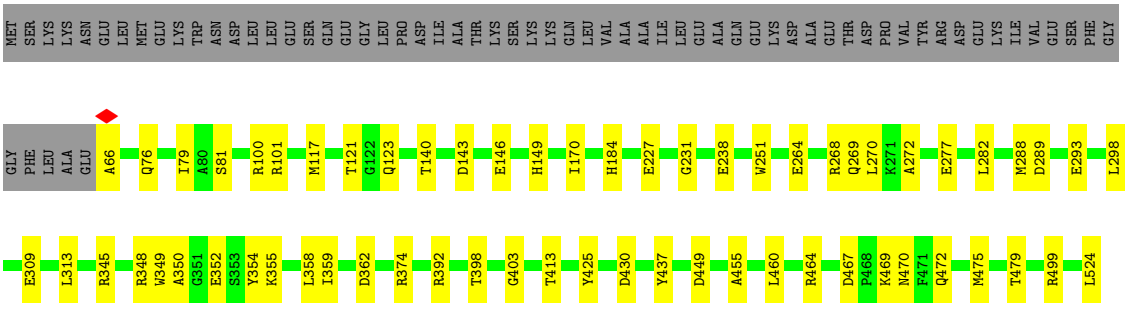




• Molecule 2: Major capsid protein

Chain K:

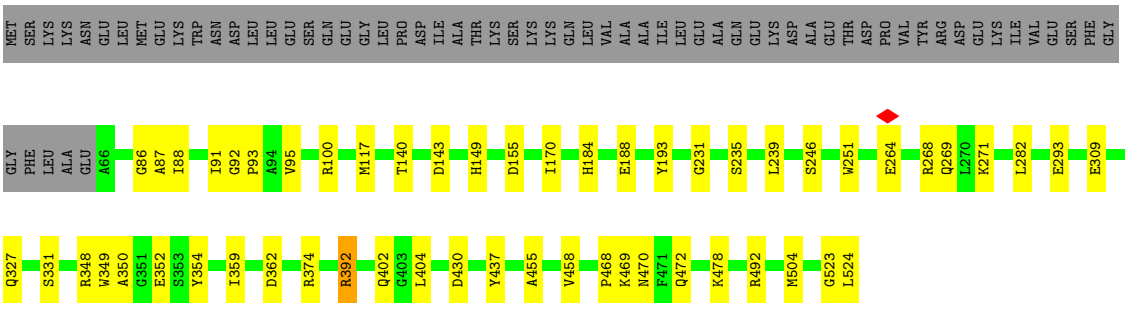




• Molecule 2: Major capsid protein

Chain L:

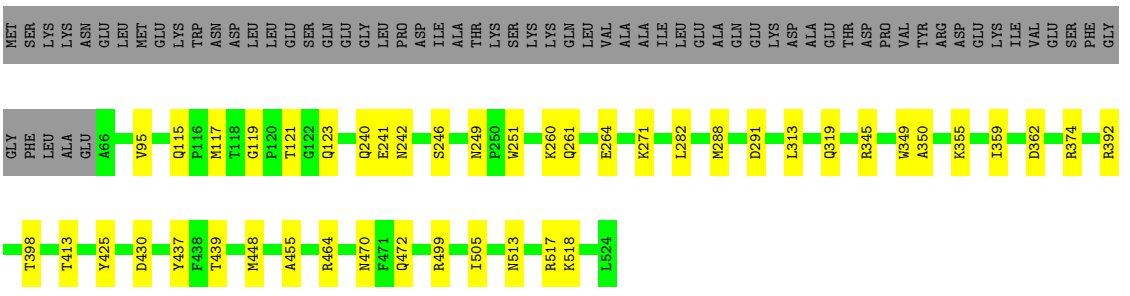




• Molecule 2: Major capsid protein

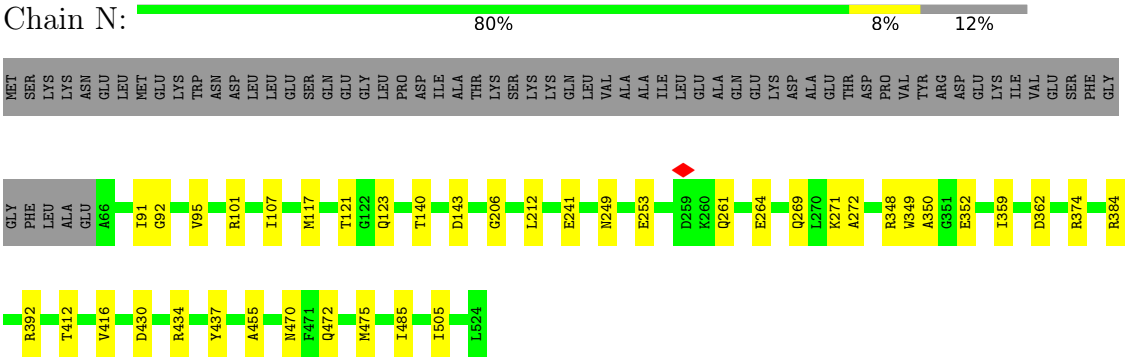
Chain M:





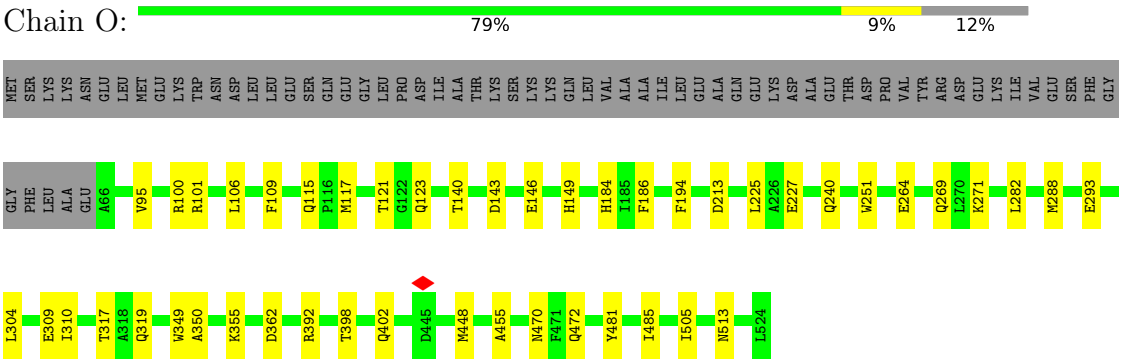
• Molecule 2: Major capsid protein

Chain N:



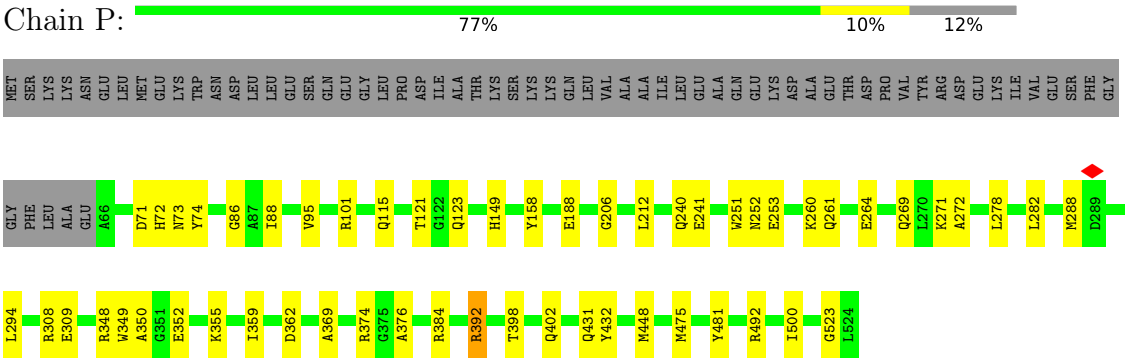
• Molecule 2: Major capsid protein

Chain O:



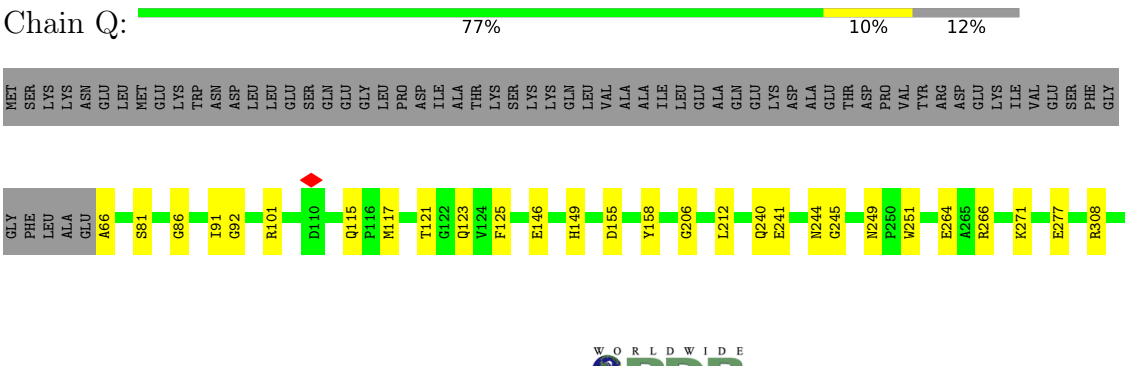
• Molecule 2: Major capsid protein

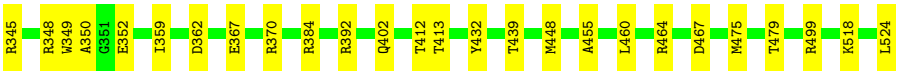
Chain P:



• Molecule 2: Major capsid protein

Chain Q:

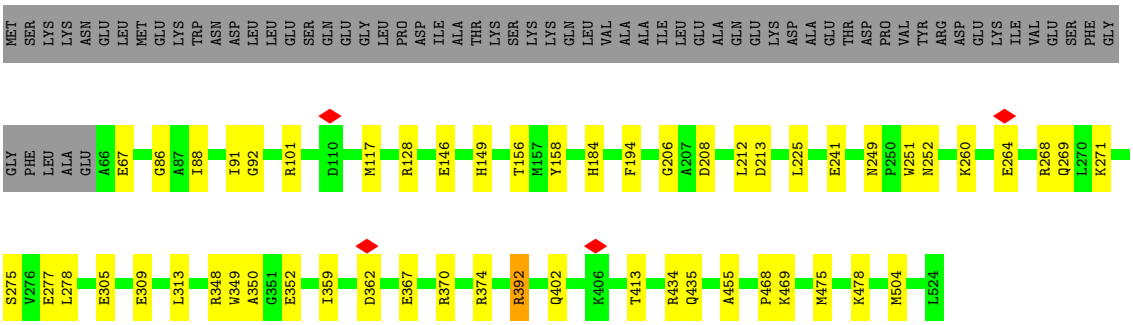




• Molecule 2: Major capsid protein

Chain R:

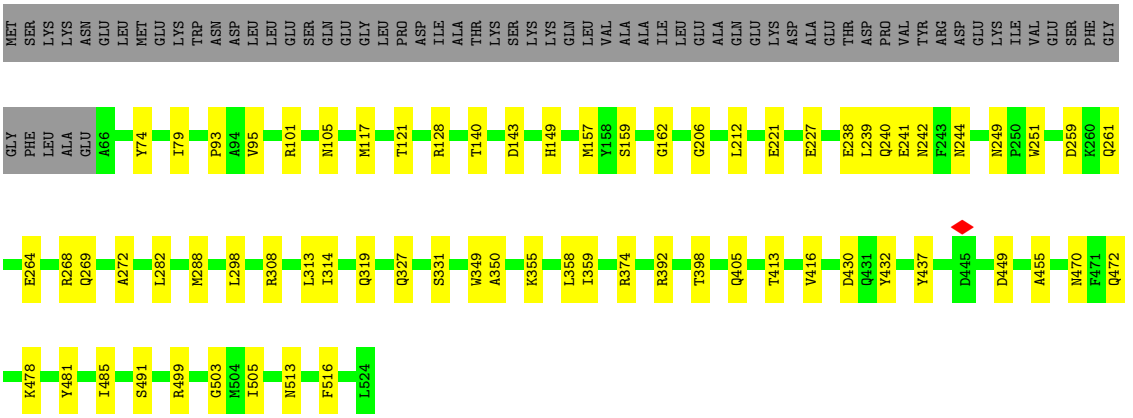




• Molecule 2: Major capsid protein

Chain S:

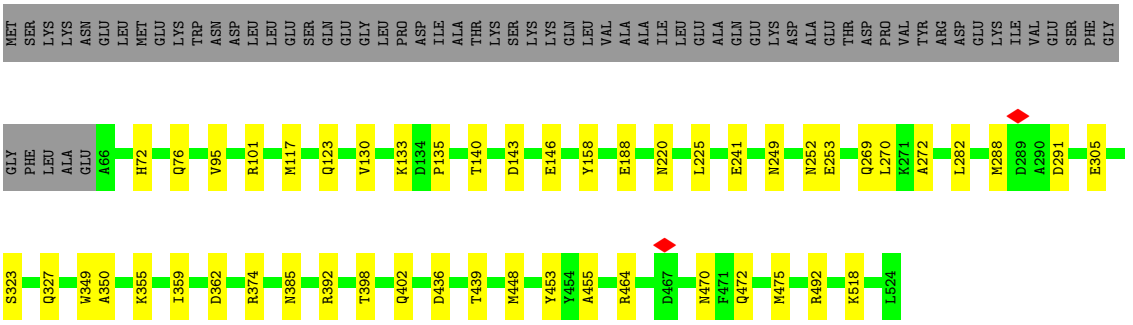




• Molecule 2: Major capsid protein

Chain T:

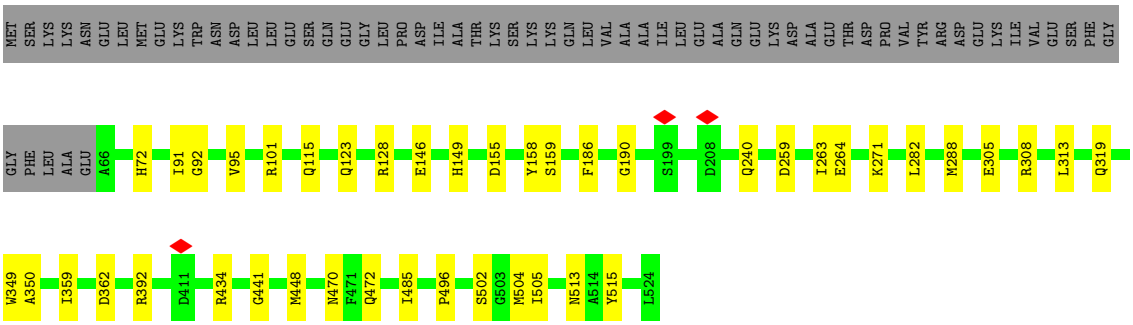




• Molecule 2: Major capsid protein

Chain U:

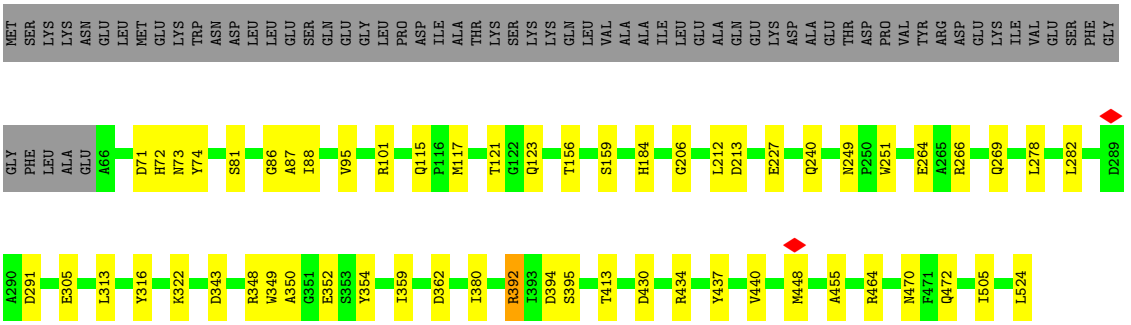




• Molecule 2: Major capsid protein

Chain V:

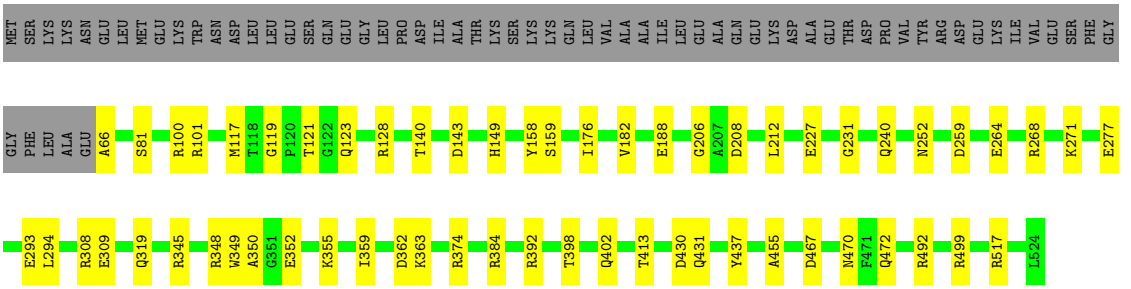




• Molecule 2: Major capsid protein

Chain W:

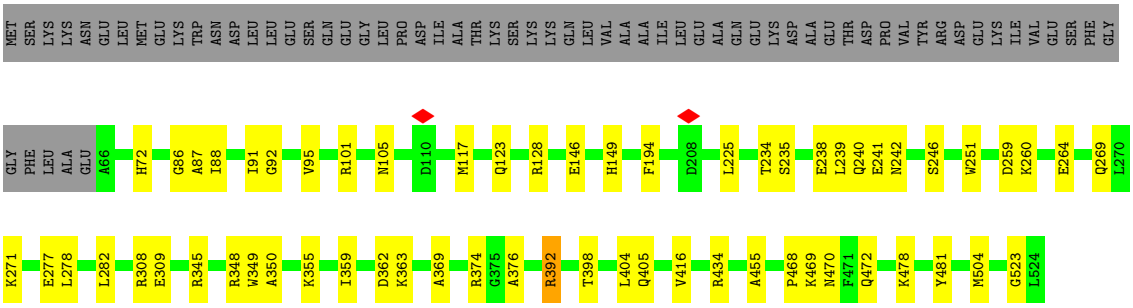




• Molecule 2: Major capsid protein

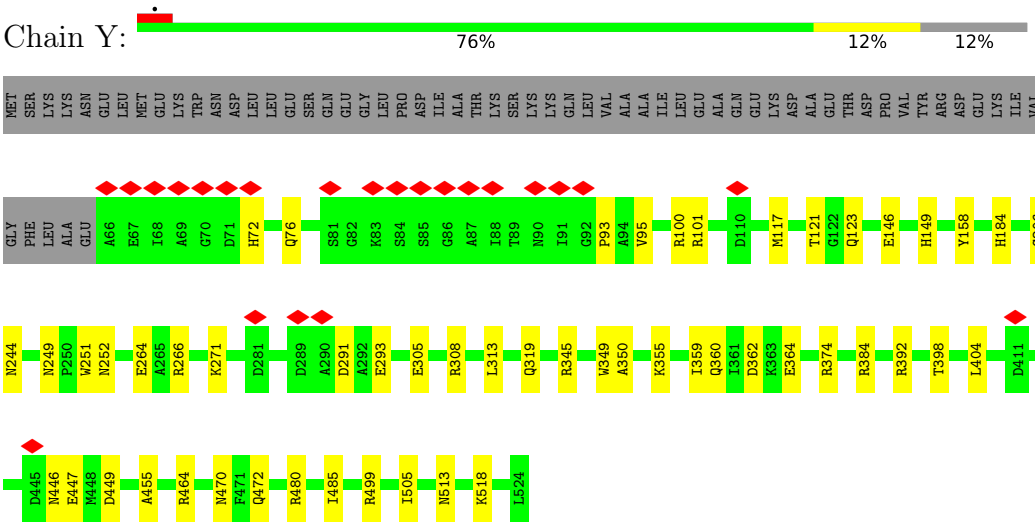
Chain X:





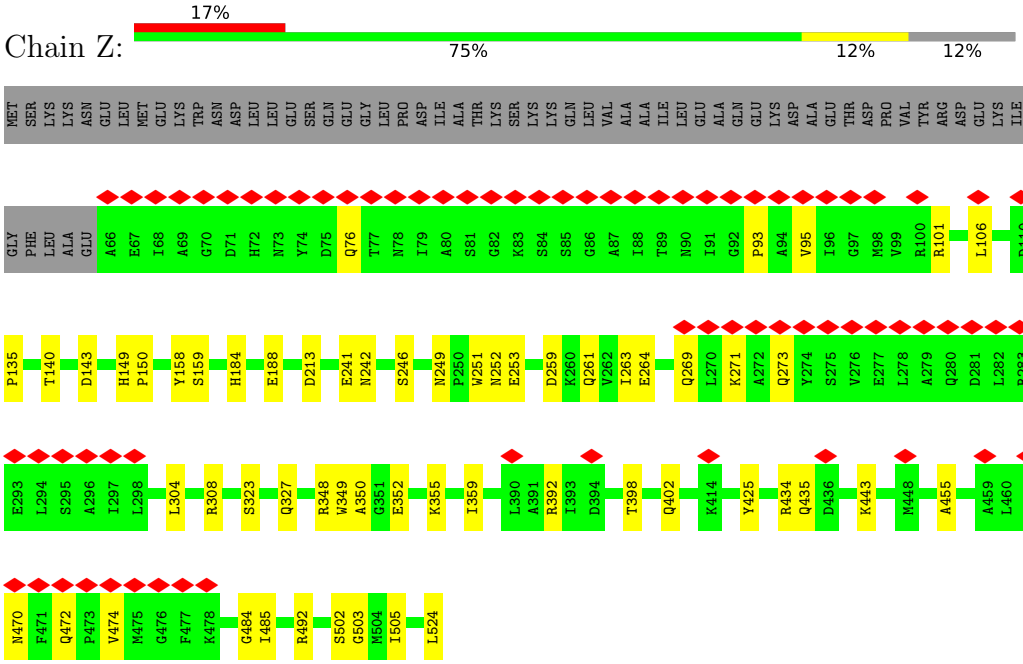
• Molecule 2: Major capsid protein

Chain Y:



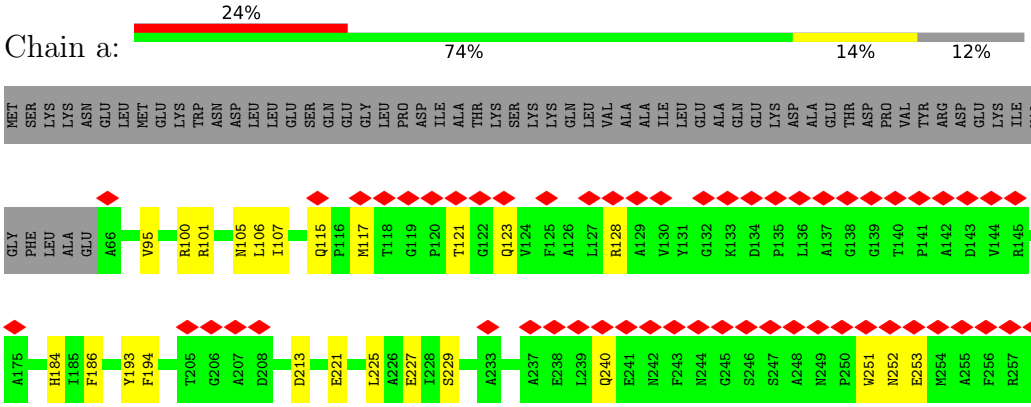
• Molecule 2: Major capsid protein

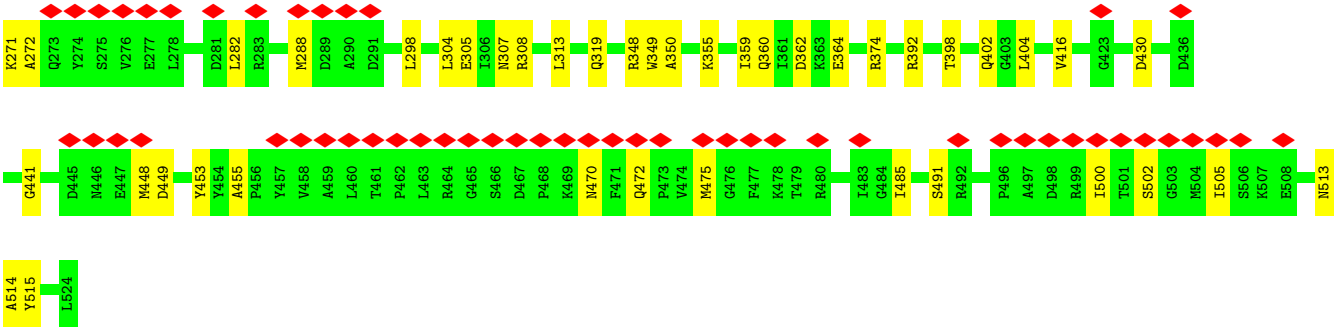
Chain Z:



