



Full wwPDB EM Validation Report ⓘ

Mar 10, 2026 – 02:34 AM UTC

PDB ID : 6MWC / pdb_00006mwc
EMDB ID : EMD-9275
Title : CryoEM structure of chimeric Eastern Equine Encephalitis Virus with Fab of
EEEV-5 antibody
Authors : Hasan, S.S.; Sun, C.; Kim, A.S.; Watanabe, Y.; Chen, C.L.; Klose, T.; Buda,
G.; Crispin, M.; Diamond, M.S.; Klimstra, W.B.; Rossmann, M.G.
Deposited on : 2018-10-29
Resolution : 7.50 Å(reported)

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

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

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

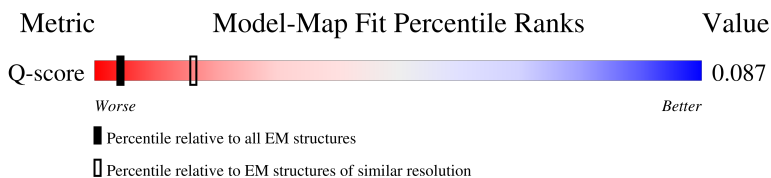