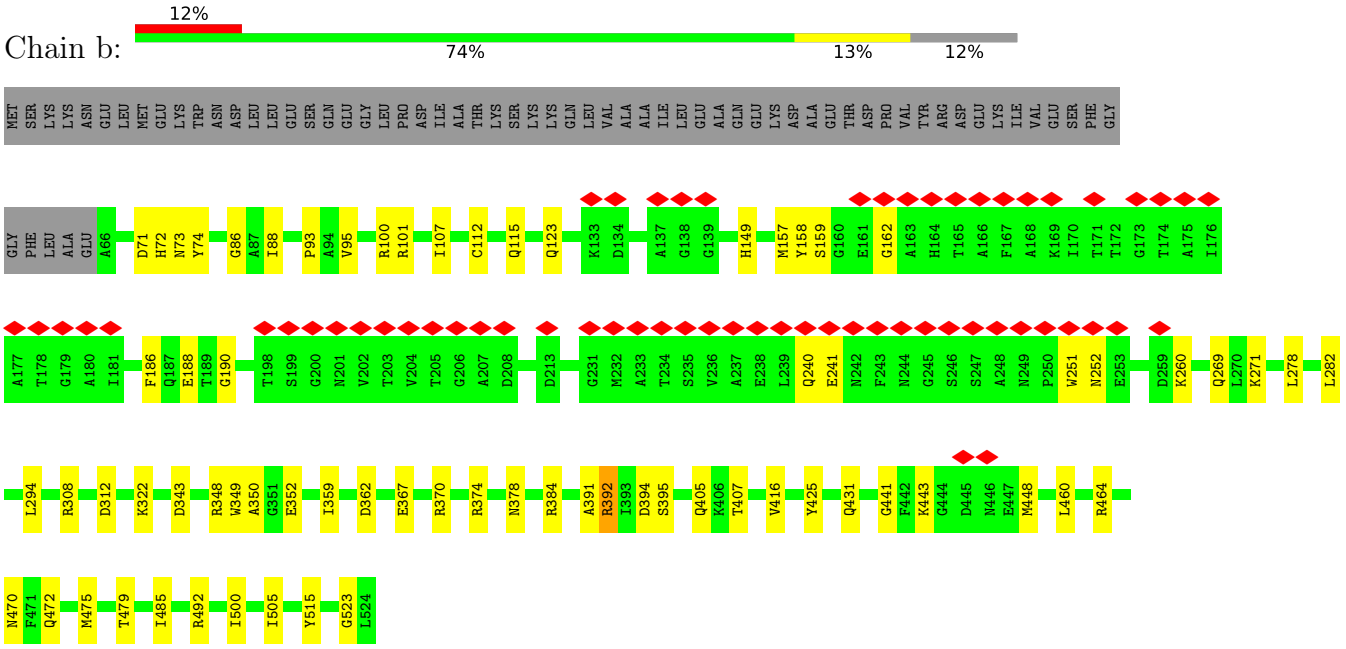
• Molecule 2: Major capsid protein

Chain a:

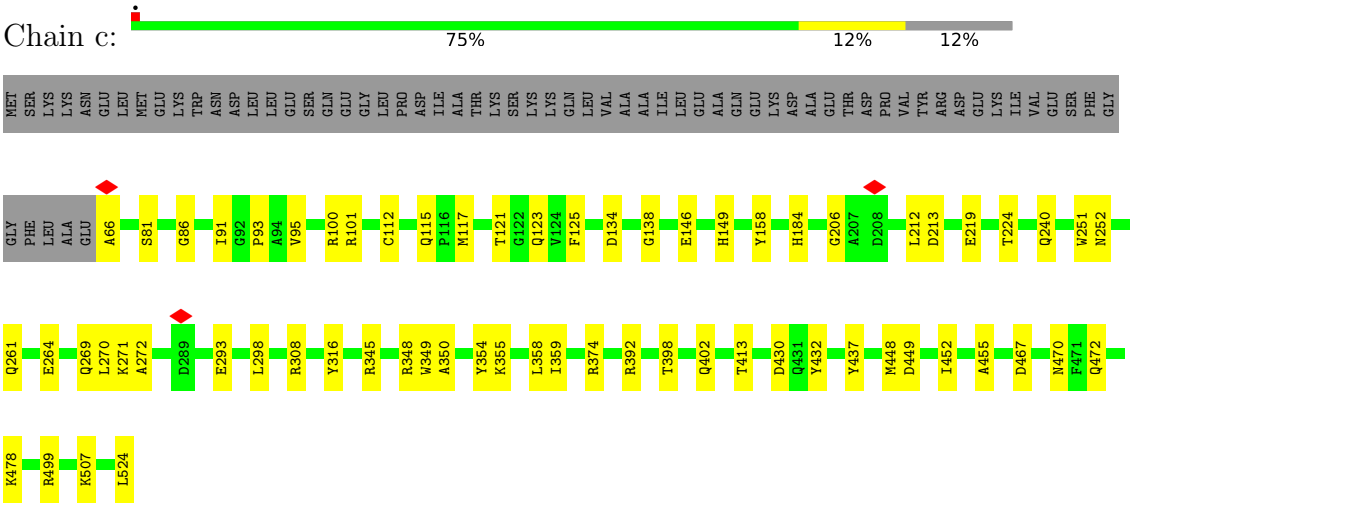




• Molecule 2: Major capsid protein

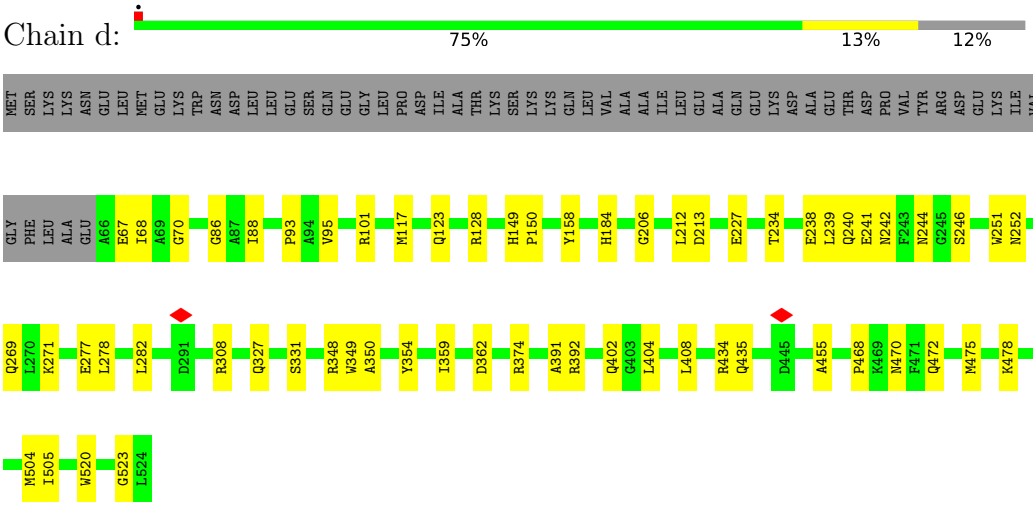


• Molecule 2: Major capsid protein



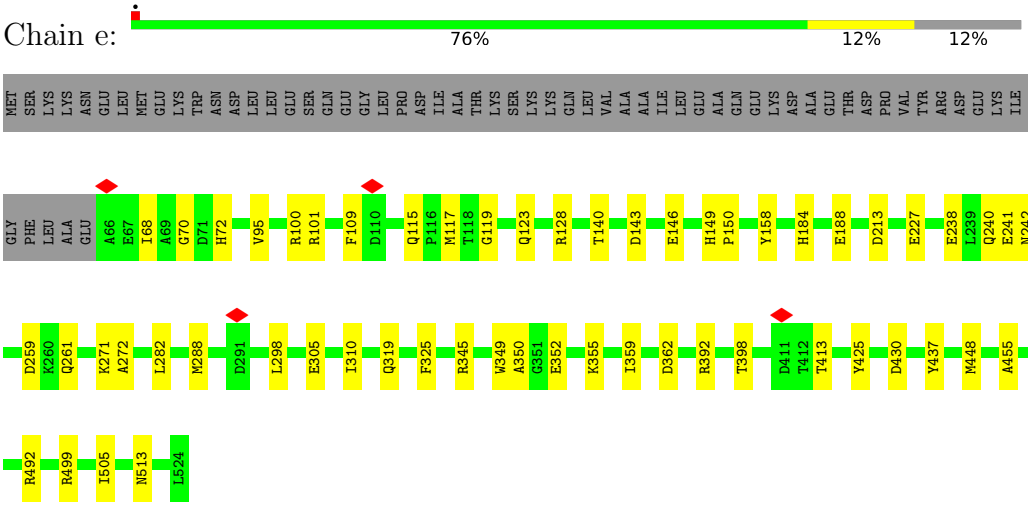
• Molecule 2: Major capsid protein

Chain d:



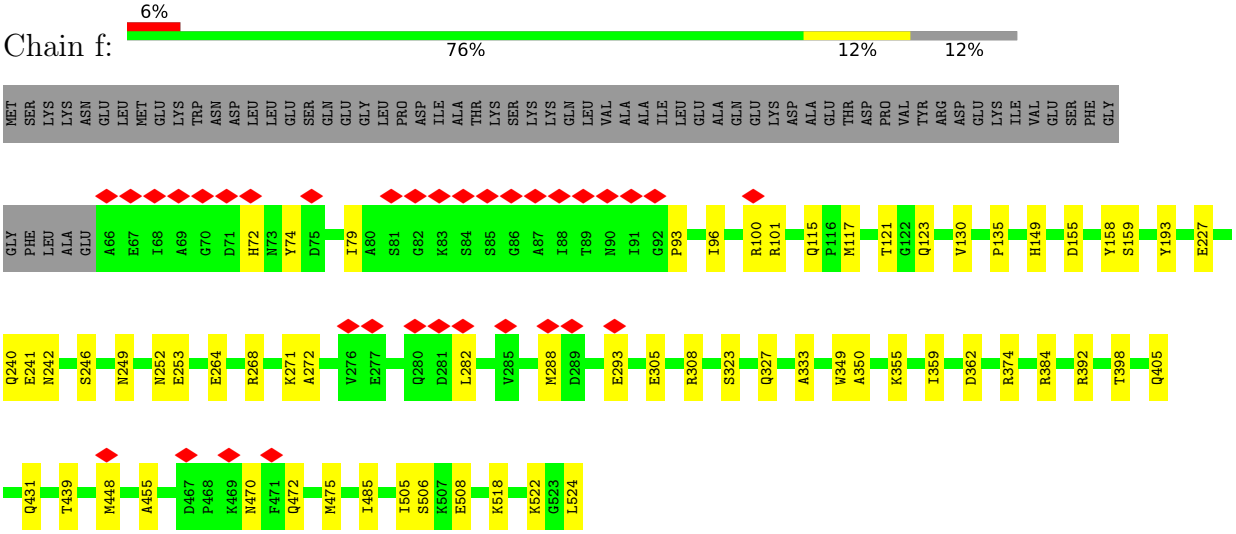
• Molecule 2: Major capsid protein

Chain e:



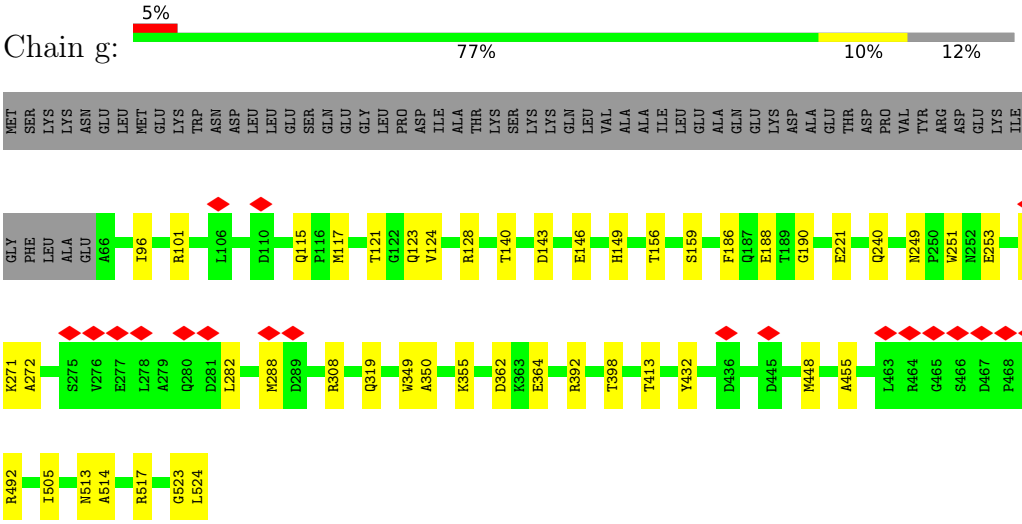
• Molecule 2: Major capsid protein

Chain f:



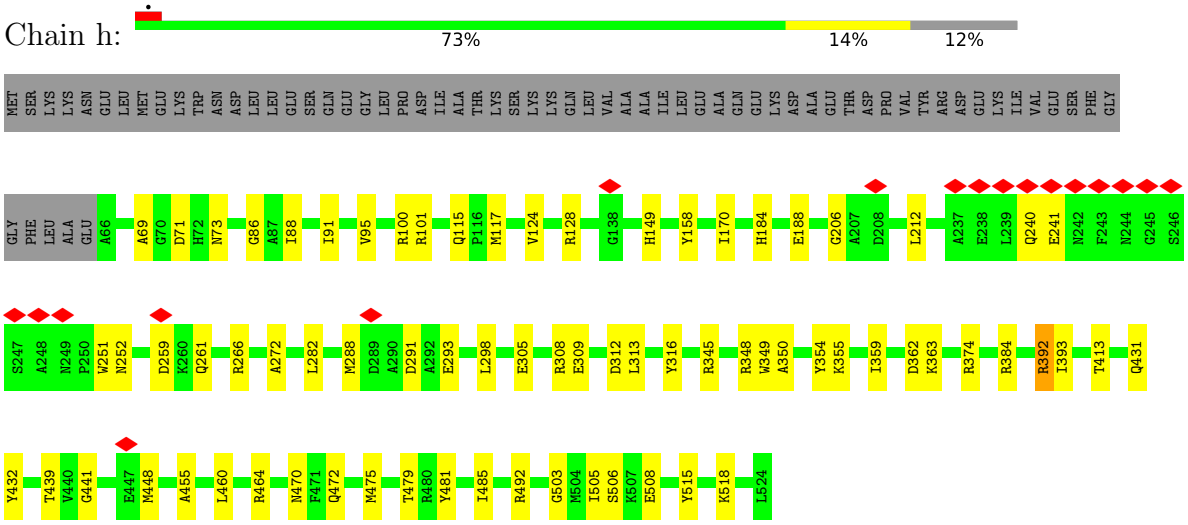
• Molecule 2: Major capsid protein

Chain g:



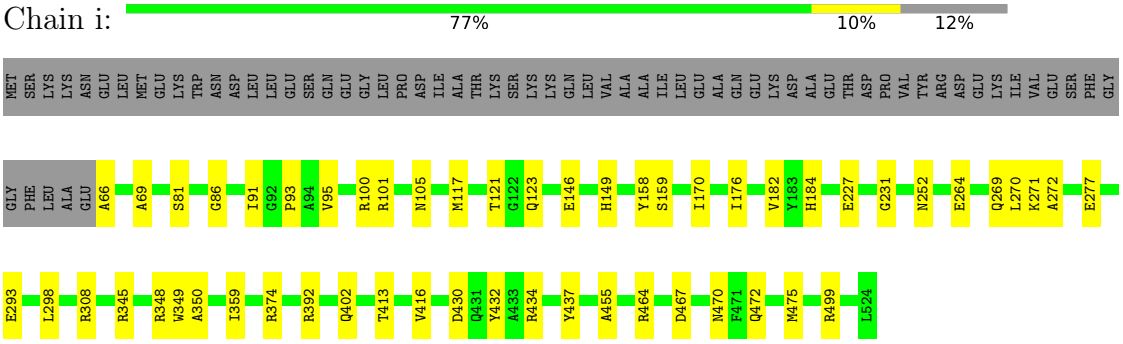
• Molecule 2: Major capsid protein

Chain h:



• Molecule 2: Major capsid protein

Chain i:



4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	641071	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/Å^2$)	40	Depositor
Minimum defocus (nm)	-700	Depositor
Maximum defocus (nm)	-2800	Depositor
Magnification	Not provided	
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	3.181	Depositor
Minimum map value	-1.855	Depositor
Average map value	0.004	Depositor
Map value standard deviation	0.146	Depositor
Recommended contour level	0.544	Depositor
Map size (Å)	500.4, 500.4, 500.4	wwPDB
Map dimensions	360, 360, 360	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.39, 1.39, 1.39	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	0.55	0/3121	0.55	0/4247
1	B	0.55	0/3121	0.58	0/4247
1	C	0.55	0/3121	0.54	0/4247
1	D	0.55	0/3121	0.57	0/4247
1	E	0.55	0/3121	0.56	0/4247
2	F	0.56	0/3518	0.59	0/4769
2	G	0.56	0/3518	0.58	0/4769
2	H	0.55	0/3518	0.58	0/4769
2	I	0.51	0/3518	0.54	0/4769
2	J	0.52	0/3518	0.54	0/4769
2	K	0.56	0/3518	0.56	0/4769
2	L	0.58	0/3518	0.58	0/4769
2	M	0.58	0/3518	0.58	0/4769
2	N	0.58	0/3518	0.58	0/4769
2	O	0.59	0/3518	0.59	0/4769
2	P	0.59	0/3518	0.61	0/4769
2	Q	0.57	0/3518	0.58	0/4769
2	R	0.57	0/3518	0.59	0/4769
2	S	0.53	0/3518	0.57	0/4769
2	T	0.48	0/3518	0.53	0/4769
2	U	0.52	0/3518	0.55	0/4769
2	V	0.56	0/3518	0.58	0/4769
2	W	0.57	0/3518	0.57	0/4769
2	X	0.54	0/3518	0.55	0/4769
2	Y	0.48	0/3518	0.51	0/4769
2	Z	0.38	0/3518	0.45	0/4769
2	a	0.33	0/3518	0.41	0/4769
2	b	0.43	0/3518	0.49	0/4769
2	c	0.50	0/3518	0.53	0/4769
2	d	0.55	0/3518	0.55	0/4769
2	e	0.52	0/3518	0.54	0/4769
2	f	0.45	0/3518	0.49	0/4769
2	g	0.38	0/3518	0.44	0/4769
2	h	0.42	0/3518	0.47	0/4769

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\#\|Z\| > 5$	RMSZ	$\#\|Z\| > 5$
2	i	0.51	0/3518	0.53	0/4769
All	All	0.52	0/121145	0.55	0/164305

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
2	F	0	1
2	J	0	1
2	L	0	1
2	P	0	1
2	R	0	1
2	U	0	1
2	V	0	1
2	X	0	1
2	Z	0	1
2	b	0	1
2	h	0	1
All	All	0	11

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (11) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	F	392	ARG	Sidechain
2	J	392	ARG	Sidechain
2	L	392	ARG	Sidechain
2	P	392	ARG	Sidechain
2	R	392	ARG	Sidechain
2	U	101	ARG	Sidechain
2	V	392	ARG	Sidechain
2	X	392	ARG	Sidechain
2	Z	308	ARG	Sidechain
2	b	392	ARG	Sidechain
2	h	392	ARG	Sidechain

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	3067	0	3010	49	0
1	B	3067	0	3010	42	0
1	C	3067	0	3010	51	0
1	D	3067	0	3010	48	0
1	E	3067	0	3010	46	0
2	F	3453	0	3402	54	0
2	G	3453	0	3402	57	0
2	H	3453	0	3402	61	0
2	I	3453	0	3402	52	0
2	J	3453	0	3402	66	0
2	K	3453	0	3402	57	0
2	L	3453	0	3402	50	0
2	M	3453	0	3402	52	0
2	N	3453	0	3402	37	0
2	O	3453	0	3402	41	0
2	P	3453	0	3402	56	0
2	Q	3453	0	3402	49	0
2	R	3453	0	3402	54	0
2	S	3453	0	3402	65	0
2	T	3453	0	3402	43	0
2	U	3453	0	3402	40	0
2	V	3453	0	3402	55	0
2	W	3453	0	3402	52	0
2	X	3453	0	3402	68	0
2	Y	3453	0	3402	58	0
2	Z	3453	0	3402	56	0
2	a	3453	0	3402	60	0
2	b	3453	0	3402	62	0
2	c	3453	0	3402	60	0
2	d	3453	0	3402	73	0
2	e	3453	0	3402	67	0
2	f	3453	0	3402	53	0
2	g	3453	0	3402	46	0
2	h	3453	0	3402	62	0
2	i	3453	0	3402	54	0
All	All	118925	0	117110	1351	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 6.

All (1351) 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:S:499:ARG:NH1	2:b:86:GLY:O	2.00	0.94
1:C:378:SER:OG	2:M:241:GLU:OE1	1.91	0.89
2:M:499:ARG:NH1	2:V:86:GLY:O	2.04	0.89
1:E:378:SER:OG	2:Y:241:GLU:OE1	1.93	0.87
2:J:86:GLY:O	2:e:499:ARG:NH1	2.08	0.85
2:g:392:ARG:HH21	2:h:362:ASP:HB2	1.42	0.83
2:a:392:ARG:HH21	2:b:362:ASP:HB2	1.44	0.83
2:K:499:ARG:NH1	2:d:86:GLY:O	2.12	0.83
1:C:354:GLY:O	1:C:394:ASN:ND2	2.12	0.82
1:E:99:ARG:NH1	1:E:123:ASP:O	2.12	0.82
2:X:86:GLY:O	2:i:499:ARG:NH1	2.10	0.82
2:N:392:ARG:HH21	2:O:362:ASP:HB2	1.46	0.81
1:A:354:GLY:O	1:A:394:ASN:ND2	2.12	0.81
2:f:392:ARG:HH21	2:g:362:ASP:HB2	1.45	0.81
1:B:244:ASN:H	1:C:431:TRP:C	1.88	0.81
2:T:269:GLN:NE2	2:U:240:GLN:OE1	2.14	0.81
2:f:121:THR:HG22	2:f:264:GLU:HG2	1.63	0.81
2:X:362:ASP:HB2	2:c:392:ARG:HH21	1.43	0.80
1:C:99:ARG:NH1	1:C:123:ASP:O	2.14	0.79
2:L:269:GLN:NE2	2:M:240:GLN:OE1	2.15	0.79
2:I:115:GLN:NE2	2:I:448:MET:SD	2.55	0.79
1:D:99:ARG:NH1	1:D:123:ASP:O	2.16	0.78
1:B:181:ARG:NH1	1:B:183:ASN:OD1	2.16	0.78
2:L:354:TYR:OH	2:M:345:ARG:NH1	2.17	0.78
1:D:162:ASP:OD1	1:E:187:ARG:NH1	2.16	0.78
1:A:93:SER:OG	1:B:189:ARG:NH1	2.16	0.78
2:G:499:ARG:NH1	2:P:86:GLY:O	2.17	0.77
2:T:72:HIS:ND1	2:U:264:GLU:OE2	2.15	0.77
2:h:158:TYR:O	2:h:252:ASN:ND2	2.16	0.77
2:d:251:TRP:HE3	2:i:271:LYS:HB2	1.50	0.77
2:F:362:ASP:HB2	2:K:392:ARG:HH21	1.50	0.77
1:B:410:ASP:OD2	1:B:413:ASN:ND2	2.18	0.76
1:D:181:ARG:NH1	1:D:183:ASN:OD1	2.18	0.76
1:E:354:GLY:O	1:E:394:ASN:ND2	2.17	0.76
1:A:377:ALA:C	2:e:241:GLU:HG3	2.10	0.76
1:D:377:ALA:C	2:S:241:GLU:HG3	2.11	0.75
2:T:392:ARG:HH21	2:U:362:ASP:HB2	1.50	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:99:ARG:NH1	1:A:123:ASP:O	2.20	0.75
2:d:362:ASP:HB2	2:i:392:ARG:HH21	1.53	0.74
2:O:402:GLN:HE22	2:P:359:ILE:HD11	1.53	0.73
2:F:269:GLN:NE2	2:G:240:GLN:OE1	2.22	0.73
2:U:392:ARG:HH12	2:V:359:ILE:HG23	1.54	0.73
2:Y:121:THR:HG22	2:Y:264:GLU:HG2	1.69	0.73
1:D:354:GLY:O	1:D:394:ASN:ND2	2.20	0.73
2:R:278:LEU:HD11	2:b:88:ILE:HD12	1.70	0.73
2:L:149:HIS:CD2	2:Q:101:ARG:HH12	2.06	0.73
2:h:101:ARG:NH1	2:i:146:GLU:OE2	2.22	0.73
2:J:115:GLN:NE2	2:J:448:MET:SD	2.61	0.73
2:S:121:THR:HG22	2:S:264:GLU:HG2	1.71	0.73
2:a:269:GLN:NE2	2:b:240:GLN:OE1	2.22	0.73
1:E:404:ARG:NH2	2:i:86:GLY:O	2.21	0.72
2:f:158:TYR:O	2:f:252:ASN:ND2	2.21	0.72
2:F:278:LEU:HD11	2:P:88:ILE:HD12	1.70	0.72
1:B:377:ALA:C	2:G:241:GLU:HG3	2.15	0.72
2:K:121:THR:HG22	2:K:264:GLU:HG2	1.70	0.72
2:e:158:TYR:O	2:e:252:ASN:ND2	2.22	0.72
2:Q:121:THR:HG22	2:Q:264:GLU:HG2	1.72	0.71
2:S:374:ARG:NH1	2:S:449:ASP:OD1	2.23	0.71
2:J:430:ASP:OD2	2:J:437:TYR:OH	2.07	0.71
2:h:354:TYR:OH	2:i:345:ARG:NH1	2.23	0.71
2:K:268:ARG:NH2	2:K:309:GLU:OE1	2.22	0.71
2:G:121:THR:HG22	2:G:264:GLU:HG2	1.71	0.71
2:e:117:MET:HG3	2:e:455:ALA:HB1	1.71	0.71
2:H:269:GLN:NE2	2:I:240:GLN:OE1	2.23	0.71
2:N:349:TRP:CD1	2:N:350:ALA:H	2.09	0.70
1:B:354:GLY:O	1:B:394:ASN:ND2	2.24	0.70
1:B:404:ARG:NH2	2:Q:86:GLY:O	2.24	0.70
2:M:95:VAL:HG22	2:N:123:GLN:HE21	1.55	0.70
2:X:469:LYS:HB3	2:d:241:GLU:HB3	1.73	0.70
2:Z:392:ARG:HH21	2:a:362:ASP:HB2	1.56	0.70
2:d:158:TYR:O	2:d:252:ASN:ND2	2.23	0.70
2:H:392:ARG:HH21	2:I:362:ASP:HB2	1.55	0.70
2:I:100:ARG:O	2:J:374:ARG:NH2	2.23	0.70
2:b:158:TYR:O	2:b:252:ASN:ND2	2.25	0.70
2:Y:470:ASN:O	2:Y:472:GLN:NE2	2.24	0.70
2:h:128:ARG:NH1	2:h:259:ASP:OD2	2.24	0.70
2:b:523:GLY:O	2:c:345:ARG:NH2	2.25	0.69
2:Z:121:THR:HG22	2:Z:264:GLU:HG2	1.73	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:e:72:HIS:ND1	2:f:264:GLU:OE2	2.26	0.69
2:a:117:MET:HG3	2:a:455:ALA:HB1	1.75	0.69
1:A:81:ASN:ND2	1:A:83:ASP:OD2	2.25	0.69
2:N:101:ARG:NH1	2:O:146:GLU:OE2	2.26	0.69
1:D:93:SER:OG	1:E:189:ARG:NH1	2.26	0.69
2:F:327:GLN:NE2	2:F:331:SER:O	2.23	0.69
2:L:430:ASP:OD2	2:L:437:TYR:OH	2.10	0.68
2:Y:499:ARG:NH1	2:h:86:GLY:O	2.17	0.68
2:Z:392:ARG:NH2	2:a:362:ASP:HB2	2.08	0.68
2:J:258:ILE:O	2:J:499:ARG:NH2	2.26	0.68
2:N:206:GLY:HA3	2:N:212:LEU:HA	1.76	0.68
1:C:95:ARG:O	1:C:165:LYS:NZ	2.27	0.68
2:N:269:GLN:NE2	2:O:240:GLN:OE1	2.27	0.68
1:D:378:SER:HB3	2:S:241:GLU:CB	2.24	0.67
2:R:206:GLY:HA3	2:R:212:LEU:HA	1.74	0.67
2:X:149:HIS:CD2	2:c:101:ARG:HH12	2.11	0.67
2:J:327:GLN:NE2	2:J:331:SER:O	2.26	0.67
2:M:349:TRP:CD1	2:M:350:ALA:H	2.12	0.67
2:T:95:VAL:HG22	2:U:123:GLN:HE21	1.59	0.67
2:Y:184:HIS:NE2	2:Y:213:ASP:OD1	2.20	0.67
2:i:158:TYR:O	2:i:252:ASN:ND2	2.27	0.67
1:A:378:SER:HB3	2:e:241:GLU:HB3	1.76	0.66
1:A:410:ASP:OD2	1:A:413:ASN:ND2	2.28	0.66
1:B:196:THR:OG1	2:G:238:GLU:OE1	2.08	0.66
2:a:158:TYR:O	2:a:252:ASN:ND2	2.26	0.66
2:V:240:GLN:NE2	2:V:249:ASN:OD1	2.26	0.66
2:Z:241:GLU:O	2:h:470:ASN:ND2	2.25	0.66
2:L:188:GLU:OE2	2:L:492:ARG:NH2	2.20	0.66
2:N:95:VAL:HG22	2:O:123:GLN:HE21	1.61	0.66
2:S:268:ARG:NH2	2:S:481:TYR:OH	2.24	0.66
2:H:121:THR:HG22	2:H:264:GLU:HG2	1.77	0.66
2:e:470:ASN:O	2:e:472:GLN:NE2	2.29	0.66
2:M:392:ARG:HH21	2:N:362:ASP:HB2	1.60	0.66
2:X:269:GLN:NE2	2:Y:240:GLN:OE1	2.28	0.66
2:H:239:LEU:O	2:H:249:ASN:ND2	2.29	0.66
2:L:362:ASP:HB2	2:Q:392:ARG:HH21	1.60	0.66
2:L:402:GLN:HE22	2:M:359:ILE:HD11	1.61	0.66
1:A:39:ASN:HD22	2:d:500:ILE:HD11	1.61	0.66
2:V:430:ASP:OD2	2:V:437:TYR:OH	2.08	0.66
2:W:384:ARG:NH2	2:W:431:GLN:O	2.29	0.66
1:A:162:ASP:OD1	1:B:187:ARG:NH1	2.29	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:S:392:ARG:HH12	2:T:359:ILE:HG23	1.60	0.66
2:i:121:THR:HG22	2:i:264:GLU:HG2	1.78	0.66
2:f:72:HIS:ND1	2:g:264:GLU:OE2	2.28	0.65
2:P:158:TYR:O	2:P:252:ASN:ND2	2.28	0.65
2:g:128:ARG:NH1	2:g:259:ASP:OD2	2.30	0.65
2:G:392:ARG:NH2	2:H:359:ILE:HA	2.12	0.65
2:N:485:ILE:HD11	2:N:505:ILE:HG12	1.79	0.65
2:a:100:ARG:O	2:b:374:ARG:NH2	2.30	0.65
2:a:355:LYS:NZ	2:a:398:THR:O	2.30	0.65
1:D:378:SER:HB3	2:S:241:GLU:HB3	1.79	0.65
2:I:392:ARG:HH21	2:J:362:ASP:HB2	1.62	0.65
2:I:271:LYS:NZ	2:J:241:GLU:OE2	2.22	0.65
2:a:282:LEU:HD21	2:a:288:MET:HB2	1.79	0.65
2:P:95:VAL:HG22	2:Q:123:GLN:HE21	1.61	0.65
2:U:434:ARG:HH12	2:V:227:GLU:CD	2.05	0.65
2:W:430:ASP:OD2	2:W:437:TYR:OH	2.12	0.65
2:V:524:LEU:OXT	2:W:363:LYS:NZ	2.29	0.64
2:F:238:GLU:HG2	2:d:277:GLU:HG3	1.79	0.64
2:f:470:ASN:HB3	2:f:472:GLN:HG2	1.79	0.64
2:F:362:ASP:HB2	2:K:392:ARG:NH2	2.12	0.64
2:O:269:GLN:NE2	2:P:240:GLN:OE1	2.31	0.64
2:Z:485:ILE:HD11	2:Z:505:ILE:HG12	1.80	0.64
2:b:349:TRP:CD1	2:b:350:ALA:H	2.16	0.64
2:X:468:PRO:HG3	2:i:467:ASP:HA	1.80	0.64
2:d:149:HIS:CD2	2:i:101:ARG:HH12	2.15	0.64
2:M:260:LYS:NZ	2:V:81:SER:O	2.30	0.64
2:V:354:TYR:OH	2:W:345:ARG:NH1	2.31	0.64
2:b:95:VAL:HG22	2:c:123:GLN:HE21	1.62	0.64
2:g:115:GLN:NE2	2:g:448:MET:SD	2.71	0.64
2:h:95:VAL:HG22	2:i:123:GLN:HE21	1.62	0.64
2:a:349:TRP:CD1	2:a:350:ALA:H	2.16	0.64
1:B:378:SER:HB2	2:G:241:GLU:HB3	1.80	0.63
2:K:374:ARG:NH1	2:K:449:ASP:OD1	2.32	0.63
2:P:115:GLN:NE2	2:P:448:MET:SD	2.71	0.63
2:c:121:THR:HG22	2:c:264:GLU:HG2	1.80	0.63
2:g:355:LYS:NZ	2:g:398:THR:O	2.31	0.63
2:g:523:GLY:O	2:h:345:ARG:NH2	2.30	0.63
2:H:470:ASN:HB3	2:H:472:GLN:HG2	1.80	0.63
2:O:349:TRP:CD1	2:O:350:ALA:H	2.16	0.63
2:g:269:GLN:NE2	2:h:240:GLN:OE1	2.30	0.63
2:J:101:ARG:NH1	2:K:146:GLU:OE2	2.31	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:R:277:GLU:OE2	2:c:478:LYS:NZ	2.24	0.63
2:X:470:ASN:HB3	2:X:472:GLN:HG2	1.81	0.63
2:d:392:ARG:NH2	2:e:359:ILE:HA	2.14	0.63
2:V:121:THR:HG22	2:V:264:GLU:HG2	1.80	0.63
2:d:392:ARG:HH12	2:e:359:ILE:HG23	1.63	0.63
1:D:181:ARG:NH2	2:c:81:SER:O	2.32	0.63
2:c:349:TRP:CD1	2:c:350:ALA:H	2.16	0.63
2:e:68:ILE:HG22	2:e:70:GLY:H	1.64	0.63
2:H:72:HIS:ND1	2:I:264:GLU:OE2	2.31	0.63
2:H:95:VAL:HG22	2:I:123:GLN:HE21	1.64	0.63
2:M:355:LYS:NZ	2:M:398:THR:O	2.31	0.63
2:P:282:LEU:HD21	2:P:288:MET:HB2	1.80	0.63
2:L:117:MET:HG3	2:L:455:ALA:HB1	1.79	0.63
2:b:157:MET:HB3	2:b:162:GLY:HA3	1.81	0.62
2:c:430:ASP:OD2	2:c:437:TYR:OH	2.09	0.62
2:G:244:ASN:HD21	2:K:66:ALA:N	1.96	0.62
2:T:470:ASN:HB3	2:T:472:GLN:HG2	1.80	0.62
2:g:392:ARG:NH2	2:h:362:ASP:HB2	2.14	0.62
1:C:162:ASP:OD1	1:D:187:ARG:NH1	2.32	0.62
2:Q:206:GLY:HA3	2:Q:212:LEU:HA	1.81	0.62
2:R:268:ARG:NH2	2:R:309:GLU:OE2	2.32	0.62
2:V:95:VAL:HG22	2:W:123:GLN:HE21	1.64	0.62
1:B:331:ASP:OD2	1:B:338:TYR:OH	2.15	0.62
2:d:269:GLN:NE2	2:e:240:GLN:OE1	2.33	0.62
1:B:99:ARG:NH1	1:B:123:ASP:O	2.31	0.62
2:T:188:GLU:OE2	2:T:492:ARG:NH2	2.24	0.62
2:I:434:ARG:HH12	2:J:227:GLU:CD	2.08	0.62
2:X:348:ARG:HH12	2:c:348:ARG:CZ	2.13	0.62
2:R:392:ARG:CZ	2:S:359:ILE:HA	2.28	0.62
2:G:95:VAL:HG22	2:H:123:GLN:HE21	1.65	0.62
2:U:271:LYS:HB2	2:V:251:TRP:CE3	2.34	0.62
2:U:319:GLN:HG3	2:U:513:ASN:O	1.99	0.62
2:F:468:PRO:HG3	2:Q:467:ASP:HA	1.82	0.61
2:R:392:ARG:NH2	2:S:358:LEU:O	2.33	0.61
2:S:485:ILE:HD11	2:S:505:ILE:HG12	1.82	0.61
2:U:186:PHE:N	2:U:190:GLY:O	2.28	0.61
2:f:101:ARG:HH12	2:g:149:HIS:CD2	2.18	0.61
2:f:485:ILE:HD11	2:f:505:ILE:HG12	1.82	0.61
1:E:39:ASN:OD1	2:X:260:LYS:NZ	2.26	0.61
2:J:367:GLU:OE2	2:J:370:ARG:NH2	2.29	0.61
1:A:181:ARG:NH2	2:K:81:SER:O	2.34	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:W:188:GLU:OE2	2:W:492:ARG:NH2	2.30	0.61
1:C:280:GLU:OE2	1:C:422:GLN:NE2	2.33	0.61
2:G:392:ARG:HH12	2:H:359:ILE:HG23	1.66	0.61
2:J:278:LEU:HD11	2:d:88:ILE:HD12	1.82	0.61
2:K:355:LYS:NZ	2:K:398:THR:O	2.33	0.61
2:R:392:ARG:NH1	2:S:359:ILE:HA	2.15	0.61
2:X:349:TRP:CD1	2:X:350:ALA:H	2.19	0.61
2:a:374:ARG:NH1	2:a:449:ASP:OD1	2.34	0.61
2:R:469:LYS:HB3	2:X:241:GLU:HG2	1.83	0.61
2:U:392:ARG:NH2	2:V:362:ASP:HB2	2.15	0.61
2:M:392:ARG:NH1	2:N:359:ILE:HG23	2.15	0.61
2:Z:112:CYS:O	2:Z:443:LYS:NZ	2.30	0.61
2:O:115:GLN:NE2	2:O:448:MET:SD	2.73	0.61
2:P:384:ARG:NH2	2:P:431:GLN:O	2.33	0.61
2:Z:106:LEU:HD21	2:Z:304:LEU:HD23	1.82	0.61
2:L:264:GLU:CD	2:L:504:MET:HG3	2.25	0.61
2:I:355:LYS:NZ	2:I:398:THR:O	2.34	0.61
2:W:348:ARG:NH2	2:W:352:GLU:OE2	2.26	0.61
2:Y:72:HIS:ND1	2:Z:264:GLU:OE2	2.33	0.61
2:M:392:ARG:NH2	2:N:362:ASP:HB2	2.16	0.60
1:C:175:THR:HG21	1:D:221:VAL:HG11	1.82	0.60
2:F:72:HIS:ND1	2:G:264:GLU:OE2	2.34	0.60
2:F:83:LYS:HE3	2:Q:499:ARG:HD2	1.82	0.60
2:H:101:ARG:HH12	2:I:149:HIS:CD2	2.18	0.60
2:X:117:MET:HG3	2:X:455:ALA:HB1	1.83	0.60
2:G:101:ARG:HH12	2:H:149:HIS:CD2	2.19	0.60
2:J:392:ARG:NH1	2:K:359:ILE:HA	2.15	0.60
2:T:241:GLU:N	2:T:249:ASN:O	2.35	0.60
2:b:107:ILE:HG12	2:b:416:VAL:HG11	1.82	0.60
2:L:404:LEU:HD21	2:M:425:TYR:HE1	1.67	0.60
2:d:240:GLN:HB2	2:d:251:TRP:HE1	1.66	0.60
2:G:392:ARG:CZ	2:H:359:ILE:HA	2.32	0.60
2:J:88:ILE:HD12	2:d:278:LEU:HD11	1.82	0.60
2:N:121:THR:HG22	2:N:264:GLU:HG2	1.83	0.60
2:g:240:GLN:NE2	2:g:249:ASN:OD1	2.31	0.60
2:K:464:ARG:NH1	2:K:475:MET:SD	2.75	0.60
2:N:349:TRP:CD1	2:N:350:ALA:N	2.70	0.60
2:O:470:ASN:HB3	2:O:472:GLN:HG2	1.83	0.60
2:Y:485:ILE:HD11	2:Y:505:ILE:HG12	1.84	0.60
2:G:117:MET:HG3	2:G:455:ALA:HB1	1.84	0.60
2:U:392:ARG:NH2	2:V:359:ILE:HA	2.16	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:J:95:VAL:HG22	2:K:123:GLN:HE21	1.66	0.60
2:L:170:ILE:HD12	2:L:184:HIS:HB2	1.84	0.60
2:U:128:ARG:NH1	2:U:259:ASP:OD2	2.34	0.60
2:Z:435:GLN:NE2	2:a:221:GLU:OE2	2.20	0.60
2:I:309:GLU:OE1	2:I:481:TYR:OH	2.15	0.60
2:M:319:GLN:HG3	2:M:513:ASN:O	2.01	0.60
1:D:39:ASN:OD1	2:R:260:LYS:NZ	2.34	0.59
2:T:133:LYS:NZ	2:T:253:GLU:OE2	2.33	0.59
2:X:95:VAL:HG22	2:Y:123:GLN:HE21	1.67	0.59
2:H:128:ARG:NH1	2:H:259:ASP:OD2	2.34	0.59
2:U:485:ILE:HD11	2:U:505:ILE:HG12	1.85	0.59
2:a:106:LEU:HD21	2:a:304:LEU:HD23	1.84	0.59
2:X:235:SER:N	2:b:71:ASP:OD1	2.35	0.59
2:N:470:ASN:HB3	2:N:472:GLN:HG2	1.83	0.59
2:W:206:GLY:HA3	2:W:212:LEU:HA	1.83	0.59
2:d:251:TRP:CE3	2:i:271:LYS:HB2	2.36	0.59
2:g:349:TRP:HB2	2:h:348:ARG:HH12	1.67	0.59
2:X:105:ASN:HB2	2:X:416:VAL:HG23	1.85	0.59
2:g:319:GLN:HG3	2:g:513:ASN:O	2.01	0.59
2:I:392:ARG:NH2	2:J:362:ASP:HB2	2.18	0.59
2:T:392:ARG:NH2	2:U:362:ASP:HB2	2.17	0.59
2:X:88:ILE:HD11	2:h:282:LEU:HD12	1.84	0.59
2:b:101:ARG:NH1	2:c:146:GLU:OE2	2.35	0.59
2:e:101:ARG:HH12	2:f:149:HIS:CD2	2.19	0.59
2:G:349:TRP:CD1	2:G:350:ALA:H	2.21	0.59
2:I:349:TRP:CD1	2:I:350:ALA:H	2.21	0.59
2:U:392:ARG:NH1	2:V:359:ILE:HG23	2.17	0.59
1:B:39:ASN:OD1	2:F:260:LYS:NZ	2.36	0.59
2:R:88:ILE:HD11	2:b:282:LEU:HD12	1.85	0.59
2:d:392:ARG:HH22	2:e:359:ILE:HA	1.67	0.59
2:F:74:TYR:HA	2:F:79:ILE:HD11	1.84	0.58
2:a:95:VAL:HG22	2:b:123:GLN:HE21	1.67	0.58
2:a:268:ARG:NH1	2:a:305:GLU:OE1	2.36	0.58
1:C:410:ASP:OD2	1:C:413:ASN:ND2	2.31	0.58
2:a:470:ASN:HB3	2:a:472:GLN:HG2	1.86	0.58
2:b:470:ASN:HB3	2:b:472:GLN:HG2	1.84	0.58
1:B:244:ASN:N	1:C:431:TRP:O	2.36	0.58
2:U:95:VAL:HG22	2:V:123:GLN:HE21	1.68	0.58
2:d:117:MET:HG3	2:d:455:ALA:HB1	1.85	0.58
2:g:101:ARG:HH12	2:h:149:HIS:CD2	2.20	0.58
2:X:355:LYS:NZ	2:X:398:THR:O	2.37	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:R:277:GLU:N	2:R:277:GLU:OE1	2.34	0.58
2:U:470:ASN:HB3	2:U:472:GLN:HG2	1.84	0.58
2:d:206:GLY:HA3	2:d:212:LEU:HA	1.85	0.58
2:e:319:GLN:HG3	2:e:513:ASN:O	2.03	0.58
2:h:316:TYR:HD2	2:i:227:GLU:O	1.86	0.58
2:V:392:ARG:HH12	2:W:359:ILE:HG23	1.68	0.58
1:C:181:ARG:NH1	1:C:183:ASN:OD1	2.36	0.58
2:F:392:ARG:CZ	2:G:359:ILE:HA	2.34	0.58
2:H:349:TRP:CD1	2:H:350:ALA:N	2.72	0.58
2:e:349:TRP:CD1	2:e:350:ALA:H	2.22	0.58
2:i:349:TRP:CD1	2:i:350:ALA:H	2.21	0.58
2:K:430:ASP:OD2	2:K:437:TYR:OH	2.13	0.58
2:O:101:ARG:HH12	2:P:149:HIS:CD2	2.21	0.58
2:h:115:GLN:NE2	2:h:448:MET:SD	2.77	0.58
1:D:67:LEU:HD12	1:E:43:GLU:HB2	1.85	0.58
2:F:345:ARG:NH1	2:K:354:TYR:OH	2.36	0.58
2:R:359:ILE:HD11	2:W:402:GLN:HE22	1.68	0.58
2:S:95:VAL:HG22	2:T:123:GLN:HE21	1.68	0.58
2:h:384:ARG:NH2	2:h:431:GLN:O	2.36	0.58
1:D:410:ASP:OD2	1:D:413:ASN:ND2	2.30	0.57
2:I:121:THR:HG22	2:I:264:GLU:HG2	1.86	0.57
2:Q:349:TRP:CD1	2:Q:350:ALA:H	2.22	0.57
2:S:349:TRP:CD1	2:S:350:ALA:H	2.22	0.57
2:b:392:ARG:CZ	2:c:359:ILE:HA	2.34	0.57
2:a:101:ARG:HH12	2:b:149:HIS:CD2	2.22	0.57
1:D:244:ASN:HB2	1:E:431:TRP:C	2.29	0.57
2:I:271:LYS:HB2	2:J:251:TRP:CE3	2.39	0.57
2:J:93:PRO:HG2	2:K:123:GLN:OE1	2.04	0.57
2:T:101:ARG:HH12	2:U:149:HIS:CD2	2.22	0.57
2:W:100:ARG:HH22	2:W:293:GLU:CD	2.11	0.57
2:e:392:ARG:NH1	2:f:359:ILE:HA	2.20	0.57
2:f:101:ARG:NH1	2:g:146:GLU:OE2	2.37	0.57
2:g:349:TRP:CD1	2:g:350:ALA:H	2.22	0.57
2:N:430:ASP:OD2	2:N:437:TYR:OH	2.20	0.57
2:T:349:TRP:CD1	2:T:350:ALA:H	2.23	0.57
2:Y:355:LYS:NZ	2:Y:398:THR:O	2.38	0.57
2:d:93:PRO:HG2	2:e:123:GLN:OE1	2.04	0.57
2:O:319:GLN:HG3	2:O:513:ASN:O	2.04	0.57
2:S:261:GLN:HE21	2:S:503:GLY:HA2	1.68	0.57
2:e:95:VAL:HG22	2:f:123:GLN:HE21	1.69	0.57
2:e:305:GLU:OE1	2:f:159:SER:OG	2.20	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:75:VAL:O	1:E:396:TYR:OH	2.22	0.57
2:H:109:PHE:HE1	2:H:310:ILE:HD12	1.68	0.57
2:J:71:ASP:HB3	2:J:73:ASN:H	1.69	0.57
2:O:95:VAL:HG22	2:P:123:GLN:HE21	1.70	0.57
2:R:367:GLU:OE2	2:R:370:ARG:NH2	2.31	0.57
2:b:71:ASP:HB3	2:b:73:ASN:H	1.70	0.57
2:P:72:HIS:ND1	2:Q:264:GLU:OE1	2.34	0.57
2:c:349:TRP:CD1	2:c:350:ALA:N	2.73	0.57
2:i:100:ARG:HH22	2:i:293:GLU:CD	2.13	0.57
1:C:182:TRP:CH2	1:C:406:ILE:HD13	2.40	0.56
2:L:88:ILE:HD12	2:V:278:LEU:HD11	1.87	0.56
2:R:392:ARG:NH2	2:S:359:ILE:HA	2.20	0.56
2:W:117:MET:HG3	2:W:455:ALA:HB1	1.86	0.56
2:Y:392:ARG:CZ	2:Z:359:ILE:HA	2.35	0.56
2:F:242:ASN:ND2	2:F:242:ASN:O	2.38	0.56
2:F:523:GLY:O	2:G:345:ARG:NH2	2.38	0.56
2:I:269:GLN:NE2	2:J:240:GLN:OE1	2.39	0.56
2:O:271:LYS:NZ	2:P:241:GLU:OE2	2.21	0.56
2:S:430:ASP:OD2	2:S:437:TYR:OH	2.18	0.56
2:d:184:HIS:NE2	2:d:213:ASP:OD1	2.26	0.56
2:e:184:HIS:NE2	2:e:213:ASP:OD1	2.30	0.56
2:e:485:ILE:HD11	2:e:505:ILE:HG12	1.85	0.56
2:f:130:VAL:HG21	2:f:135:PRO:HA	1.86	0.56
2:S:117:MET:HG3	2:S:455:ALA:HB1	1.88	0.56
2:V:71:ASP:HB3	2:V:73:ASN:H	1.70	0.56
2:W:140:THR:OG1	2:W:143:ASP:OD2	2.17	0.56
2:Z:188:GLU:OE2	2:Z:492:ARG:NH2	2.37	0.56
2:Y:244:ASN:HD21	2:c:66:ALA:N	2.02	0.56
1:A:288:ASP:OD1	1:A:289:ALA:N	2.39	0.56
1:D:231:ILE:HG21	1:D:331:ASP:OD2	2.05	0.56
2:I:349:TRP:HB2	2:J:348:ARG:HH12	1.71	0.56
2:K:349:TRP:CD1	2:K:350:ALA:H	2.24	0.56
2:L:392:ARG:NH1	2:M:359:ILE:HG23	2.20	0.56
2:P:349:TRP:CD1	2:P:350:ALA:H	2.23	0.56
2:e:282:LEU:HD21	2:e:288:MET:HB2	1.88	0.56
2:f:241:GLU:N	2:f:249:ASN:O	2.39	0.56
2:T:355:LYS:NZ	2:T:398:THR:O	2.39	0.56
2:W:128:ARG:NH1	2:W:259:ASP:OD2	2.39	0.56
2:W:349:TRP:CD1	2:W:350:ALA:N	2.74	0.56
2:M:470:ASN:HB3	2:M:472:GLN:HG2	1.88	0.56
2:d:470:ASN:HB3	2:d:472:GLN:HG2	1.87	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:g:524:LEU:OXT	2:h:363:LYS:NZ	2.30	0.56
2:F:354:TYR:OH	2:G:345:ARG:NH1	2.38	0.56
2:L:349:TRP:CD1	2:L:350:ALA:H	2.24	0.56
2:N:241:GLU:O	2:V:470:ASN:ND2	2.32	0.56
2:O:121:THR:HG22	2:O:264:GLU:HG2	1.87	0.56
2:R:468:PRO:HG3	2:c:467:ASP:HA	1.88	0.56
2:b:367:GLU:OE2	2:b:370:ARG:NH2	2.35	0.56
1:D:196:THR:OG1	2:S:238:GLU:OE1	2.15	0.56
2:R:158:TYR:O	2:R:252:ASN:ND2	2.31	0.56
2:W:349:TRP:CD1	2:W:350:ALA:H	2.24	0.56
2:a:392:ARG:NH2	2:b:362:ASP:HB2	2.18	0.56
2:L:95:VAL:HG22	2:M:123:GLN:HE21	1.71	0.56
1:E:331:ASP:OD2	1:E:338:TYR:OH	2.24	0.55
2:G:206:GLY:HA3	2:G:212:LEU:HA	1.88	0.55
2:I:101:ARG:HH12	2:J:149:HIS:CD2	2.23	0.55
2:d:523:GLY:O	2:e:345:ARG:NH2	2.39	0.55
2:f:349:TRP:CD1	2:f:350:ALA:H	2.23	0.55
2:I:392:ARG:HH12	2:J:359:ILE:HG23	1.72	0.55
2:I:470:ASN:HB3	2:I:472:GLN:HG2	1.88	0.55
2:N:117:MET:HG3	2:N:455:ALA:HB1	1.87	0.55
2:L:91:ILE:HG23	2:W:123:GLN:HE22	1.70	0.55
2:L:392:ARG:NH2	2:M:362:ASP:HB2	2.21	0.55
2:I:319:GLN:HG3	2:I:513:ASN:O	2.05	0.55
2:b:349:TRP:CD1	2:b:350:ALA:N	2.74	0.55
1:A:378:SER:HB3	2:e:241:GLU:CB	2.37	0.55
2:F:392:ARG:NH2	2:G:359:ILE:HA	2.22	0.55
2:Q:241:GLU:N	2:Q:249:ASN:O	2.37	0.55
2:R:91:ILE:HG12	2:c:125:PHE:HZ	1.72	0.55
2:V:392:ARG:NH2	2:W:362:ASP:HB2	2.22	0.55
2:Z:76:GLN:HB3	2:a:502:SER:HB2	1.88	0.55
2:a:115:GLN:NE2	2:a:448:MET:SD	2.79	0.55
2:g:188:GLU:OE2	2:g:492:ARG:NH2	2.35	0.55
1:E:406:ILE:HG22	1:E:408:GLY:H	1.72	0.55
2:V:269:GLN:NE2	2:W:240:GLN:OE1	2.40	0.55
2:X:251:TRP:HE3	2:c:271:LYS:HB2	1.71	0.55
2:X:278:LEU:HD11	2:h:88:ILE:HD12	1.88	0.55
2:J:101:ARG:HH12	2:K:149:HIS:CD2	2.25	0.55
2:L:271:LYS:HB2	2:M:251:TRP:CE3	2.41	0.55
2:P:355:LYS:NZ	2:P:398:THR:O	2.39	0.55
2:d:392:ARG:NH1	2:e:359:ILE:HA	2.21	0.55
2:g:272:ALA:HB3	2:g:475:MET:HB2	1.87	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:198:GLU:OE2	2:R:478:LYS:HE2	2.07	0.55
1:E:378:SER:OG	2:Y:241:GLU:HB3	2.07	0.55
2:J:271:LYS:HB2	2:K:251:TRP:CE3	2.42	0.55
2:W:158:TYR:O	2:W:252:ASN:ND2	2.33	0.55
2:e:430:ASP:OD2	2:e:437:TYR:OH	2.21	0.55
2:H:241:GLU:N	2:H:249:ASN:O	2.38	0.55
2:H:349:TRP:CD1	2:H:350:ALA:H	2.24	0.55
2:J:206:GLY:HA3	2:J:212:LEU:HA	1.89	0.55
2:L:392:ARG:HH12	2:M:359:ILE:HG23	1.71	0.55
2:N:241:GLU:H	2:N:249:ASN:HB3	1.72	0.55
2:g:485:ILE:HD11	2:g:505:ILE:HG12	1.89	0.55
1:C:181:ARG:NH2	2:W:81:SER:O	2.40	0.55
2:F:117:MET:HG3	2:F:455:ALA:HB1	1.88	0.55
2:L:100:ARG:O	2:M:374:ARG:NH2	2.40	0.55
2:d:354:TYR:OH	2:e:345:ARG:NH1	2.40	0.55
2:g:470:ASN:HB3	2:g:472:GLN:HG2	1.88	0.55
1:A:361:TYR:CE2	1:A:363:GLU:HB2	2.42	0.54
2:J:354:TYR:OH	2:K:345:ARG:NH1	2.39	0.54
2:X:251:TRP:CE3	2:c:271:LYS:HB2	2.43	0.54
2:Z:349:TRP:CD1	2:Z:350:ALA:H	2.25	0.54
2:F:188:GLU:OE2	2:F:492:ARG:NH2	2.32	0.54
2:O:349:TRP:CD1	2:O:350:ALA:N	2.76	0.54
2:R:269:GLN:OE1	2:R:478:LYS:HE3	2.07	0.54
2:V:392:ARG:NH2	2:W:359:ILE:HA	2.22	0.54
1:A:375:ASP:OD1	1:A:382:LYS:HE3	2.08	0.54
2:L:251:TRP:HE3	2:Q:271:LYS:HB2	1.72	0.54
2:R:184:HIS:NE2	2:R:213:ASP:OD1	2.27	0.54
2:G:485:ILE:HD11	2:G:505:ILE:HG12	1.88	0.54
2:Y:349:TRP:CD1	2:Y:350:ALA:H	2.26	0.54
2:a:349:TRP:CD1	2:a:350:ALA:N	2.75	0.54
2:b:72:HIS:HB2	2:c:264:GLU:OE2	2.06	0.54
2:I:128:ARG:NH1	2:I:259:ASP:OD2	2.40	0.54
2:M:319:GLN:OE1	2:M:517:ARG:NH1	2.40	0.54
2:P:101:ARG:NH1	2:Q:146:GLU:OE2	2.38	0.54
2:b:322:LYS:NZ	2:b:343:ASP:OD2	2.38	0.54
2:h:241:GLU:HG3	2:h:251:TRP:CD1	2.42	0.54
2:W:268:ARG:NH2	2:W:309:GLU:OE1	2.40	0.54
2:e:392:ARG:CZ	2:f:359:ILE:HA	2.38	0.54
2:f:355:LYS:NZ	2:f:398:THR:O	2.41	0.54
2:G:271:LYS:HB2	2:H:251:TRP:CE3	2.43	0.54
2:S:470:ASN:O	2:S:472:GLN:NE2	2.40	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:b:485:ILE:HD11	2:b:505:ILE:HG12	1.90	0.54
2:h:170:ILE:HD12	2:h:184:HIS:HB2	1.89	0.54
2:J:88:ILE:HD13	2:d:282:LEU:HD13	1.90	0.54
2:R:241:GLU:N	2:R:249:ASN:O	2.37	0.54
2:g:392:ARG:NH1	2:h:359:ILE:HG23	2.23	0.54
2:R:117:MET:HG3	2:R:455:ALA:HB1	1.89	0.54
2:a:121:THR:HG22	2:a:264:GLU:HG2	1.89	0.54
1:D:182:TRP:CZ2	1:D:395:PRO:HA	2.43	0.54
2:P:71:ASP:HB3	2:P:73:ASN:H	1.73	0.53
2:R:149:HIS:CD2	2:W:101:ARG:HH12	2.26	0.53
2:V:349:TRP:CD1	2:V:350:ALA:H	2.26	0.53
2:W:355:LYS:NZ	2:W:398:THR:O	2.42	0.53
2:i:308:ARG:NH2	2:i:432:TYR:HD2	2.06	0.53
1:E:58:GLU:OE1	1:E:329:TYR:OH	2.23	0.53
2:R:251:TRP:CE3	2:W:271:LYS:HB2	2.43	0.53
2:b:392:ARG:NH1	2:c:359:ILE:HA	2.23	0.53
2:d:392:ARG:CZ	2:e:359:ILE:HA	2.39	0.53
2:I:68:ILE:HG23	2:K:238:GLU:OE1	2.08	0.53
2:L:468:PRO:HG3	2:W:467:ASP:HA	1.89	0.53
2:Q:384:ARG:NH1	2:Q:412:THR:OG1	2.41	0.53
2:Y:439:THR:HG22	2:Y:518:LYS:HA	1.91	0.53
2:Z:158:TYR:O	2:Z:252:ASN:ND2	2.40	0.53
2:M:117:MET:HG3	2:M:455:ALA:HB1	1.90	0.53
2:T:282:LEU:HD21	2:T:288:MET:HB2	1.90	0.53
2:X:277:GLU:HB3	2:d:238:GLU:CD	2.34	0.53
2:Z:323:SER:HA	2:Z:327:GLN:HB2	1.89	0.53
2:a:107:ILE:O	2:a:307:ASN:ND2	2.41	0.53
2:g:121:THR:HG22	2:g:264:GLU:HG2	1.89	0.53
1:C:198:GLU:OE2	2:L:478:LYS:HE2	2.09	0.53
2:S:240:GLN:O	2:S:241:GLU:HB3	2.08	0.53
2:c:355:LYS:NZ	2:c:398:THR:O	2.41	0.53
1:A:175:THR:HG21	1:B:221:VAL:HG11	1.90	0.53
2:F:208:ASP:O	2:F:212:LEU:N	2.35	0.53
2:O:117:MET:HG3	2:O:455:ALA:HB1	1.91	0.53
2:Q:348:ARG:HH21	2:Q:352:GLU:CD	2.17	0.53
2:V:115:GLN:NE2	2:V:448:MET:SD	2.82	0.53
2:X:271:LYS:HB2	2:Y:251:TRP:CE3	2.44	0.53
1:A:198:GLU:OE2	2:d:478:LYS:HE2	2.09	0.53
2:L:327:GLN:NE2	2:L:331:SER:O	2.35	0.53
2:M:349:TRP:CD1	2:M:350:ALA:N	2.77	0.53
2:X:392:ARG:CZ	2:Y:359:ILE:HA	2.38	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:X:392:ARG:NH1	2:Y:359:ILE:HA	2.24	0.53
2:M:241:GLU:N	2:M:249:ASN:O	2.32	0.53
2:W:319:GLN:OE1	2:W:517:ARG:NH1	2.42	0.53
2:Y:101:ARG:HH12	2:Z:149:HIS:CD2	2.27	0.53
2:h:470:ASN:HB3	2:h:472:GLN:HG2	1.91	0.53
2:T:305:GLU:OE1	2:U:159:SER:OG	2.22	0.53
2:Z:271:LYS:HB2	2:a:251:TRP:HE3	1.75	0.53
2:b:241:GLU:HG3	2:b:251:TRP:CD1	2.44	0.53
1:A:189:ARG:NH1	1:E:93:SER:OG	2.42	0.52
2:H:280:GLN:O	2:H:284:ALA:N	2.33	0.52
2:J:404:LEU:HD21	2:K:425:TYR:HE2	1.74	0.52
2:K:117:MET:HG3	2:K:455:ALA:HB1	1.91	0.52
2:L:268:ARG:NH2	2:L:309:GLU:OE2	2.42	0.52
2:P:188:GLU:CD	2:P:492:ARG:HH22	2.16	0.52
2:U:392:ARG:HH21	2:V:362:ASP:HB2	1.74	0.52
2:h:101:ARG:HH12	2:i:149:HIS:CD2	2.26	0.52
2:G:155:ASP:CG	2:G:158:TYR:HB2	2.34	0.52
2:I:392:ARG:NH1	2:J:359:ILE:HG23	2.23	0.52
2:L:235:SER:N	2:P:71:ASP:OD1	2.42	0.52
1:D:65:THR:HG21	1:D:70:ALA:HB2	1.91	0.52
2:O:392:ARG:NH2	2:P:362:ASP:HB2	2.25	0.52
2:e:355:LYS:NZ	2:e:398:THR:O	2.42	0.52
2:V:392:ARG:NH1	2:W:359:ILE:HG23	2.25	0.52
2:X:128:ARG:NE	2:X:146:GLU:OE2	2.41	0.52
2:Z:434:ARG:HD3	2:a:186:PHE:CE2	2.45	0.52
2:e:188:GLU:HB3	2:e:325:PHE:HE2	1.74	0.52
2:M:241:GLU:O	2:M:241:GLU:CD	2.53	0.52
2:P:523:GLY:O	2:Q:345:ARG:NH2	2.40	0.52
2:T:349:TRP:CD1	2:T:350:ALA:N	2.78	0.52
1:A:289:ALA:HA	1:A:343:CYS:HB3	1.91	0.52
2:J:278:LEU:HD22	2:d:67:GLU:HB3	1.91	0.52
2:X:282:LEU:HD13	2:h:88:ILE:HD13	1.90	0.52
2:F:470:ASN:HB3	2:F:472:GLN:HG2	1.92	0.52
2:O:100:ARG:O	2:P:374:ARG:NH2	2.41	0.52
2:S:327:GLN:NE2	2:S:331:SER:O	2.40	0.52
2:a:402:GLN:HE22	2:b:359:ILE:HD11	1.74	0.52
1:E:181:ARG:NH2	2:i:81:SER:O	2.43	0.52
2:K:349:TRP:CD1	2:K:350:ALA:N	2.78	0.52
2:N:271:LYS:HB2	2:O:251:TRP:CE3	2.45	0.52
2:P:72:HIS:HB2	2:Q:264:GLU:OE2	2.09	0.52
1:A:182:TRP:CZ3	1:A:406:ILE:HD13	2.45	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:288:ASP:OD1	1:E:289:ALA:N	2.43	0.52
2:S:105:ASN:HB2	2:S:416:VAL:HG23	1.91	0.52
2:U:349:TRP:CD1	2:U:350:ALA:H	2.28	0.52
2:G:308:ARG:NH2	2:G:432:TYR:HD2	2.08	0.52
2:Y:404:LEU:HD21	2:Z:425:TYR:HE2	1.74	0.52
2:Z:392:ARG:NH1	2:a:359:ILE:HG23	2.24	0.52
2:b:100:ARG:O	2:c:374:ARG:NH2	2.41	0.52
1:D:406:ILE:HG22	1:D:408:GLY:H	1.75	0.51
2:F:251:TRP:HE1	2:K:269:GLN:HG3	1.74	0.51
2:H:309:GLU:OE1	2:H:481:TYR:OH	2.14	0.51
2:S:244:ASN:HD21	2:W:66:ALA:N	2.08	0.51
2:S:319:GLN:HG3	2:S:513:ASN:O	2.11	0.51
2:Z:402:GLN:HE21	2:a:355:LYS:HB3	1.76	0.51
2:f:349:TRP:CD1	2:f:350:ALA:N	2.78	0.51
2:L:100:ARG:HH22	2:L:293:GLU:CD	2.18	0.51
2:O:106:LEU:HD21	2:O:304:LEU:HD23	1.92	0.51
2:R:349:TRP:CD1	2:R:350:ALA:H	2.28	0.51
2:h:71:ASP:HB3	2:h:73:ASN:H	1.76	0.51
2:h:272:ALA:HB3	2:h:475:MET:HB2	1.91	0.51
1:C:377:ALA:HB1	2:M:241:GLU:CD	2.36	0.51
1:D:75:VAL:O	1:D:396:TYR:OH	2.23	0.51
2:J:349:TRP:CD1	2:J:350:ALA:H	2.28	0.51
2:d:95:VAL:HG22	2:e:123:GLN:HE21	1.76	0.51
2:f:115:GLN:NE2	2:f:448:MET:SD	2.84	0.51
1:E:65:THR:HG21	1:E:70:ALA:HB2	1.91	0.51
1:E:91:THR:O	1:E:99:ARG:NH2	2.43	0.51
1:E:398:THR:HG22	1:E:406:ILE:HD11	1.92	0.51
2:P:392:ARG:NH2	2:Q:359:ILE:HA	2.26	0.51
2:X:374:ARG:O	2:c:413:THR:HG21	2.10	0.51
1:C:406:ILE:HG22	1:C:408:GLY:H	1.75	0.51
2:X:240:GLN:OE1	2:c:269:GLN:NE2	2.44	0.51
2:Y:313:LEU:HD13	2:Y:505:ILE:HD12	1.93	0.51
2:Z:140:THR:OG1	2:Z:143:ASP:OD2	2.15	0.51
2:Z:392:ARG:NH2	2:a:359:ILE:HA	2.26	0.51
2:h:309:GLU:OE1	2:h:481:TYR:OH	2.23	0.51
1:B:378:SER:HB2	2:G:241:GLU:CB	2.41	0.51
2:F:101:ARG:NH1	2:G:146:GLU:OE2	2.38	0.51
2:H:206:GLY:HA3	2:H:212:LEU:HA	1.93	0.51
2:I:402:GLN:HE22	2:J:359:ILE:HD11	1.75	0.51
2:K:282:LEU:HD21	2:K:288:MET:HB2	1.93	0.51
2:R:208:ASP:O	2:R:212:LEU:N	2.32	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:R:413:THR:HG21	2:S:374:ARG:O	2.10	0.51
2:d:392:ARG:HH12	2:e:359:ILE:HA	1.75	0.51
2:h:308:ARG:NH2	2:h:312:ASP:OD1	2.44	0.51
1:D:58:GLU:OE1	1:D:329:TYR:OH	2.27	0.51
2:L:349:TRP:CD1	2:L:350:ALA:N	2.79	0.51
2:Z:241:GLU:H	2:Z:249:ASN:HB3	1.74	0.51
2:d:241:GLU:HG3	2:d:251:TRP:CD1	2.46	0.51
1:A:377:ALA:O	2:e:241:GLU:HG3	2.11	0.51
2:G:269:GLN:NE2	2:H:240:GLN:OE1	2.39	0.51
2:H:485:ILE:HD11	2:H:505:ILE:HG12	1.93	0.51
2:c:184:HIS:NE2	2:c:213:ASP:OD1	2.21	0.51
2:f:271:LYS:HB2	2:g:251:TRP:CE3	2.46	0.51
1:C:361:TYR:CE2	1:C:363:GLU:HB2	2.45	0.51
1:D:378:SER:HB3	2:S:241:GLU:CG	2.41	0.51
2:J:117:MET:HG3	2:J:455:ALA:HB1	1.92	0.51
2:P:271:LYS:HB2	2:Q:251:TRP:CE3	2.46	0.51
2:Y:241:GLU:O	2:Y:241:GLU:CD	2.54	0.51
2:H:188:GLU:OE2	2:H:492:ARG:NH1	2.35	0.51
2:L:251:TRP:CE3	2:Q:271:LYS:HB2	2.46	0.51
2:T:117:MET:HG3	2:T:455:ALA:HB1	1.93	0.51
2:T:448:MET:O	2:T:453:TYR:OH	2.23	0.51
2:V:470:ASN:HB3	2:V:472:GLN:HG2	1.92	0.51
2:Y:384:ARG:NH2	2:Y:431:GLN:O	2.44	0.51
2:h:272:ALA:HB2	2:h:298:LEU:HD11	1.92	0.51
2:c:115:GLN:NE2	2:c:448:MET:SD	2.84	0.50
2:c:117:MET:HG3	2:c:455:ALA:HB1	1.92	0.50
2:h:282:LEU:HD21	2:h:288:MET:HB2	1.92	0.50
2:S:157:MET:HB3	2:S:162:GLY:HA3	1.93	0.50
2:T:140:THR:OG1	2:T:143:ASP:OD2	2.24	0.50
2:V:101:ARG:HH12	2:W:149:HIS:CD2	2.30	0.50
1:A:221:VAL:HG11	1:E:175:THR:HG21	1.93	0.50
2:H:123:GLN:HA	2:H:261:GLN:O	2.11	0.50
2:R:67:GLU:HB3	2:b:278:LEU:HD22	1.92	0.50
2:d:101:ARG:NH1	2:e:146:GLU:OE2	2.39	0.50
1:A:179:MET:HE3	1:B:208:PHE:CZ	2.46	0.50
1:A:398:THR:HG22	1:A:406:ILE:HD11	1.93	0.50
2:F:392:ARG:NH1	2:G:359:ILE:HG23	2.27	0.50
2:S:268:ARG:HH21	2:S:481:TYR:HH	1.52	0.50
2:W:470:ASN:HB3	2:W:472:GLN:HG2	1.93	0.50
2:X:392:ARG:NH2	2:Y:359:ILE:HA	2.27	0.50
2:b:384:ARG:NH2	2:b:431:GLN:O	2.44	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:410:ASP:OD2	1:E:413:ASN:ND2	2.43	0.50
2:Y:95:VAL:HG22	2:Z:123:GLN:HE21	1.76	0.50
2:Y:241:GLU:N	2:Y:249:ASN:O	2.33	0.50
2:d:128:ARG:NH1	2:d:259:ASP:OD2	2.42	0.50
1:A:377:ALA:HB3	2:e:241:GLU:OE2	2.12	0.50
1:C:294:CYS:HB2	1:C:299:THR:OG1	2.12	0.50
2:F:319:GLN:OE1	2:F:517:ARG:NH1	2.44	0.50
2:G:392:ARG:NH1	2:H:359:ILE:HA	2.27	0.50
2:K:170:ILE:HD12	2:K:184:HIS:HB2	1.94	0.50
2:L:392:ARG:CZ	2:M:359:ILE:HA	2.42	0.50
2:O:349:TRP:HB2	2:P:348:ARG:HH12	1.75	0.50
2:Q:349:TRP:CD1	2:Q:350:ALA:N	2.80	0.50
2:S:149:HIS:NE2	2:S:491:SER:O	2.40	0.50
2:S:239:LEU:O	2:S:249:ASN:ND2	2.44	0.50
2:d:271:LYS:HB2	2:e:251:TRP:CE3	2.47	0.50
2:Q:460:LEU:HD23	2:Q:479:THR:HB	1.94	0.50
2:b:392:ARG:NH2	2:c:358:LEU:O	2.44	0.50
2:d:123:GLN:OE1	2:i:93:PRO:HG2	2.11	0.50
2:i:430:ASP:OD2	2:i:437:TYR:OH	2.21	0.50
1:A:182:TRP:CH2	1:A:406:ILE:HD13	2.47	0.50
1:B:377:ALA:O	2:G:241:GLU:HG3	2.10	0.50
2:J:485:ILE:HD11	2:J:505:ILE:HG12	1.94	0.50
2:O:309:GLU:OE1	2:O:481:TYR:OH	2.23	0.50
2:d:101:ARG:HH12	2:e:149:HIS:CD2	2.29	0.50
2:e:115:GLN:NE2	2:e:448:MET:SD	2.85	0.50
1:B:288:ASP:OD1	1:B:289:ALA:N	2.45	0.50
1:D:93:SER:HB3	1:E:191:PHE:CE2	2.47	0.50
1:D:182:TRP:CE2	1:D:395:PRO:HA	2.47	0.50
2:c:219:GLU:OE1	2:c:224:THR:OG1	2.17	0.50
2:F:88:ILE:HD12	2:P:278:LEU:HD11	1.94	0.49
2:P:392:ARG:NH1	2:Q:359:ILE:HG23	2.27	0.49
2:X:123:GLN:HE21	2:c:95:VAL:HG22	1.77	0.49
2:i:277:GLU:OE1	2:i:277:GLU:N	2.37	0.49
1:E:239:LYS:HB2	1:E:418:SER:O	2.12	0.49
2:J:392:ARG:NH2	2:K:362:ASP:OD2	2.45	0.49
2:T:158:TYR:O	2:T:252:ASN:ND2	2.40	0.49
2:d:259:ASP:CG	2:d:496:PRO:HG3	2.37	0.49
2:i:349:TRP:CD1	2:i:350:ALA:N	2.80	0.49
1:A:77:TYR:O	1:A:85:THR:HG23	2.12	0.49
2:Z:355:LYS:NZ	2:Z:398:THR:O	2.45	0.49
2:b:392:ARG:NH2	2:c:359:ILE:HA	2.27	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:264:GLU:CD	2:F:504:MET:HG3	2.38	0.49
2:J:72:HIS:HB2	2:K:264:GLU:OE2	2.12	0.49
2:X:349:TRP:CD1	2:X:350:ALA:N	2.79	0.49
2:f:272:ALA:HB3	2:f:475:MET:HB2	1.93	0.49
2:G:74:TYR:HD1	2:H:264:GLU:OE1	1.95	0.49
2:L:404:LEU:HD21	2:M:425:TYR:CE1	2.46	0.49
2:R:194:PHE:HB3	2:R:225:LEU:HB3	1.92	0.49
2:G:430:ASP:OD2	2:G:437:TYR:OH	2.26	0.49
2:M:313:LEU:HD13	2:M:505:ILE:HD12	1.95	0.49
2:O:140:THR:OG1	2:O:143:ASP:OD2	2.17	0.49
1:B:179:MET:HE3	1:C:208:PHE:CZ	2.47	0.49
1:C:288:ASP:OD1	1:C:289:ALA:N	2.46	0.49
2:I:100:ARG:HH22	2:I:293:GLU:CD	2.20	0.49
2:N:101:ARG:HH12	2:O:149:HIS:CD2	2.31	0.49
2:T:272:ALA:HB3	2:T:475:MET:HB2	1.94	0.49
2:T:392:ARG:NH1	2:U:359:ILE:HG23	2.27	0.49
2:Z:117:MET:HG3	2:Z:455:ALA:HB1	1.95	0.49
2:Z:128:ARG:NH1	2:Z:259:ASP:OD2	2.42	0.49
2:a:184:HIS:NE2	2:a:213:ASP:OD1	2.27	0.49
2:a:308:ARG:NH1	2:a:430:ASP:OD1	2.35	0.49
2:d:485:ILE:HD11	2:d:505:ILE:HG12	1.94	0.49
2:e:188:GLU:OE2	2:e:492:ARG:NH2	2.41	0.49
2:g:282:LEU:HD21	2:g:288:MET:HB2	1.95	0.49
1:A:58:GLU:OE1	1:A:329:TYR:OH	2.14	0.49
2:J:392:ARG:HH12	2:K:359:ILE:HA	1.76	0.49
2:V:72:HIS:HB2	2:W:264:GLU:OE2	2.13	0.49
1:C:398:THR:HG22	1:C:406:ILE:HD11	1.94	0.49
2:I:485:ILE:HD11	2:I:505:ILE:HG12	1.93	0.49
2:R:101:ARG:HH12	2:S:149:HIS:CD2	2.30	0.49
2:U:155:ASP:CG	2:U:158:TYR:HB2	2.38	0.49
2:K:348:ARG:NH2	2:K:352:GLU:OE2	2.36	0.48
2:W:121:THR:HG22	2:W:264:GLU:HG2	1.94	0.48
2:g:96:ILE:HB	2:h:124:VAL:HG22	1.95	0.48
1:A:120:ASP:OD1	1:A:120:ASP:N	2.46	0.48
1:B:182:TRP:CH2	1:B:406:ILE:HD13	2.48	0.48
1:B:406:ILE:HG22	1:B:408:GLY:H	1.78	0.48
2:S:272:ALA:HB2	2:S:298:LEU:HD11	1.95	0.48
2:R:271:LYS:HB2	2:S:251:TRP:CE3	2.48	0.48
2:X:72:HIS:ND1	2:Y:264:GLU:OE2	2.44	0.48
2:N:392:ARG:NH2	2:O:362:ASP:HB2	2.23	0.48
2:V:117:MET:HG3	2:V:455:ALA:HB1	1.96	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:e:140:THR:OG1	2:e:143:ASP:OD2	2.14	0.48
1:B:380:GLN:HE22	2:F:478:LYS:NZ	2.11	0.48
2:F:384:ARG:NH1	2:F:412:THR:OG1	2.46	0.48
2:N:123:GLN:HA	2:N:261:GLN:O	2.14	0.48
2:V:305:GLU:OE1	2:W:159:SER:OG	2.25	0.48
2:h:392:ARG:CZ	2:i:359:ILE:HA	2.43	0.48
2:K:470:ASN:HB3	2:K:472:GLN:HG2	1.95	0.48
2:a:305:GLU:OE1	2:b:159:SER:HB3	2.12	0.48
2:d:242:ASN:HA	2:d:246:SER:HB3	1.96	0.48
2:K:467:ASP:HA	2:d:468:PRO:HG3	1.95	0.48
2:N:140:THR:OG1	2:N:143:ASP:OD2	2.25	0.48
2:R:362:ASP:HB2	2:W:392:ARG:HH21	1.79	0.48
2:V:291:ASP:CG	2:V:464:ARG:HH22	2.22	0.48
2:a:105:ASN:HB2	2:a:416:VAL:HG23	1.96	0.48
2:d:404:LEU:HD21	2:e:425:TYR:HE1	1.79	0.48
2:h:206:GLY:HA3	2:h:212:LEU:HA	1.95	0.48
1:D:361:TYR:CE2	1:D:363:GLU:HB2	2.49	0.48
2:G:319:GLN:HG3	2:G:513:ASN:O	2.14	0.48
2:G:392:ARG:HH22	2:H:359:ILE:HA	1.79	0.48
2:M:117:MET:HE2	2:M:119:GLY:O	2.14	0.48
2:O:355:LYS:NZ	2:O:398:THR:O	2.46	0.48
2:P:392:ARG:HH12	2:Q:359:ILE:HG23	1.78	0.48
2:X:194:PHE:HB3	2:X:225:LEU:HB3	1.95	0.48
2:b:394:ASP:OD1	2:b:395:SER:N	2.46	0.48
2:h:349:TRP:CD1	2:h:350:ALA:H	2.32	0.48
2:S:355:LYS:NZ	2:S:398:THR:O	2.47	0.48
2:V:434:ARG:HH22	2:W:227:GLU:CD	2.21	0.48
2:X:269:GLN:OE1	2:X:478:LYS:HE3	2.14	0.48
2:e:349:TRP:CD1	2:e:350:ALA:N	2.82	0.48
1:C:72:LEU:HD13	1:D:46:SER:HB3	1.96	0.48
2:F:251:TRP:NE1	2:K:269:GLN:HG3	2.29	0.48
2:F:374:ARG:O	2:K:413:THR:HG21	2.13	0.48
2:L:392:ARG:NH2	2:M:359:ILE:HA	2.28	0.48
2:Z:130:VAL:HG21	2:Z:135:PRO:HA	1.96	0.48
2:c:158:TYR:O	2:c:252:ASN:ND2	2.42	0.48
1:D:288:ASP:OD1	1:D:289:ALA:N	2.47	0.47
2:d:359:ILE:HG23	2:i:392:ARG:CZ	2.44	0.47
2:g:349:TRP:CD1	2:g:350:ALA:N	2.82	0.47
2:h:100:ARG:HH22	2:h:293:GLU:CD	2.22	0.47
1:D:77:TYR:O	1:D:85:THR:HG23	2.14	0.47
1:D:120:ASP:OD1	1:D:120:ASP:N	2.45	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:O:271:LYS:O	2:P:253:GLU:HA	2.14	0.47
2:O:392:ARG:CZ	2:P:359:ILE:HA	2.44	0.47
2:S:269:GLN:OE1	2:S:478:LYS:NZ	2.32	0.47
2:T:323:SER:HA	2:T:327:GLN:HB2	1.96	0.47
2:Z:261:GLN:HE21	2:Z:503:GLY:HA2	1.79	0.47
2:a:392:ARG:NH1	2:b:359:ILE:HG23	2.28	0.47
2:S:140:THR:OG1	2:S:143:ASP:OD2	2.30	0.47
2:X:91:ILE:HG23	2:i:123:GLN:HE22	1.77	0.47
2:a:513:ASN:OD1	2:a:514:ALA:N	2.48	0.47
1:C:99:ARG:NH1	1:C:125:VAL:HG23	2.29	0.47
2:F:170:ILE:HD12	2:F:184:HIS:HB2	1.97	0.47
2:R:91:ILE:HG12	2:c:125:PHE:CZ	2.49	0.47
2:a:117:MET:CG	2:a:455:ALA:HB1	2.43	0.47
2:d:374:ARG:O	2:i:413:THR:HG21	2.14	0.47
2:h:413:THR:HG21	2:i:374:ARG:O	2.15	0.47
1:E:46:SER:OG	1:E:47:LEU:N	2.47	0.47
2:X:242:ASN:HA	2:X:246:SER:HB3	1.96	0.47
2:X:309:GLU:OE1	2:X:481:TYR:OH	2.27	0.47
2:h:305:GLU:OE1	2:i:159:SER:OG	2.21	0.47
1:A:406:ILE:HG22	1:A:408:GLY:H	1.79	0.47
1:B:198:GLU:OE2	2:F:478:LYS:HE2	2.15	0.47
1:B:269:MET:HE3	1:C:260:ALA:HA	1.97	0.47
2:F:206:GLY:HA3	2:F:212:LEU:HA	1.95	0.47
2:H:268:ARG:NH2	2:H:309:GLU:OE2	2.48	0.47
2:Y:392:ARG:NH1	2:Z:359:ILE:HA	2.28	0.47
2:g:240:GLN:HA	2:g:249:ASN:ND2	2.30	0.47
2:h:261:GLN:HE21	2:h:503:GLY:HA2	1.79	0.47
2:h:413:THR:HG21	2:i:374:ARG:C	2.40	0.47
2:F:359:ILE:HG23	2:K:392:ARG:NH1	2.30	0.47
2:G:240:GLN:HA	2:G:249:ASN:CG	2.40	0.47
2:P:309:GLU:OE1	2:P:481:TYR:OH	2.30	0.47
2:R:275:SER:OG	2:X:238:GLU:OE2	2.18	0.47
2:Z:269:GLN:NE2	2:a:240:GLN:OE1	2.48	0.47
2:c:316:TYR:OH	2:c:507:LYS:HA	2.15	0.47
1:A:41:ARG:HE	2:i:91:ILE:HG22	1.79	0.47
1:C:239:LYS:HB2	1:C:418:SER:O	2.15	0.47
1:D:170:GLU:OE1	1:D:170:GLU:N	2.48	0.47
2:I:109:PHE:HE1	2:I:310:ILE:HD12	1.80	0.47
2:S:241:GLU:CG	2:S:241:GLU:O	2.63	0.47
2:Y:117:MET:HG3	2:Y:455:ALA:HB1	1.97	0.47
2:b:115:GLN:NE2	2:b:448:MET:SD	2.88	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:b:464:ARG:NH1	2:b:475:MET:SD	2.88	0.47
2:f:100:ARG:HH22	2:f:293:GLU:CD	2.19	0.47
1:D:404:ARG:NH2	2:c:86:GLY:O	2.48	0.47
2:H:282:LEU:HD21	2:H:288:MET:HB2	1.97	0.47
2:e:244:ASN:HD21	2:i:66:ALA:N	2.13	0.47
2:i:272:ALA:HB2	2:i:298:LEU:HD11	1.97	0.47
1:B:71:THR:HG23	1:C:42:PRO:HB3	1.96	0.46
1:B:378:SER:HB2	2:G:241:GLU:OE1	2.15	0.46
2:W:208:ASP:O	2:W:212:LEU:N	2.38	0.46
2:X:404:LEU:HD21	2:Y:425:TYR:HE1	1.79	0.46
2:X:523:GLY:O	2:Y:345:ARG:NH2	2.48	0.46
2:b:348:ARG:NH2	2:b:352:GLU:OE2	2.48	0.46
2:b:391:ALA:HA	2:b:407:THR:OG1	2.15	0.46
2:f:323:SER:HA	2:f:327:GLN:HB2	1.96	0.46
2:N:434:ARG:HH22	2:O:227:GLU:CD	2.23	0.46
2:a:404:LEU:HD21	2:b:425:TYR:CE2	2.50	0.46
2:c:470:ASN:HB3	2:c:472:GLN:HG2	1.96	0.46
2:d:240:GLN:OE1	2:i:269:GLN:NE2	2.48	0.46
2:F:158:TYR:O	2:F:252:ASN:ND2	2.45	0.46
2:F:349:TRP:CD1	2:F:350:ALA:H	2.33	0.46
2:X:101:ARG:NH1	2:Y:146:GLU:OE2	2.41	0.46
2:c:134:ASP:OD2	2:c:138:GLY:N	2.43	0.46
2:f:96:ILE:HB	2:g:124:VAL:HG22	1.96	0.46
2:i:105:ASN:HB2	2:i:416:VAL:HG23	1.97	0.46
1:A:322:LEU:HD12	1:A:326:TYR:HB2	1.98	0.46
1:B:149:VAL:HG21	1:C:336:PHE:CZ	2.50	0.46
1:B:161:ALA:O	1:C:187:ARG:HB3	2.15	0.46
1:D:175:THR:HG21	1:E:221:VAL:HG11	1.97	0.46
2:J:384:ARG:NH2	2:J:431:GLN:O	2.48	0.46
2:O:101:ARG:NH1	2:P:149:HIS:CD2	2.82	0.46
2:P:101:ARG:HH12	2:Q:149:HIS:CD2	2.33	0.46
2:S:74:TYR:HA	2:S:79:ILE:HD11	1.98	0.46
2:Z:133:LYS:NZ	2:Z:253:GLU:OE2	2.38	0.46
2:f:74:TYR:HA	2:f:79:ILE:HD11	1.97	0.46
2:H:109:PHE:CE1	2:H:310:ILE:HD12	2.49	0.46
2:O:184:HIS:NE2	2:O:213:ASP:OD1	2.28	0.46
2:Y:76:GLN:OE1	2:Z:502:SER:N	2.48	0.46
2:a:194:PHE:HB3	2:a:225:LEU:HB3	1.98	0.46
2:a:360:GLN:O	2:a:364:GLU:HG2	2.15	0.46
2:e:188:GLU:CD	2:e:492:ARG:HH22	2.22	0.46
2:h:392:ARG:NH1	2:i:359:ILE:HG23	2.30	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:182:TRP:CE2	1:C:395:PRO:HA	2.51	0.46
2:F:68:ILE:HD11	2:H:243:PHE:HD2	1.80	0.46
2:I:349:TRP:CD1	2:I:350:ALA:N	2.84	0.46
2:N:348:ARG:HH21	2:N:352:GLU:CD	2.23	0.46
2:S:241:GLU:O	2:S:242:ASN:HB2	2.16	0.46
2:Z:349:TRP:CD1	2:Z:350:ALA:N	2.83	0.46
2:d:348:ARG:HH12	2:i:348:ARG:CZ	2.29	0.46
2:d:349:TRP:CD1	2:d:350:ALA:H	2.34	0.46
1:E:377:ALA:HB1	2:Y:241:GLU:CD	2.40	0.46
2:F:349:TRP:NE1	2:G:352:GLU:HB3	2.31	0.46
2:H:84:SER:HB3	2:H:88:ILE:O	2.15	0.46
2:L:86:GLY:O	2:W:499:ARG:NH1	2.35	0.46
2:N:272:ALA:HB3	2:N:475:MET:HB2	1.98	0.46
2:O:485:ILE:HD11	2:O:505:ILE:HG12	1.98	0.46
2:Q:155:ASP:CG	2:Q:158:TYR:HB2	2.41	0.46
2:J:448:MET:O	2:J:453:TYR:OH	2.31	0.46
2:d:327:GLN:NE2	2:d:331:SER:O	2.42	0.46
2:f:271:LYS:HB2	2:g:251:TRP:HE3	1.80	0.46
1:A:93:SER:HB3	1:B:191:PHE:CE2	2.51	0.46
2:G:72:HIS:ND1	2:H:264:GLU:OE2	2.49	0.46
2:G:475:MET:HE3	2:G:475:MET:HB3	1.86	0.46
2:Y:271:LYS:O	2:Z:253:GLU:HA	2.15	0.46
1:B:181:ARG:NH2	2:Q:81:SER:O	2.48	0.46
1:D:280:GLU:OE2	1:D:422:GLN:NE2	2.49	0.46
2:K:100:ARG:HH22	2:K:293:GLU:CD	2.24	0.46
2:U:259:ASP:CG	2:U:496:PRO:HG3	2.41	0.46
2:U:392:ARG:CZ	2:V:359:ILE:HA	2.46	0.46
2:X:392:ARG:NH1	2:Y:359:ILE:HG23	2.31	0.46
2:Y:349:TRP:NE1	2:Z:352:GLU:HB3	2.31	0.46
2:g:308:ARG:NH2	2:g:432:TYR:HD2	2.14	0.46
2:I:95:VAL:HG22	2:J:123:GLN:HE21	1.80	0.45
2:I:259:ASP:CG	2:I:496:PRO:HG3	2.41	0.45
2:J:392:ARG:CZ	2:K:359:ILE:HA	2.46	0.45
2:O:282:LEU:HD21	2:O:288:MET:HB2	1.98	0.45
2:Q:464:ARG:NH1	2:Q:475:MET:SD	2.88	0.45
2:X:264:GLU:CD	2:X:504:MET:HG3	2.41	0.45
2:Y:206:GLY:HA3	2:Y:212:LEU:HA	1.97	0.45
2:Y:360:GLN:NE2	2:Y:364:GLU:OE2	2.48	0.45
1:C:375:ASP:OD1	1:C:382:LYS:HE3	2.16	0.45
2:H:272:ALA:HB2	2:H:298:LEU:HD11	1.97	0.45
2:L:374:ARG:O	2:Q:413:THR:HG21	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:V:184:HIS:NE2	2:V:213:ASP:OD1	2.24	0.45
2:Y:374:ARG:NH1	2:Y:449:ASP:OD1	2.48	0.45
2:b:101:ARG:HH12	2:c:149:HIS:CD2	2.34	0.45
2:b:271:LYS:HB2	2:c:251:TRP:CE3	2.51	0.45
2:h:460:LEU:HD23	2:h:479:THR:HB	1.97	0.45
2:H:379:PHE:CE1	2:H:441:GLY:HA3	2.51	0.45
2:P:392:ARG:CZ	2:Q:359:ILE:HA	2.47	0.45
2:R:392:ARG:NH1	2:S:359:ILE:HG23	2.31	0.45
2:X:239:LEU:HG	2:X:246:SER:HB2	1.98	0.45
2:c:350:ALA:HB1	2:c:402:GLN:HE22	1.81	0.45
2:d:123:GLN:HE21	2:i:95:VAL:HG22	1.80	0.45
2:e:109:PHE:HE1	2:e:310:ILE:HD12	1.81	0.45
2:N:241:GLU:N	2:N:249:ASN:O	2.50	0.45
2:U:441:GLY:HA2	2:U:515:TYR:O	2.17	0.45
2:X:470:ASN:C	2:X:472:GLN:H	2.25	0.45
2:Y:266:ARG:O	2:Y:480:ARG:HA	2.16	0.45
2:f:240:GLN:HA	2:f:249:ASN:CG	2.42	0.45
2:f:271:LYS:O	2:g:253:GLU:HA	2.15	0.45
2:h:100:ARG:O	2:i:374:ARG:NH2	2.49	0.45
2:h:392:ARG:NH2	2:i:359:ILE:HA	2.32	0.45
1:A:182:TRP:CD1	1:A:182:TRP:N	2.84	0.45
2:H:149:HIS:ND1	2:H:150:PRO:HD2	2.31	0.45
2:Y:100:ARG:HH22	2:Y:293:GLU:CD	2.22	0.45
2:b:93:PRO:HG2	2:c:123:GLN:OE1	2.16	0.45
2:e:100:ARG:O	2:f:374:ARG:NH2	2.49	0.45
1:A:42:PRO:HB3	1:E:71:THR:HG23	1.98	0.45
1:C:120:ASP:OD1	1:C:120:ASP:N	2.47	0.45
1:D:375:ASP:OD1	1:D:382:LYS:HE3	2.16	0.45
2:F:294:LEU:HD23	2:F:294:LEU:HA	1.74	0.45
2:I:384:ARG:NH2	2:I:431:GLN:O	2.49	0.45
2:S:392:ARG:NH1	2:T:359:ILE:HG23	2.28	0.45
2:T:402:GLN:NE2	2:U:359:ILE:HD11	2.31	0.45
2:V:392:ARG:CZ	2:W:359:ILE:HA	2.47	0.45
2:d:149:HIS:ND1	2:d:150:PRO:HD2	2.32	0.45
2:d:392:ARG:NH1	2:e:359:ILE:HG23	2.29	0.45
2:d:434:ARG:HH12	2:e:227:GLU:CD	2.25	0.45
1:E:294:CYS:HB2	1:E:299:THR:OG1	2.17	0.45
2:I:155:ASP:CG	2:I:158:TYR:HB2	2.41	0.45
2:S:240:GLN:HA	2:S:249:ASN:CG	2.41	0.45
2:h:266:ARG:HD2	2:i:231:GLY:O	2.17	0.45
1:A:71:THR:HG23	1:B:42:PRO:HB3	1.97	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:177:PHE:HE2	1:A:179:MET:SD	2.39	0.45
1:A:263:ALA:HB3	1:A:264:PRO:HD3	1.98	0.45
1:D:182:TRP:CD1	1:D:182:TRP:N	2.84	0.45
1:D:398:THR:HG22	1:D:406:ILE:HD11	1.99	0.45
2:Q:367:GLU:OE2	2:Q:370:ARG:NH2	2.39	0.45
2:R:86:GLY:O	2:c:499:ARG:NH1	2.33	0.45
2:T:402:GLN:HE22	2:U:359:ILE:HD11	1.82	0.45
2:U:349:TRP:HB2	2:V:348:ARG:HH12	1.82	0.45
2:W:294:LEU:HD23	2:W:294:LEU:HA	1.81	0.45
2:b:308:ARG:NH2	2:b:312:ASP:OD1	2.49	0.45
2:g:117:MET:HG3	2:g:455:ALA:HB1	1.98	0.45
1:A:182:TRP:CE2	1:A:395:PRO:HA	2.52	0.45
1:C:127:GLU:OE2	1:C:155:ARG:NE	2.41	0.45
2:L:155:ASP:OD1	2:L:193:TYR:OH	2.28	0.45
2:M:115:GLN:NE2	2:M:448:MET:SD	2.90	0.45
2:O:109:PHE:HE1	2:O:310:ILE:HD12	1.81	0.45
2:Y:308:ARG:O	2:Y:308:ARG:HD3	2.16	0.45
2:e:149:HIS:ND1	2:e:150:PRO:HD2	2.32	0.45
2:f:93:PRO:HG2	2:g:123:GLN:OE1	2.17	0.45
1:C:95:ARG:NE	1:C:159:GLU:OE1	2.49	0.44
2:F:278:LEU:HD11	2:P:88:ILE:CD1	2.44	0.44
2:H:323:SER:HA	2:H:327:GLN:HB2	1.98	0.44
2:M:430:ASP:OD2	2:M:437:TYR:OH	2.32	0.44
2:R:264:GLU:OE1	2:R:504:MET:HG3	2.17	0.44
2:U:115:GLN:NE2	2:U:448:MET:SD	2.90	0.44
2:a:271:LYS:HB2	2:b:251:TRP:HE3	1.82	0.44
2:c:206:GLY:HA3	2:c:212:LEU:HA	1.99	0.44
2:f:242:ASN:HA	2:f:246:SER:O	2.18	0.44
1:A:431:TRP:C	1:E:244:ASN:HB2	2.42	0.44
2:G:308:ARG:O	2:G:308:ARG:HD3	2.17	0.44
2:K:362:ASP:OD1	2:K:425:TYR:OH	2.30	0.44
2:L:140:THR:OG1	2:L:143:ASP:OD2	2.33	0.44
2:R:269:GLN:NE2	2:S:240:GLN:OE1	2.50	0.44
2:Z:434:ARG:HD3	2:a:186:PHE:CD2	2.53	0.44
2:Z:470:ASN:HB3	2:Z:472:GLN:HG2	1.99	0.44
2:e:392:ARG:NH2	2:f:359:ILE:HA	2.32	0.44
2:f:327:GLN:NE2	2:f:333:ALA:HB2	2.32	0.44
1:A:46:SER:OG	1:A:47:LEU:N	2.50	0.44
1:E:198:GLU:OE2	2:X:478:LYS:HE2	2.17	0.44
2:I:107:ILE:HG12	2:I:416:VAL:HG11	1.99	0.44
2:J:188:GLU:OE2	2:J:492:ARG:NH2	2.26	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:g:140:THR:OG1	2:g:143:ASP:OD2	2.35	0.44
2:H:188:GLU:CD	2:H:492:ARG:HH12	2.23	0.44
2:J:155:ASP:CG	2:J:158:TYR:HB2	2.43	0.44
2:K:272:ALA:HB2	2:K:298:LEU:HD11	1.99	0.44
2:O:392:ARG:NH1	2:P:359:ILE:HG23	2.32	0.44
2:P:392:ARG:NH2	2:Q:362:ASP:HB2	2.32	0.44
2:S:128:ARG:NH1	2:S:259:ASP:OD2	2.50	0.44
2:Z:348:ARG:CZ	2:a:348:ARG:HH12	2.30	0.44
2:e:271:LYS:O	2:f:253:GLU:HA	2.16	0.44
2:h:485:ILE:HD11	2:h:505:ILE:HG12	1.99	0.44
2:H:240:GLN:HA	2:H:249:ASN:ND2	2.32	0.44
2:J:367:GLU:CD	2:J:370:ARG:HE	2.25	0.44
2:Q:439:THR:HG22	2:Q:518:LYS:HA	1.99	0.44
2:S:93:PRO:HG2	2:T:123:GLN:OE1	2.17	0.44
2:S:241:GLU:O	2:S:242:ASN:CB	2.66	0.44
2:S:313:LEU:HD13	2:S:505:ILE:HD12	1.99	0.44
2:X:149:HIS:CD2	2:c:101:ARG:NH1	2.83	0.44
2:F:149:HIS:CD2	2:K:101:ARG:HH12	2.36	0.44
2:J:282:LEU:HD12	2:d:88:ILE:CD1	2.48	0.44
2:L:523:GLY:O	2:M:345:ARG:NH2	2.51	0.44
2:Q:117:MET:HG3	2:Q:455:ALA:HB1	1.99	0.44
2:V:349:TRP:CD1	2:V:350:ALA:N	2.85	0.44
2:X:392:ARG:HH12	2:Y:359:ILE:HG23	1.83	0.44
2:H:106:LEU:HD21	2:H:304:LEU:HD23	2.00	0.44
2:J:261:GLN:HE21	2:J:503:GLY:HA2	1.83	0.44
2:K:392:ARG:HG2	2:K:403:GLY:O	2.17	0.44
2:N:384:ARG:NH1	2:N:412:THR:OG1	2.51	0.44
2:X:87:ALA:C	2:i:499:ARG:HH22	2.26	0.44
2:e:128:ARG:NH1	2:e:259:ASP:OD2	2.50	0.44
2:f:155:ASP:CG	2:f:158:TYR:HB2	2.42	0.44
2:f:193:TYR:O	2:f:227:GLU:HA	2.18	0.44
1:C:46:SER:OG	1:C:47:LEU:N	2.51	0.44
1:C:71:THR:HG23	1:D:42:PRO:HB3	1.99	0.44
1:C:182:TRP:CZ3	1:C:406:ILE:HD13	2.53	0.44
2:G:434:ARG:HD3	2:H:186:PHE:CD2	2.53	0.44
2:H:115:GLN:NE2	2:H:448:MET:SD	2.91	0.44
2:M:499:ARG:HH22	2:V:87:ALA:C	2.25	0.44
2:Q:115:GLN:NE2	2:Q:448:MET:SD	2.91	0.44
2:T:220:ASN:ND2	2:T:225:LEU:O	2.45	0.44
2:T:439:THR:HG22	2:T:518:LYS:HA	1.99	0.44
2:U:72:HIS:HB2	2:V:264:GLU:OE2	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:U:349:TRP:NE1	2:V:352:GLU:HB3	2.33	0.44
2:V:313:LEU:HD22	2:V:505:ILE:HD13	2.00	0.44
2:f:241:GLU:H	2:f:249:ASN:HB3	1.82	0.44
2:H:271:LYS:HB2	2:I:251:TRP:HE3	1.83	0.44
2:I:392:ARG:NH2	2:J:359:ILE:HA	2.33	0.44
2:U:308:ARG:HG3	2:V:156:THR:HG21	1.99	0.44
1:C:378:SER:OG	2:M:241:GLU:HB3	2.18	0.43
2:G:158:TYR:O	2:G:252:ASN:ND2	2.45	0.43
2:H:117:MET:HG3	2:H:455:ALA:HB1	2.00	0.43
2:K:460:LEU:HD23	2:K:479:THR:HB	1.99	0.43
2:X:277:GLU:CD	2:h:69:ALA:HB3	2.43	0.43
2:Y:100:ARG:NH2	2:Y:293:GLU:OE2	2.38	0.43
2:Z:524:LEU:HD23	2:Z:524:LEU:HA	1.85	0.43
2:a:404:LEU:HD21	2:b:425:TYR:HE2	1.82	0.43
1:A:187:ARG:NH1	1:E:162:ASP:OD1	2.51	0.43
1:B:93:SER:HB3	1:C:191:PHE:CE2	2.53	0.43
1:C:407:LYS:HE3	1:C:407:LYS:HB2	1.90	0.43
2:F:95:VAL:HG22	2:G:123:GLN:HE21	1.83	0.43
2:F:434:ARG:HH22	2:G:227:GLU:CD	2.24	0.43
2:L:93:PRO:HG2	2:M:123:GLN:OE1	2.18	0.43
2:L:231:GLY:O	2:Q:266:ARG:NH1	2.51	0.43
2:R:156:THR:HG21	2:W:308:ARG:HG3	1.99	0.43
2:S:413:THR:HG21	2:T:374:ARG:O	2.18	0.43
2:Z:241:GLU:HG2	2:Z:249:ASN:O	2.18	0.43
2:b:367:GLU:CD	2:b:370:ARG:HE	2.26	0.43
2:d:374:ARG:C	2:i:413:THR:HG21	2.43	0.43
1:A:196:THR:OG1	2:e:238:GLU:OE1	2.28	0.43
1:C:182:TRP:CD1	1:C:182:TRP:N	2.85	0.43
1:C:201:GLN:CD	2:L:458:VAL:HG21	2.43	0.43
1:E:181:ARG:NH1	1:E:183:ASN:OD1	2.51	0.43
2:I:404:LEU:HD21	2:J:425:TYR:HE2	1.82	0.43
2:K:76:GLN:HA	2:K:79:ILE:HD12	2.00	0.43
2:M:242:ASN:HA	2:M:246:SER:OG	2.19	0.43
2:P:294:LEU:HA	2:P:294:LEU:HD23	1.78	0.43
2:P:348:ARG:NH2	2:P:352:GLU:OE2	2.51	0.43
2:X:392:ARG:NH2	2:Y:362:ASP:HB2	2.33	0.43
2:Y:291:ASP:CG	2:Y:464:ARG:HH22	2.27	0.43
2:a:485:ILE:HD11	2:a:505:ILE:HG12	1.99	0.43
2:c:308:ARG:NH2	2:c:432:TYR:HD2	2.16	0.43
2:d:475:MET:HE3	2:d:475:MET:HB3	1.88	0.43
2:f:405:GLN:NE2	2:g:362:ASP:HB3	2.33	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:i:464:ARG:NH1	2:i:475:MET:SD	2.92	0.43
1:C:41:ARG:HE	2:Q:91:ILE:HG22	1.83	0.43
2:M:123:GLN:HA	2:M:261:GLN:O	2.17	0.43
2:M:282:LEU:HD21	2:M:288:MET:HB2	1.99	0.43
2:P:402:GLN:HE22	2:Q:359:ILE:HD11	1.83	0.43
2:X:123:GLN:NE2	2:c:95:VAL:HG22	2.32	0.43
2:e:392:ARG:NH1	2:f:359:ILE:HG23	2.33	0.43
2:f:384:ARG:NH2	2:f:431:GLN:O	2.51	0.43
2:F:271:LYS:HB2	2:G:251:TRP:CE3	2.54	0.43
2:G:392:ARG:NH2	2:H:362:ASP:HB2	2.34	0.43
2:I:413:THR:HG21	2:J:374:ARG:O	2.18	0.43
2:Q:308:ARG:NH2	2:Q:432:TYR:HD2	2.16	0.43
2:R:402:GLN:HE22	2:S:359:ILE:HD11	1.84	0.43
2:S:392:ARG:NH2	2:T:362:ASP:HB2	2.33	0.43
2:X:363:LYS:NZ	2:c:524:LEU:OXT	2.44	0.43
2:Y:319:GLN:HG3	2:Y:513:ASN:O	2.18	0.43
2:a:448:MET:O	2:a:453:TYR:OH	2.27	0.43
2:d:239:LEU:HD11	2:d:244:ASN:HB2	2.00	0.43
1:C:194:GLU:O	2:Q:66:ALA:HB3	2.18	0.43
2:G:392:ARG:NH1	2:H:359:ILE:HG23	2.31	0.43
2:I:308:ARG:HG3	2:J:156:THR:HG21	2.00	0.43
2:J:394:ASP:OD1	2:J:395:SER:N	2.51	0.43
2:N:107:ILE:HG12	2:N:416:VAL:HG11	2.00	0.43
2:P:206:GLY:HA3	2:P:212:LEU:HA	2.00	0.43
2:X:242:ASN:O	2:X:242:ASN:ND2	2.50	0.43
2:X:308:ARG:HA	2:X:308:ARG:HD2	1.77	0.43
2:I:176:ILE:HD13	2:I:182:VAL:HG21	1.99	0.43
2:K:270:LEU:HD23	2:K:270:LEU:HA	1.81	0.43
2:L:87:ALA:C	2:W:499:ARG:HH22	2.26	0.43
2:L:282:LEU:HD13	2:V:88:ILE:HD13	2.01	0.43
2:L:470:ASN:HB3	2:L:472:GLN:HG2	2.00	0.43
2:P:74:TYR:N	2:P:74:TYR:CD1	2.87	0.43
2:Q:277:GLU:OE1	2:Q:277:GLU:N	2.47	0.43
2:R:305:GLU:OE1	2:S:159:SER:OG	2.27	0.43
2:S:101:ARG:NH1	2:T:146:GLU:OE2	2.37	0.43
2:h:298:LEU:HD23	2:h:298:LEU:HA	1.79	0.43
2:h:439:THR:HG22	2:h:518:LYS:HA	2.00	0.43
1:D:406:ILE:HG22	1:D:408:GLY:N	2.32	0.43
2:G:101:ARG:NH1	2:H:149:HIS:CD2	2.85	0.43
2:I:441:GLY:HA2	2:I:515:TYR:O	2.19	0.43
2:N:271:LYS:HB2	2:O:251:TRP:HE3	1.83	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:R:128:ARG:NE	2:R:146:GLU:OE2	2.47	0.43
2:U:305:GLU:OE1	2:V:159:SER:HB3	2.18	0.43
2:V:394:ASP:OD1	2:V:395:SER:N	2.50	0.43
2:W:277:GLU:OE1	2:W:277:GLU:N	2.47	0.43
2:X:374:ARG:C	2:c:413:THR:HG21	2.43	0.43
2:Z:101:ARG:HH22	2:a:491:SER:HA	1.84	0.43
2:d:241:GLU:OE2	2:i:271:LYS:NZ	2.49	0.43
2:f:117:MET:HG3	2:f:455:ALA:HB1	2.01	0.43
2:f:522:LYS:NZ	2:g:221:GLU:OE1	2.39	0.43
2:h:291:ASP:OD1	2:h:464:ARG:NH2	2.47	0.43
2:H:117:MET:HE2	2:H:119:GLY:O	2.19	0.43
2:R:362:ASP:CB	2:W:392:ARG:HH21	2.31	0.43
2:T:76:GLN:HB3	2:U:502:SER:HB2	2.01	0.43
2:V:74:TYR:N	2:V:74:TYR:CD1	2.87	0.43
2:d:149:HIS:CD2	2:i:101:ARG:NH1	2.85	0.43
1:E:375:ASP:OD1	1:E:382:LYS:HE3	2.19	0.43
2:H:319:GLN:OE1	2:H:517:ARG:NH1	2.52	0.43
2:P:475:MET:HE3	2:P:475:MET:HB3	1.86	0.43
2:Y:93:PRO:HG2	2:Z:123:GLN:OE1	2.19	0.43
2:d:234:THR:HB	2:h:71:ASP:OD1	2.19	0.43
2:d:308:ARG:HA	2:d:308:ARG:HD2	1.78	0.43
2:e:123:GLN:HA	2:e:261:GLN:O	2.19	0.43
1:B:170:GLU:OE1	1:B:170:GLU:N	2.50	0.42
1:C:182:TRP:CZ3	1:C:406:ILE:HG21	2.54	0.42
2:F:308:ARG:HD2	2:F:308:ARG:HA	1.74	0.42
2:I:349:TRP:NE1	2:J:352:GLU:HB3	2.34	0.42
2:J:71:ASP:CB	2:J:73:ASN:H	2.32	0.42
2:J:266:ARG:HD2	2:K:231:GLY:O	2.19	0.42
2:J:404:LEU:HD21	2:K:425:TYR:CE2	2.52	0.42
2:P:308:ARG:NH1	2:P:432:TYR:HD2	2.17	0.42
2:S:282:LEU:HD21	2:S:288:MET:HB2	2.01	0.42
2:S:349:TRP:CD1	2:S:350:ALA:N	2.86	0.42
2:a:272:ALA:HB3	2:a:475:MET:HB2	2.00	0.42
2:d:240:GLN:HB2	2:d:251:TRP:NE1	2.33	0.42
2:d:359:ILE:HG23	2:i:392:ARG:NH1	2.34	0.42
2:f:308:ARG:HG3	2:g:156:THR:HG21	2.00	0.42
2:h:313:LEU:HD13	2:h:505:ILE:HD12	2.01	0.42
1:B:120:ASP:OD1	1:B:120:ASP:N	2.51	0.42
1:B:240:ARG:HA	1:B:240:ARG:HD3	1.89	0.42
1:E:274:ALA:HA	1:E:277:MET:HE3	2.00	0.42
2:G:93:PRO:HG2	2:H:123:GLN:OE1	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:I:117:MET:HG3	2:I:455:ALA:HB1	2.01	0.42
2:S:405:GLN:HG3	2:T:362:ASP:OD2	2.19	0.42
2:Z:273:GLN:HG2	2:Z:474:VAL:HG13	2.00	0.42
2:d:264:GLU:OE1	2:d:504:MET:HG3	2.20	0.42
2:h:506:SER:OG	2:h:508:GLU:OE1	2.31	0.42
1:B:297:ARG:HD2	1:B:431:TRP:HZ2	1.84	0.42
1:E:41:ARG:HE	2:c:91:ILE:CG2	2.33	0.42
2:H:240:GLN:HA	2:H:249:ASN:CG	2.44	0.42
2:M:241:GLU:O	2:M:242:ASN:CB	2.67	0.42
2:M:241:GLU:O	2:M:242:ASN:HB2	2.19	0.42
2:P:121:THR:HG22	2:P:264:GLU:HG2	2.00	0.42
2:S:392:ARG:CZ	2:T:359:ILE:HA	2.49	0.42
2:X:91:ILE:HG22	2:X:92:GLY:N	2.34	0.42
2:X:123:GLN:OE1	2:c:93:PRO:HG2	2.19	0.42
2:Y:446:ASN:OD1	2:Y:447:GLU:N	2.52	0.42
2:Z:242:ASN:HA	2:Z:246:SER:O	2.19	0.42
2:i:69:ALA:O	2:i:86:GLY:HA3	2.19	0.42
1:A:182:TRP:CZ2	1:A:395:PRO:HA	2.54	0.42
1:D:378:SER:N	2:S:241:GLU:HG3	2.35	0.42
2:F:269:GLN:OE1	2:F:478:LYS:HE3	2.19	0.42
2:R:91:ILE:HG22	2:R:92:GLY:N	2.34	0.42
2:R:374:ARG:NH2	2:W:100:ARG:O	2.47	0.42
2:S:392:ARG:NH2	2:T:359:ILE:HA	2.34	0.42
2:Z:95:VAL:HG22	2:a:123:GLN:HE21	1.85	0.42
2:d:404:LEU:HD21	2:e:425:TYR:CE1	2.54	0.42
2:f:506:SER:OG	2:f:508:GLU:OE1	2.30	0.42
2:F:235:SER:N	2:J:71:ASP:OD1	2.44	0.42
2:I:186:PHE:N	2:I:190:GLY:O	2.39	0.42
2:I:282:LEU:HD21	2:I:288:MET:HB2	2.00	0.42
2:J:434:ARG:HH22	2:K:227:GLU:CD	2.28	0.42
2:L:239:LEU:HG	2:L:246:SER:HB2	2.00	0.42
2:O:271:LYS:HB2	2:P:251:TRP:CE3	2.54	0.42
2:R:374:ARG:O	2:W:413:THR:HG21	2.20	0.42
2:U:313:LEU:HD22	2:U:505:ILE:HD13	2.01	0.42
2:V:316:TYR:HD2	2:W:227:GLU:O	2.03	0.42
2:V:413:THR:HG21	2:W:374:ARG:O	2.19	0.42
2:Z:149:HIS:ND1	2:Z:150:PRO:HD2	2.34	0.42
2:a:193:TYR:O	2:a:227:GLU:HA	2.20	0.42
1:E:406:ILE:HG22	1:E:408:GLY:N	2.34	0.42
2:I:91:ILE:HG22	2:I:92:GLY:N	2.34	0.42
2:R:313:LEU:HA	2:R:313:LEU:HD23	1.88	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:U:263:ILE:HG23	2:U:504:MET:SD	2.59	0.42
2:Y:305:GLU:OE1	2:Z:159:SER:OG	2.30	0.42
2:c:272:ALA:HB2	2:c:298:LEU:HD11	2.01	0.42
1:B:377:ALA:HB3	2:G:241:GLU:OE2	2.20	0.42
2:H:241:GLU:H	2:H:249:ASN:HB3	1.84	0.42
2:I:162:GLY:HA2	2:I:167:PHE:CE2	2.54	0.42
2:J:413:THR:HG21	2:K:374:ARG:O	2.20	0.42
2:J:475:MET:HE3	2:J:475:MET:HB3	1.89	0.42
2:N:117:MET:CG	2:N:455:ALA:HB1	2.50	0.42
2:Q:91:ILE:HG22	2:Q:92:GLY:N	2.35	0.42
2:R:264:GLU:CD	2:R:504:MET:HG3	2.45	0.42
2:h:117:MET:HG3	2:h:455:ALA:HB1	2.02	0.42
1:C:263:ALA:HB3	1:C:264:PRO:HD3	2.02	0.42
1:D:129:ILE:HD11	1:D:155:ARG:HB3	2.00	0.42
2:J:392:ARG:NH2	2:K:358:LEU:O	2.53	0.42
2:K:277:GLU:OE1	2:K:277:GLU:N	2.50	0.42
2:S:314:ILE:HG23	2:S:516:PHE:CD2	2.54	0.42
2:W:176:ILE:HD13	2:W:182:VAL:HG21	2.02	0.42
2:X:345:ARG:NH1	2:c:354:TYR:OH	2.53	0.42
2:f:524:LEU:HD23	2:f:524:LEU:HA	1.87	0.42
2:h:355:LYS:HG2	2:h:393:ILE:HD12	2.00	0.42
2:i:270:LEU:HD23	2:i:270:LEU:HA	1.89	0.42
1:E:120:ASP:OD1	1:E:120:ASP:N	2.52	0.42
2:H:140:THR:OG1	2:H:143:ASP:OD2	2.31	0.42
2:H:355:LYS:NZ	2:H:398:THR:O	2.53	0.42
2:M:291:ASP:CG	2:M:464:ARG:HH22	2.27	0.42
2:P:272:ALA:HB3	2:P:475:MET:HB2	2.00	0.42
2:Q:244:ASN:CG	2:Q:245:GLY:H	2.28	0.42
2:R:475:MET:HE3	2:R:475:MET:HB3	1.89	0.42
2:X:362:ASP:HB2	2:c:392:ARG:NH2	2.24	0.42
2:X:405:GLN:HE21	2:X:405:GLN:HB2	1.62	0.42
2:Y:271:LYS:HB2	2:Z:251:TRP:CE3	2.55	0.42
2:b:74:TYR:N	2:b:74:TYR:CD1	2.84	0.42
2:d:269:GLN:OE1	2:d:478:LYS:HE3	2.19	0.42
2:h:188:GLU:OE2	2:h:492:ARG:NH2	2.41	0.42
1:D:269:MET:HB2	1:E:263:ALA:HB2	2.02	0.42
2:K:140:THR:OG1	2:K:143:ASP:OD2	2.31	0.42
2:L:91:ILE:HG22	2:L:92:GLY:N	2.34	0.42
2:R:435:GLN:NE2	2:S:221:GLU:OE2	2.38	0.42
2:S:308:ARG:NH2	2:S:432:TYR:HD2	2.18	0.42
2:V:71:ASP:CB	2:V:73:ASN:H	2.32	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:V:266:ARG:HD2	2:W:231:GLY:O	2.19	0.42
2:a:313:LEU:HD13	2:a:505:ILE:HD12	2.02	0.42
2:b:186:PHE:N	2:b:190:GLY:O	2.36	0.42
2:f:305:GLU:OE1	2:g:159:SER:OG	2.28	0.42
2:H:270:LEU:HD23	2:H:270:LEU:HA	1.89	0.41
2:K:313:LEU:HD23	2:K:313:LEU:HA	1.88	0.41
2:L:348:ARG:HH21	2:L:352:GLU:CD	2.27	0.41
2:N:349:TRP:CG	2:N:350:ALA:N	2.88	0.41
2:N:434:ARG:HD3	2:O:186:PHE:CE2	2.55	0.41
2:P:369:ALA:HB2	2:P:376:ALA:HB2	2.02	0.41
2:X:359:ILE:HG23	2:c:392:ARG:NH1	2.35	0.41
2:a:441:GLY:HA2	2:a:515:TYR:O	2.20	0.41
2:b:71:ASP:CB	2:b:73:ASN:H	2.32	0.41
2:c:100:ARG:HH22	2:c:293:GLU:CD	2.28	0.41
1:B:398:THR:HG22	1:B:406:ILE:HD11	2.01	0.41
2:F:105:ASN:HB2	2:F:416:VAL:HG23	2.02	0.41
2:I:460:LEU:HD23	2:I:460:LEU:HA	1.92	0.41
2:K:289:ASP:O	2:K:293:GLU:HG2	2.20	0.41
2:O:100:ARG:HH22	2:O:293:GLU:CD	2.28	0.41
2:b:188:GLU:CD	2:b:492:ARG:HH22	2.27	0.41
2:b:241:GLU:HG3	2:b:251:TRP:NE1	2.34	0.41
2:b:378:ASN:O	2:b:425:TYR:HA	2.20	0.41
2:d:349:TRP:NE1	2:e:352:GLU:HB3	2.35	0.41
2:d:359:ILE:HD11	2:i:402:GLN:HE22	1.85	0.41
2:i:117:MET:HG3	2:i:455:ALA:HB1	2.02	0.41
1:A:132:ILE:HD12	1:A:132:ILE:HA	1.93	0.41
1:C:81:ASN:ND2	1:C:83:ASP:OD2	2.53	0.41
2:F:235:SER:OG	2:J:71:ASP:OD2	2.33	0.41
2:F:240:GLN:HG3	2:K:269:GLN:NE2	2.35	0.41
2:I:107:ILE:HD12	2:I:311:VAL:HG21	2.02	0.41
2:J:390:LEU:HA	2:J:390:LEU:HD23	1.80	0.41
2:S:206:GLY:HA3	2:S:212:LEU:HA	2.01	0.41
2:T:101:ARG:HD2	2:U:146:GLU:OE2	2.20	0.41
2:T:291:ASP:CG	2:T:464:ARG:HH22	2.27	0.41
2:f:282:LEU:HD21	2:f:288:MET:HB2	2.03	0.41
2:f:439:THR:HG22	2:f:518:LYS:HA	2.03	0.41
2:g:117:MET:CG	2:g:455:ALA:HB1	2.50	0.41
1:C:145:LEU:HD23	1:C:145:LEU:HA	1.90	0.41
1:D:354:GLY:H	1:D:394:ASN:ND2	2.18	0.41
2:G:434:ARG:HD3	2:H:186:PHE:CE2	2.55	0.41
2:M:121:THR:HG22	2:M:264:GLU:HG2	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:P:282:LEU:HD23	2:P:282:LEU:C	2.45	0.41
2:T:270:LEU:HA	2:T:270:LEU:HD23	1.84	0.41
1:A:281:MET:SD	1:A:289:ALA:HB2	2.60	0.41
1:B:297:ARG:HD2	1:B:431:TRP:CZ2	2.55	0.41
1:D:182:TRP:CH2	1:D:406:ILE:HD13	2.55	0.41
2:F:129:ALA:O	2:F:147:ALA:N	2.48	0.41
2:G:294:LEU:HD23	2:G:294:LEU:HA	1.85	0.41
2:G:413:THR:HG21	2:H:374:ARG:O	2.21	0.41
2:P:349:TRP:NE1	2:Q:352:GLU:HB3	2.35	0.41
2:Y:392:ARG:NH2	2:Z:359:ILE:HA	2.35	0.41
2:Z:184:HIS:NE2	2:Z:213:ASP:OD1	2.26	0.41
2:Z:271:LYS:O	2:a:253:GLU:HA	2.19	0.41
2:b:260:LYS:HB3	2:b:500:ILE:HG12	2.03	0.41
2:b:294:LEU:HA	2:b:294:LEU:HD23	1.82	0.41
2:b:405:GLN:HE21	2:b:405:GLN:HB2	1.71	0.41
2:c:270:LEU:HD23	2:c:270:LEU:HA	1.87	0.41
2:e:117:MET:HE2	2:e:119:GLY:O	2.20	0.41
2:e:392:ARG:NH2	2:f:362:ASP:HB2	2.36	0.41
1:A:67:LEU:HD23	1:A:67:LEU:HA	1.88	0.41
1:E:291:TYR:CZ	1:E:342:GLY:HA3	2.56	0.41
2:O:194:PHE:HB3	2:O:225:LEU:HB3	2.02	0.41
2:X:369:ALA:HB2	2:X:376:ALA:HB2	2.03	0.41
2:a:158:TYR:CE2	2:a:252:ASN:HB3	2.56	0.41
2:c:374:ARG:NH1	2:c:449:ASP:OD1	2.53	0.41
2:d:227:GLU:OE1	2:i:434:ARG:NH2	2.32	0.41
2:i:170:ILE:HD12	2:i:184:HIS:HB2	2.02	0.41
1:C:77:TYR:CE1	1:D:217:ILE:HG12	2.56	0.41
1:E:281:MET:HE1	1:E:342:GLY:C	2.45	0.41
2:L:469:LYS:HB3	2:R:241:GLU:HB3	2.03	0.41
2:M:413:THR:HG21	2:N:374:ARG:O	2.21	0.41
2:R:348:ARG:HH21	2:R:352:GLU:CD	2.29	0.41
2:T:130:VAL:HG21	2:T:135:PRO:HA	2.02	0.41
2:W:117:MET:HE2	2:W:119:GLY:O	2.21	0.41
2:a:319:GLN:HG3	2:a:513:ASN:O	2.20	0.41
2:e:413:THR:HG21	2:f:374:ARG:O	2.20	0.41
2:h:308:ARG:HH11	2:h:432:TYR:HD2	1.68	0.41
2:J:369:ALA:HB2	2:J:376:ALA:HB2	2.02	0.41
2:L:88:ILE:HD13	2:V:282:LEU:HD12	2.02	0.41
2:L:524:LEU:HD23	2:L:524:LEU:HA	1.88	0.41
2:P:349:TRP:CD1	2:P:350:ALA:N	2.88	0.41
2:R:392:ARG:HH12	2:S:359:ILE:HA	1.86	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:X:234:THR:HB	2:b:71:ASP:OD1	2.20	0.41
2:a:260:LYS:HB3	2:a:500:ILE:HG12	2.03	0.41
1:D:244:ASN:H	1:E:431:TRP:C	2.29	0.41
1:E:77:TYR:O	1:E:85:THR:HG23	2.21	0.41
2:G:349:TRP:CD1	2:G:350:ALA:N	2.87	0.41
2:H:105:ASN:ND2	2:H:412:THR:O	2.53	0.41
2:I:323:SER:HA	2:I:327:GLN:HB2	2.03	0.41
2:I:349:TRP:CG	2:I:350:ALA:N	2.89	0.41
2:M:349:TRP:CG	2:M:350:ALA:N	2.88	0.41
2:N:91:ILE:HG22	2:N:92:GLY:N	2.36	0.41
2:O:317:THR:HB	2:O:513:ASN:HB2	2.03	0.41
2:P:123:GLN:HA	2:P:261:GLN:O	2.21	0.41
2:P:269:GLN:NE2	2:Q:240:GLN:OE1	2.54	0.41
2:T:385:ASN:ND2	2:T:436:ASP:OD1	2.33	0.41
2:V:322:LYS:NZ	2:V:343:ASP:OD1	2.52	0.41
2:Y:101:ARG:NH1	2:Z:149:HIS:CD2	2.89	0.41
2:Y:158:TYR:O	2:Y:252:ASN:ND2	2.50	0.41
2:d:402:GLN:HE21	2:d:402:GLN:HB3	1.59	0.41
2:g:186:PHE:N	2:g:190:GLY:O	2.39	0.41
2:g:413:THR:HG21	2:h:374:ARG:C	2.45	0.41
1:B:182:TRP:CD1	1:B:182:TRP:N	2.88	0.41
2:F:244:ASN:HD21	2:J:66:ALA:HB1	1.86	0.41
2:K:524:LEU:HD23	2:K:524:LEU:HA	1.78	0.41
2:M:392:ARG:NH2	2:N:359:ILE:HA	2.35	0.41
2:U:91:ILE:HG22	2:U:92:GLY:N	2.36	0.41
2:b:460:LEU:HD23	2:b:479:THR:HB	2.03	0.41
2:e:240:GLN:O	2:e:241:GLU:HB3	2.21	0.41
2:e:241:GLU:O	2:e:242:ASN:CB	2.68	0.41
2:g:364:GLU:OE1	2:g:517:ARG:NE	2.39	0.41
2:i:176:ILE:HD13	2:i:182:VAL:HG21	2.02	0.41
1:A:239:LYS:HB2	1:A:418:SER:O	2.21	0.40
1:C:377:ALA:CB	2:M:241:GLU:CD	2.94	0.40
1:E:145:LEU:HA	1:E:145:LEU:HD23	1.88	0.40
1:E:170:GLU:OE1	2:K:469:LYS:HD3	2.21	0.40
2:G:321:GLY:HA2	2:G:517:ARG:NH2	2.37	0.40
2:G:524:LEU:HD23	2:G:524:LEU:HA	1.89	0.40
2:M:439:THR:HG22	2:M:518:LYS:HA	2.02	0.40
2:Q:524:LEU:HA	2:Q:524:LEU:HD23	1.86	0.40
2:X:128:ARG:NH1	2:X:259:ASP:OD2	2.55	0.40
2:Z:93:PRO:HG2	2:a:123:GLN:OE1	2.20	0.40
2:a:157:MET:HE2	2:a:229:SER:HA	2.04	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:g:513:ASN:OD1	2:g:514:ALA:N	2.54	0.40
1:A:406:ILE:HG22	1:A:408:GLY:N	2.37	0.40
1:B:129:ILE:HD11	1:B:155:ARG:HB3	2.03	0.40
1:C:95:ARG:N	1:C:159:GLU:O	2.38	0.40
2:F:91:ILE:HG12	2:Q:125:PHE:HZ	1.86	0.40
2:X:434:ARG:HH12	2:Y:227:GLU:CD	2.30	0.40
2:b:269:GLN:NE2	2:c:240:GLN:OE1	2.54	0.40
2:b:441:GLY:HA2	2:b:515:TYR:O	2.21	0.40
2:c:123:GLN:HA	2:c:261:GLN:O	2.21	0.40
2:e:241:GLU:O	2:e:241:GLU:CG	2.69	0.40
2:e:272:ALA:HB2	2:e:298:LEU:HD11	2.03	0.40
2:g:271:LYS:HB2	2:h:251:TRP:CE3	2.56	0.40
2:G:348:ARG:CZ	2:H:348:ARG:HH12	2.34	0.40
2:M:439:THR:HA	2:M:517:ARG:O	2.22	0.40
2:P:260:LYS:HB3	2:P:500:ILE:HG12	2.03	0.40
2:U:282:LEU:HD21	2:U:288:MET:HB2	2.02	0.40
2:X:278:LEU:HD11	2:h:88:ILE:CD1	2.52	0.40
2:b:112:CYS:O	2:b:443:LYS:NZ	2.33	0.40
2:f:268:ARG:NH1	2:g:159:SER:OG	2.41	0.40
1:C:240:ARG:HA	1:C:240:ARG:HD3	1.85	0.40
1:D:91:THR:O	1:D:99:ARG:NH2	2.53	0.40
2:J:469:LYS:HB3	2:f:241:GLU:HB3	2.04	0.40
2:P:392:ARG:NH1	2:Q:359:ILE:HA	2.37	0.40
2:T:241:GLU:H	2:T:249:ASN:HB3	1.86	0.40
2:a:128:ARG:NH1	2:a:259:ASP:OD2	2.49	0.40
2:d:391:ALA:HB2	2:d:408:LEU:HB2	2.03	0.40
2:i:470:ASN:HB3	2:i:472:GLN:HG2	2.03	0.40
1:A:378:SER:HB3	2:e:241:GLU:OE1	2.20	0.40
1:E:99:ARG:NH1	1:E:125:VAL:HG23	2.36	0.40
2:L:359:ILE:HD11	2:Q:402:GLN:HE22	1.86	0.40
2:M:271:LYS:O	2:N:253:GLU:HA	2.21	0.40
2:R:434:ARG:NH1	2:S:227:GLU:OE2	2.27	0.40
2:V:206:GLY:HA3	2:V:212:LEU:HA	2.03	0.40
2:V:380:ILE:HG12	2:V:440:VAL:HG22	2.03	0.40
2:X:101:ARG:HH12	2:Y:149:HIS:CD2	2.40	0.40
2:Y:123:GLN:HE22	2:h:91:ILE:HG23	1.87	0.40
2:Z:263:ILE:HD13	2:Z:484:GLY:HA3	2.04	0.40
2:a:272:ALA:HB2	2:a:298:LEU:HD11	2.03	0.40
2:c:112:CYS:HB2	2:c:452:ILE:O	2.21	0.40
2:d:68:ILE:HG22	2:d:70:GLY:N	2.36	0.40
2:d:392:ARG:NH2	2:e:362:ASP:OD2	2.48	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:d:435:GLN:HB2	2:d:520:TRP:HZ3	1.86	0.40
2:h:441:GLY:HA2	2:h:515:TYR:O	2.22	0.40

There are no symmetry-related clashes.

5.3 Torsion angles (i)

5.3.1 Protein backbone (i)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	394/440 (90%)	384 (98%)	10 (2%)	0	100	100
1	B	394/440 (90%)	381 (97%)	13 (3%)	0	100	100
1	C	394/440 (90%)	382 (97%)	12 (3%)	0	100	100
1	D	394/440 (90%)	382 (97%)	12 (3%)	0	100	100
1	E	394/440 (90%)	379 (96%)	15 (4%)	0	100	100
2	F	457/524 (87%)	440 (96%)	17 (4%)	0	100	100
2	G	457/524 (87%)	445 (97%)	12 (3%)	0	100	100
2	H	457/524 (87%)	443 (97%)	14 (3%)	0	100	100
2	I	457/524 (87%)	445 (97%)	12 (3%)	0	100	100
2	J	457/524 (87%)	439 (96%)	18 (4%)	0	100	100
2	K	457/524 (87%)	443 (97%)	14 (3%)	0	100	100
2	L	457/524 (87%)	442 (97%)	15 (3%)	0	100	100
2	M	457/524 (87%)	442 (97%)	15 (3%)	0	100	100
2	N	457/524 (87%)	446 (98%)	11 (2%)	0	100	100
2	O	457/524 (87%)	444 (97%)	13 (3%)	0	100	100
2	P	457/524 (87%)	441 (96%)	16 (4%)	0	100	100
2	Q	457/524 (87%)	442 (97%)	15 (3%)	0	100	100
2	R	457/524 (87%)	445 (97%)	12 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	S	457/524 (87%)	442 (97%)	15 (3%)	0	100	100
2	T	457/524 (87%)	445 (97%)	12 (3%)	0	100	100
2	U	457/524 (87%)	444 (97%)	13 (3%)	0	100	100
2	V	457/524 (87%)	440 (96%)	17 (4%)	0	100	100
2	W	457/524 (87%)	445 (97%)	12 (3%)	0	100	100
2	X	457/524 (87%)	442 (97%)	15 (3%)	0	100	100
2	Y	457/524 (87%)	443 (97%)	14 (3%)	0	100	100
2	Z	457/524 (87%)	445 (97%)	12 (3%)	0	100	100
2	a	457/524 (87%)	448 (98%)	9 (2%)	0	100	100
2	b	457/524 (87%)	440 (96%)	17 (4%)	0	100	100
2	c	457/524 (87%)	443 (97%)	14 (3%)	0	100	100
2	d	457/524 (87%)	446 (98%)	11 (2%)	0	100	100
2	e	457/524 (87%)	443 (97%)	14 (3%)	0	100	100
2	f	457/524 (87%)	443 (97%)	14 (3%)	0	100	100
2	g	457/524 (87%)	446 (98%)	11 (2%)	0	100	100
2	h	457/524 (87%)	441 (96%)	16 (4%)	0	100	100
2	i	457/524 (87%)	444 (97%)	13 (3%)	0	100	100
All	All	15680/17920 (88%)	15205 (97%)	475 (3%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains (i)

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	340/381 (89%)	340 (100%)	0	100	100
1	B	340/381 (89%)	340 (100%)	0	100	100
1	C	340/381 (89%)	340 (100%)	0	100	100
1	D	340/381 (89%)	340 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	E	340/381 (89%)	340 (100%)	0	100	100
2	F	352/408 (86%)	352 (100%)	0	100	100
2	G	352/408 (86%)	352 (100%)	0	100	100
2	H	352/408 (86%)	352 (100%)	0	100	100
2	I	352/408 (86%)	352 (100%)	0	100	100
2	J	352/408 (86%)	352 (100%)	0	100	100
2	K	352/408 (86%)	352 (100%)	0	100	100
2	L	352/408 (86%)	352 (100%)	0	100	100
2	M	352/408 (86%)	352 (100%)	0	100	100
2	N	352/408 (86%)	352 (100%)	0	100	100
2	O	352/408 (86%)	352 (100%)	0	100	100
2	P	352/408 (86%)	352 (100%)	0	100	100
2	Q	352/408 (86%)	352 (100%)	0	100	100
2	R	352/408 (86%)	352 (100%)	0	100	100
2	S	352/408 (86%)	352 (100%)	0	100	100
2	T	352/408 (86%)	352 (100%)	0	100	100
2	U	352/408 (86%)	352 (100%)	0	100	100
2	V	352/408 (86%)	352 (100%)	0	100	100
2	W	352/408 (86%)	352 (100%)	0	100	100
2	X	352/408 (86%)	352 (100%)	0	100	100
2	Y	352/408 (86%)	352 (100%)	0	100	100
2	Z	352/408 (86%)	352 (100%)	0	100	100
2	a	352/408 (86%)	352 (100%)	0	100	100
2	b	352/408 (86%)	352 (100%)	0	100	100
2	c	352/408 (86%)	352 (100%)	0	100	100
2	d	352/408 (86%)	352 (100%)	0	100	100
2	e	352/408 (86%)	352 (100%)	0	100	100
2	f	352/408 (86%)	352 (100%)	0	100	100
2	g	352/408 (86%)	352 (100%)	0	100	100
2	h	352/408 (86%)	352 (100%)	0	100	100
2	i	352/408 (86%)	352 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
All	All	12260/14145 (87%)	12260 (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 (79) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	52	ASN
1	B	227	ASN
1	B	333	ASN
1	B	380	GLN
1	C	422	GLN
1	D	57	HIS
1	E	422	GLN
2	F	73	ASN
2	F	307	ASN
2	F	409	ASN
2	G	307	ASN
2	G	405	GLN
2	G	409	ASN
2	H	164	HIS
2	H	249	ASN
2	H	269	GLN
2	H	273	GLN
2	H	286	HIS
2	H	366	ASN
2	I	402	GLN
2	J	307	ASN
2	K	470	ASN
2	L	242	ASN
2	L	402	GLN
2	M	307	ASN
2	N	164	HIS
2	O	73	ASN
2	O	402	GLN
2	P	164	HIS
2	P	286	HIS
2	P	402	GLN
2	Q	261	GLN
2	Q	286	HIS
2	Q	470	ASN
2	R	242	ASN

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Mol	Chain	Res	Type
2	R	366	ASN
2	S	261	GLN
2	S	307	ASN
2	S	409	ASN
2	T	269	GLN
2	T	286	HIS
2	T	405	GLN
2	U	164	HIS
2	U	307	ASN
2	U	366	ASN
2	V	164	HIS
2	V	307	ASN
2	V	409	ASN
2	W	123	GLN
2	W	273	GLN
2	W	402	GLN
2	W	405	GLN
2	X	73	ASN
2	X	242	ASN
2	X	366	ASN
2	Y	123	GLN
2	Y	244	ASN
2	Y	273	GLN
2	Y	409	ASN
2	Z	273	GLN
2	b	307	ASN
2	b	405	GLN
2	c	90	ASN
2	c	273	GLN
2	c	366	ASN
2	c	409	ASN
2	d	286	HIS
2	d	402	GLN
2	e	244	ASN
2	e	286	HIS
2	e	409	ASN
2	f	73	ASN
2	f	273	GLN
2	g	73	ASN
2	h	164	HIS
2	h	286	HIS
2	i	123	GLN

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Mol	Chain	Res	Type
2	i	242	ASN
2	i	366	ASN

5.3.3 RNA (i)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates (i)

There are no oligosaccharides in this entry.

5.6 Ligand geometry (i)

There are no ligands in this entry.

5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

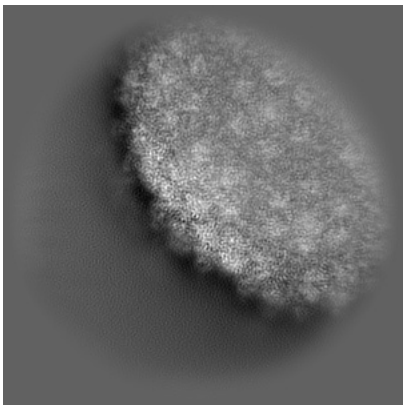
6 Map visualisation

This section contains visualisations of the EMDB entry EMD-80026. These allow visual inspection of the internal detail of the map and identification of artifacts.

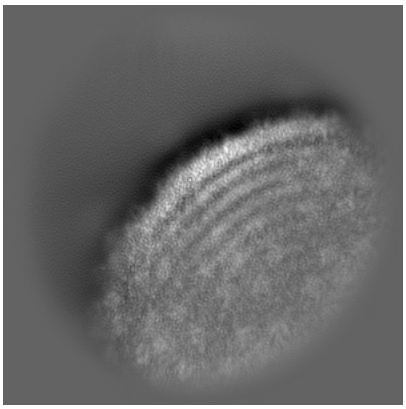
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections

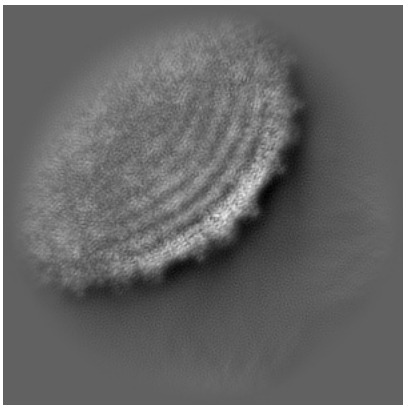
6.1.1 Primary map



X

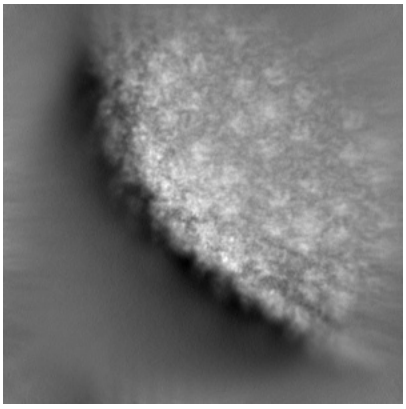


Y

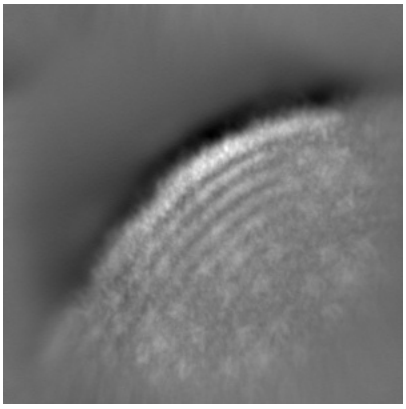


Z

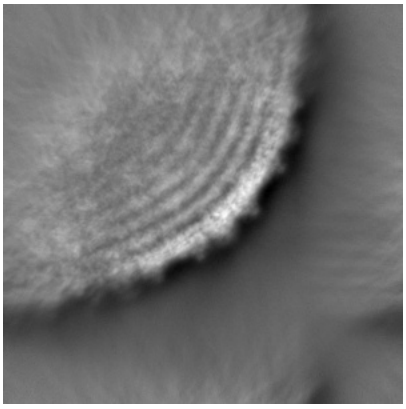
6.1.2 Raw map



X



Y

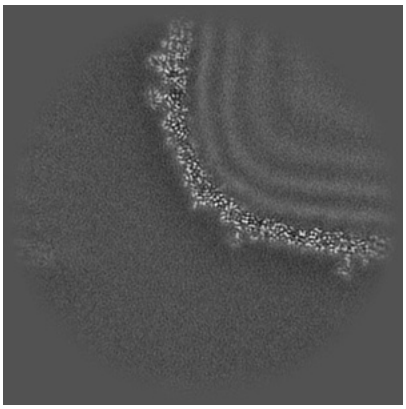


Z

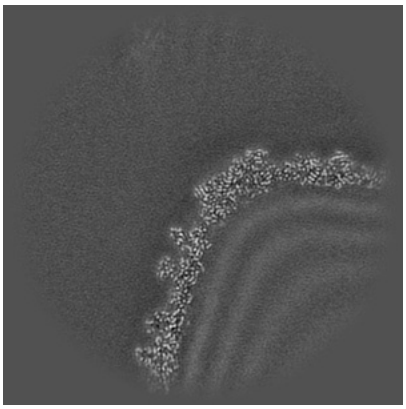
The images above show the map projected in three orthogonal directions.

6.2 Central slices (i)

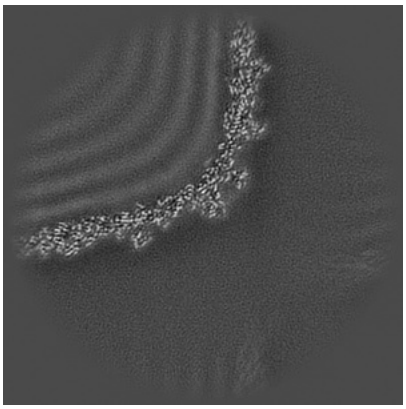
6.2.1 Primary map



X Index: 180

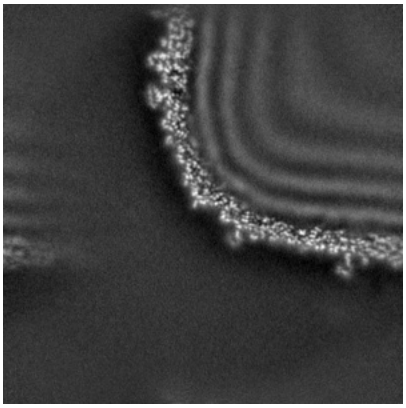


Y Index: 180

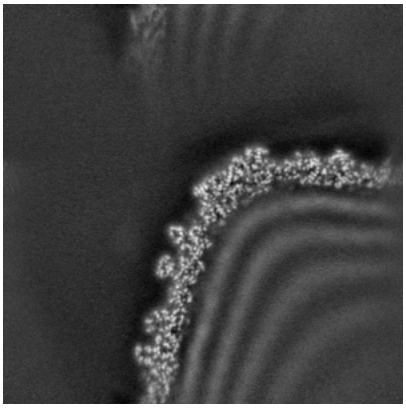


Z Index: 180

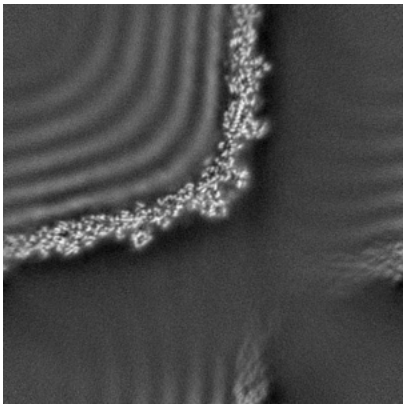
6.2.2 Raw map



X Index: 180



Y Index: 180

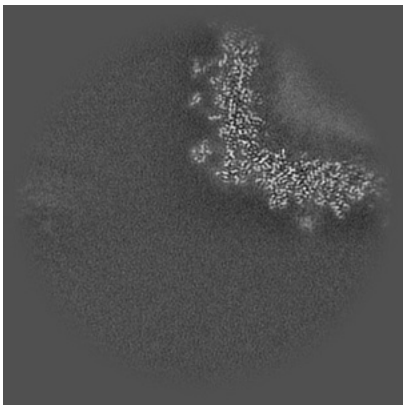


Z Index: 180

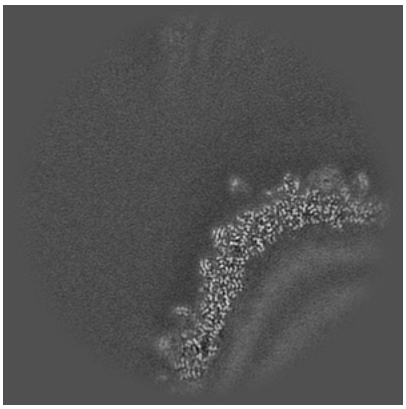
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

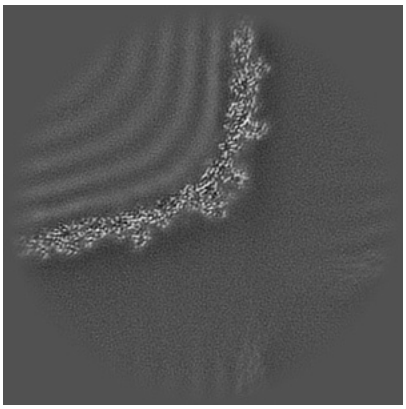
6.3.1 Primary map



X Index: 228

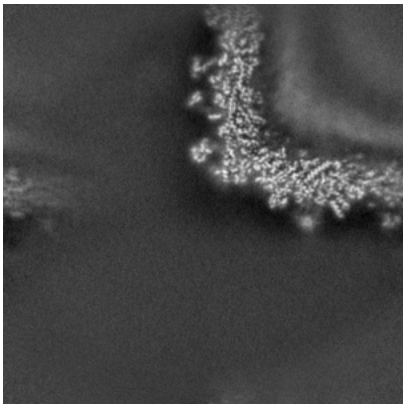


Y Index: 152

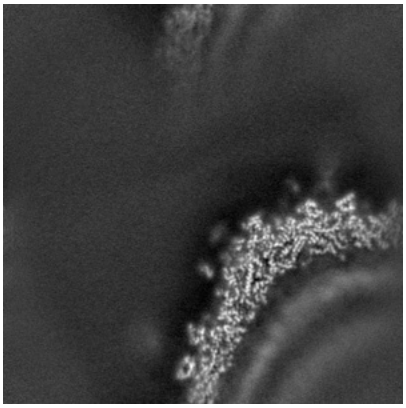


Z Index: 181

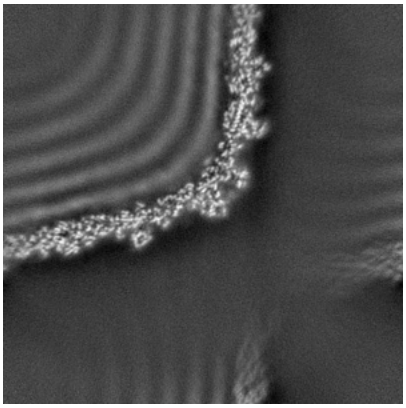
6.3.2 Raw map



X Index: 228



Y Index: 140

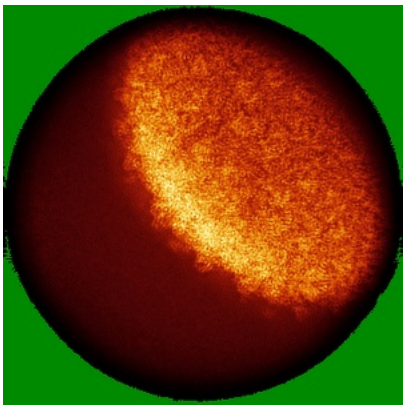


Z Index: 180

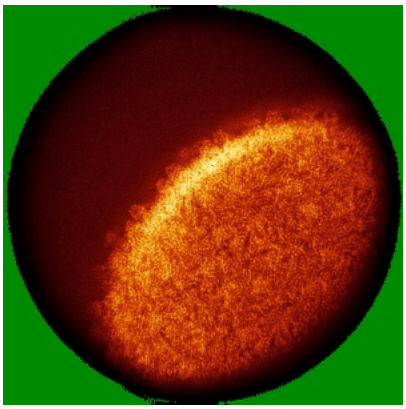
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) (i)

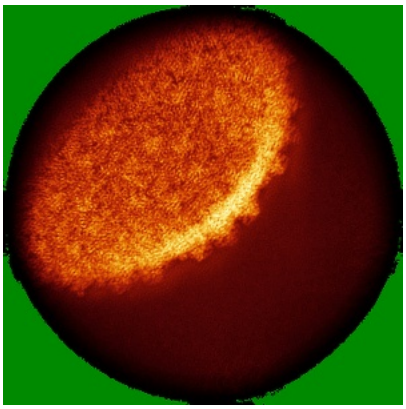
6.4.1 Primary map



X

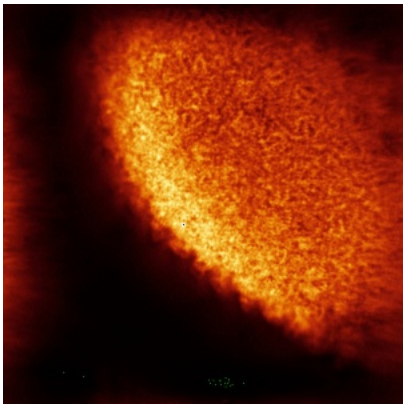


Y

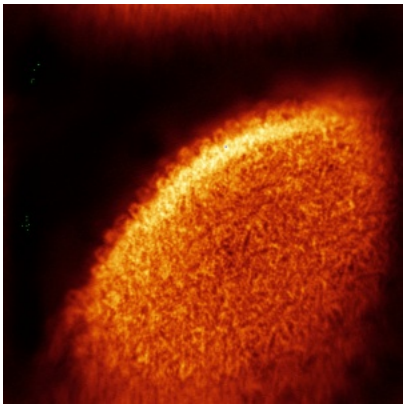


Z

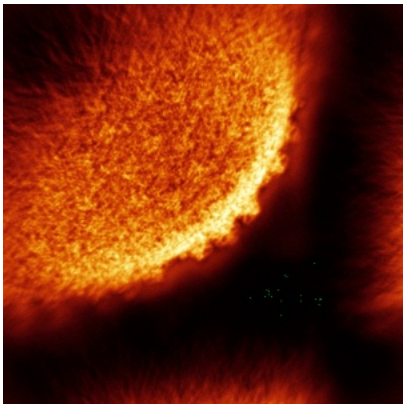
6.4.2 Raw map



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)

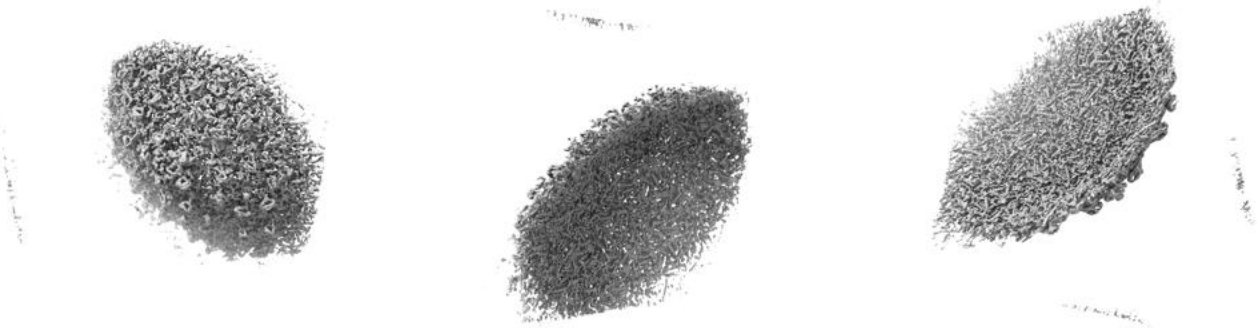
6.5.1 Primary map



X Y Z

The images above show the 3D surface view of the map at the recommended contour level 0.544. 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.

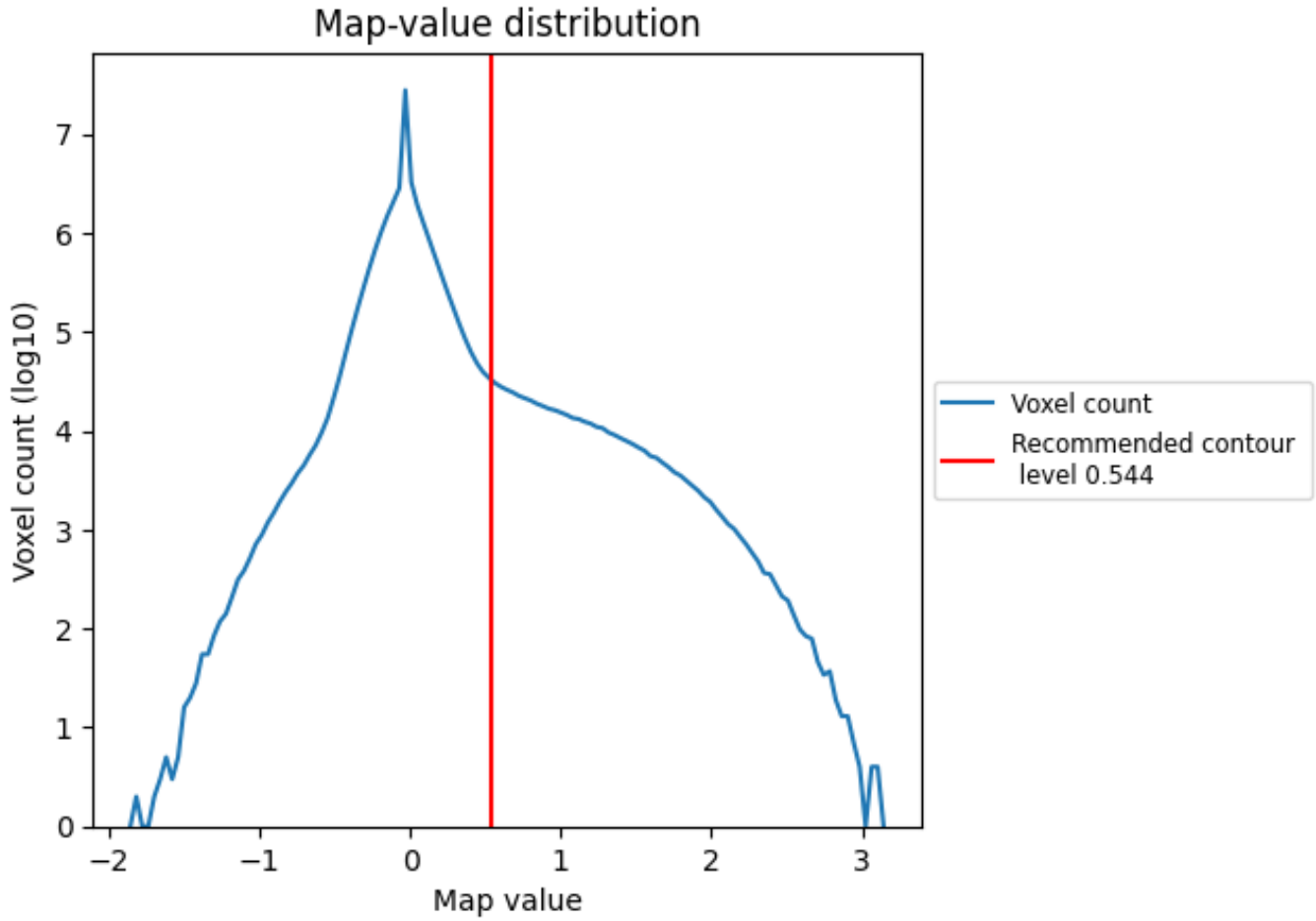
6.6 Mask visualisation (i)

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

7 Map analysis

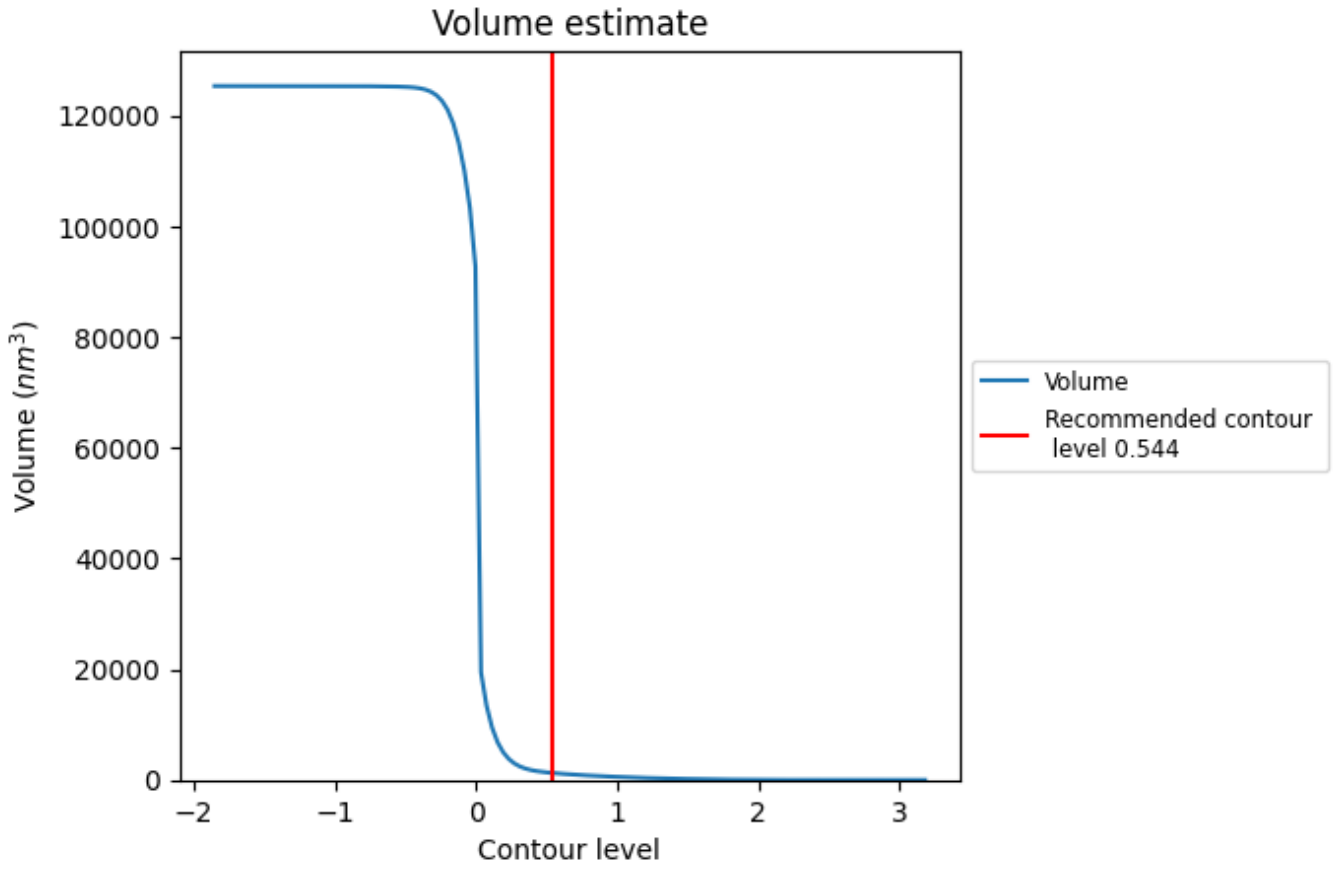
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution



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.

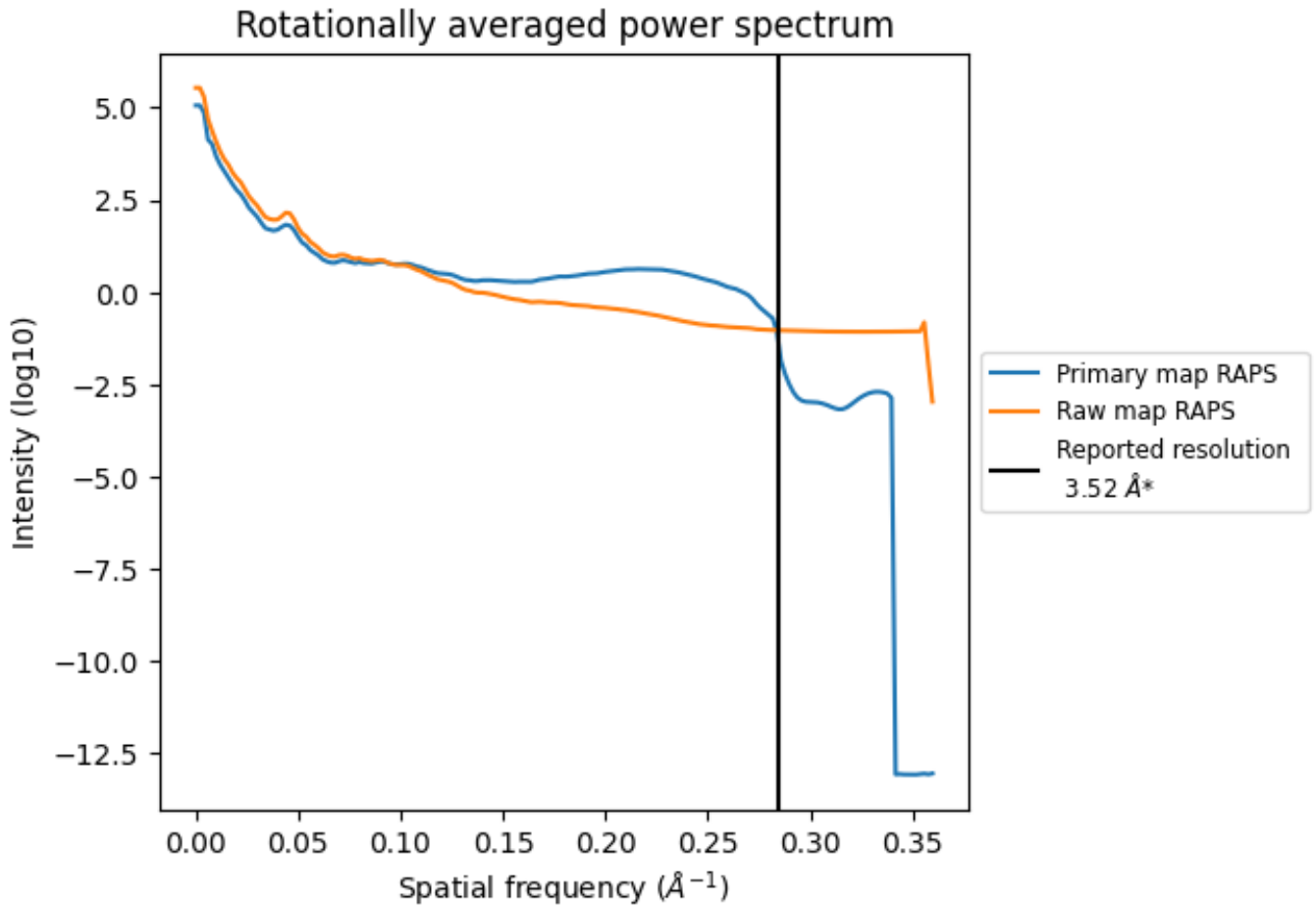
7.2 Volume estimate



The volume at the recommended contour level is 1251 nm^3; this corresponds to an approximate mass of 1130 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)

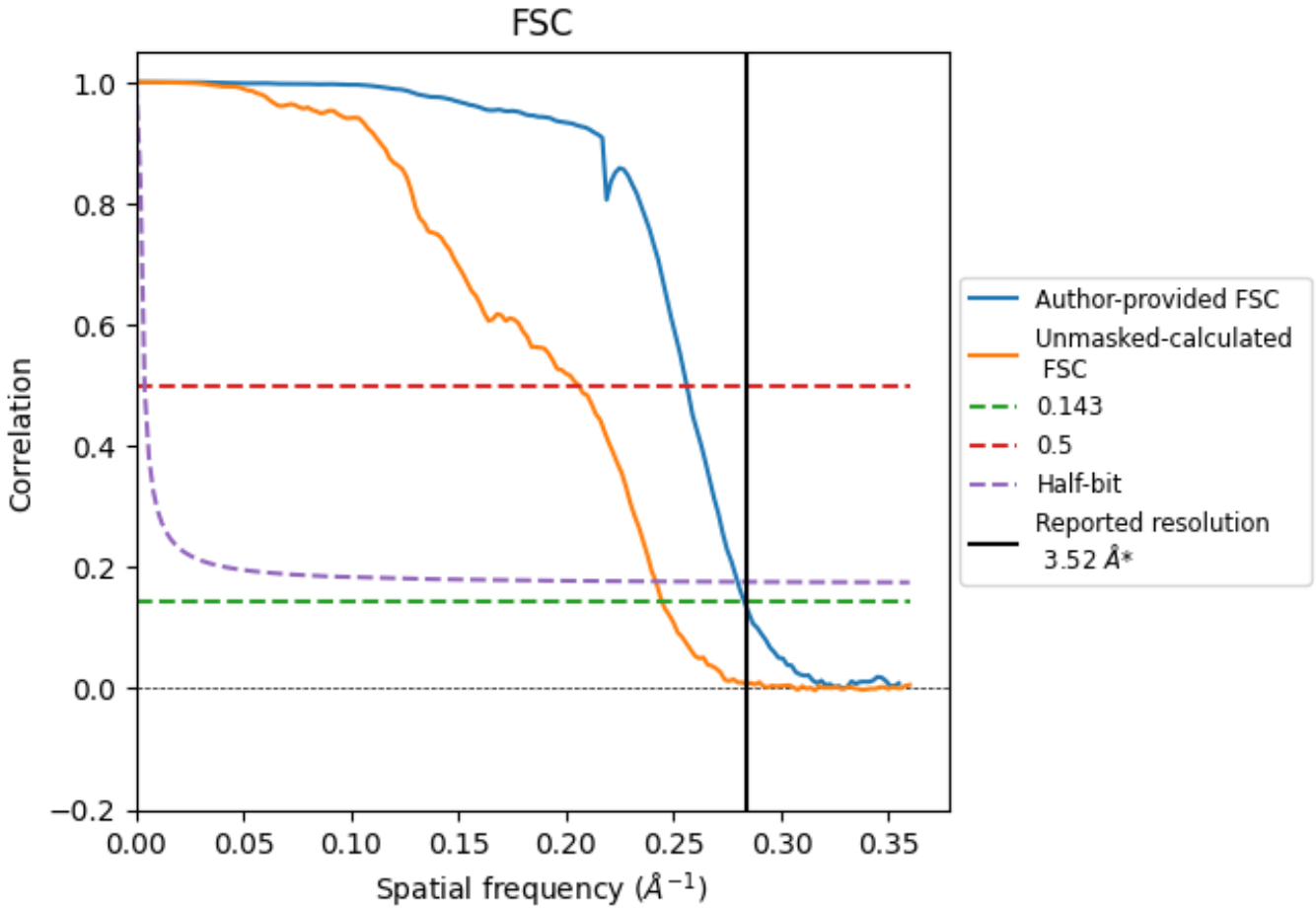


*Reported resolution corresponds to spatial frequency of 0.284 $Å^{-1}$

8 Fourier-Shell correlation

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



*Reported resolution corresponds to spatial frequency of 0.284 Å^{-1}

8.2 Resolution estimates (i)

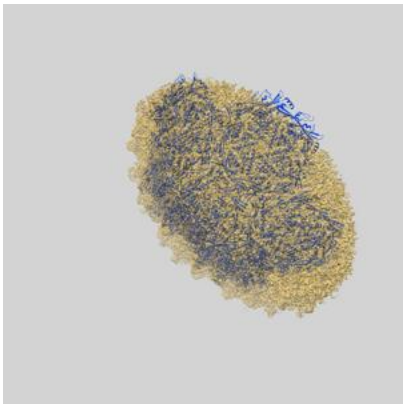
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.52	-	-
Author-provided FSC curve	3.54	3.90	3.58
Unmasked-calculated*	4.09	4.86	4.14

*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 4.09 differs from the reported value 3.52 by more than 10 %

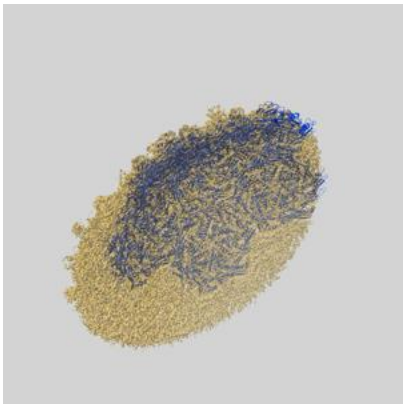
9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-80026 and PDB model 25DE. Per-residue inclusion information can be found in section 3 on page 7.

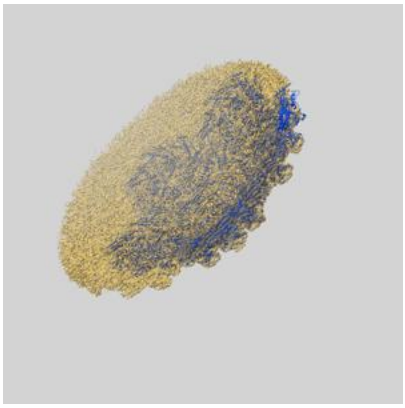
9.1 Map-model overlay



X



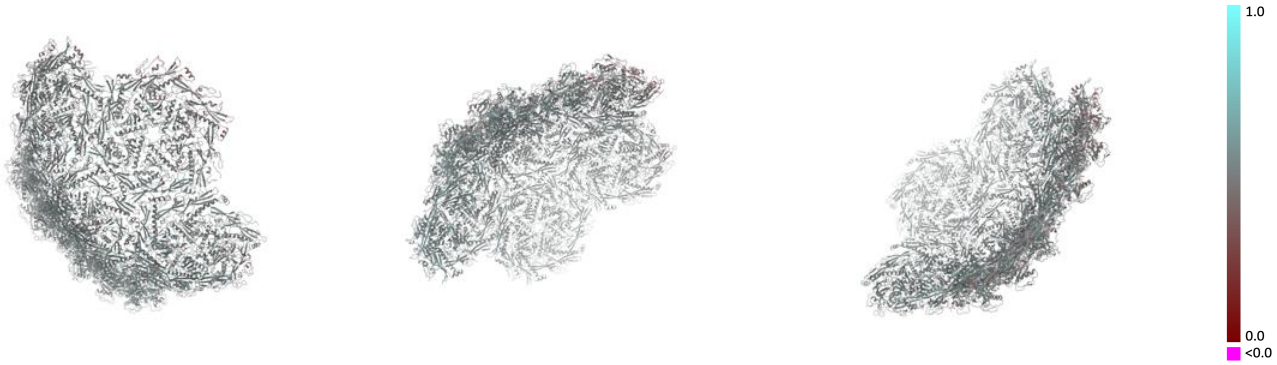
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.544 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.

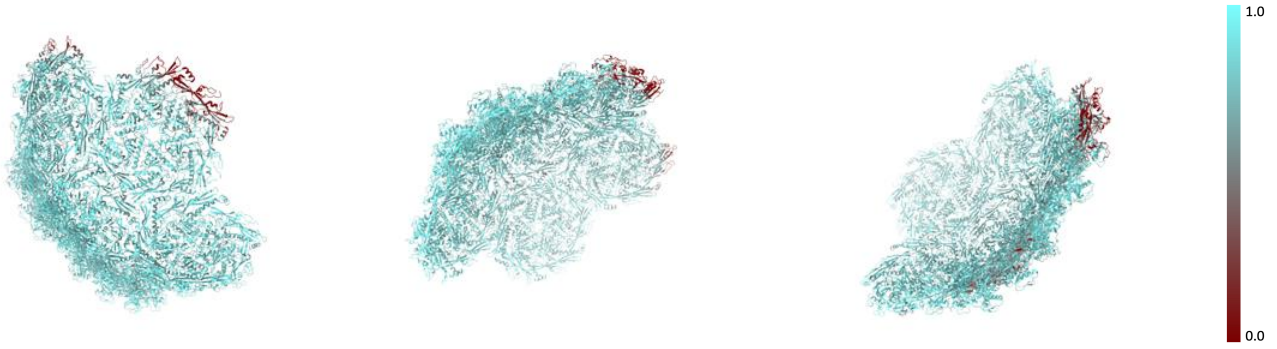
9.2 Q-score mapped to coordinate model (i)



X Y Z

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

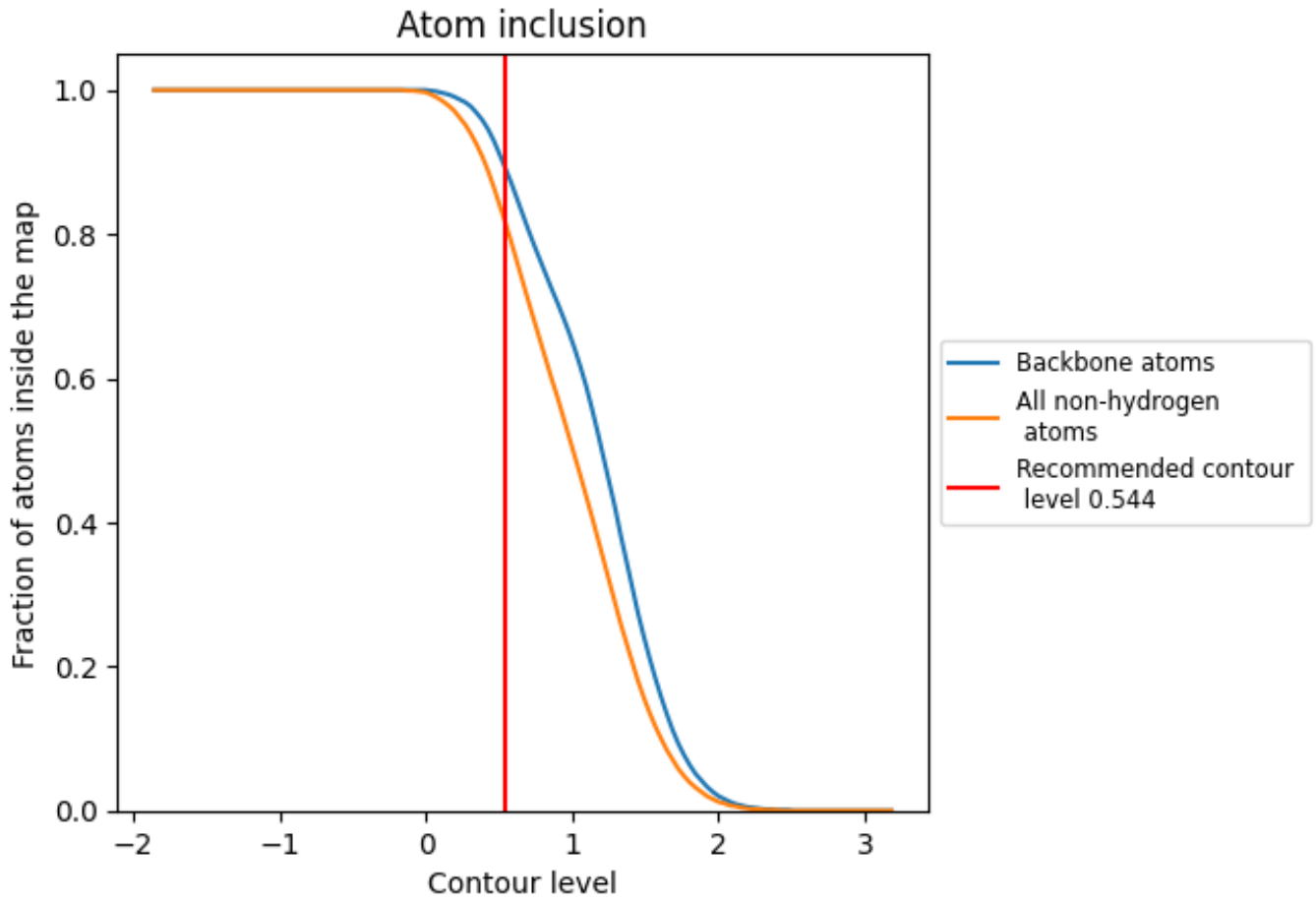
9.3 Atom inclusion mapped to coordinate model (i)



X Y Z

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 (0.544).

9.4 Atom inclusion (i)



At the recommended contour level, 89% of all backbone atoms, 82% 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 (0.544) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.8160	0.5050
A	0.8440	0.5050
B	0.8360	0.5090
C	0.8340	0.5010
D	0.8400	0.5030
E	0.8310	0.5030
F	0.8540	0.5110
G	0.8460	0.5120
H	0.8470	0.5140
I	0.8380	0.5040
J	0.8370	0.5070
K	0.8450	0.5120
L	0.8470	0.5150
M	0.8540	0.5220
N	0.8510	0.5240
O	0.8560	0.5240
P	0.8620	0.5180
Q	0.8530	0.5160
R	0.8630	0.5110
S	0.8540	0.5090
T	0.8260	0.5000
U	0.8280	0.5030
V	0.8470	0.5140
W	0.8560	0.5180
X	0.8380	0.5080
Y	0.7910	0.4940
Z	0.6450	0.4730
a	0.5740	0.4660
b	0.7240	0.4850
c	0.8280	0.5070
d	0.8370	0.5050
e	0.8230	0.5030
f	0.7590	0.4960
g	0.7280	0.4840
h	0.7570	0.4910
i	0.8200	0.5020

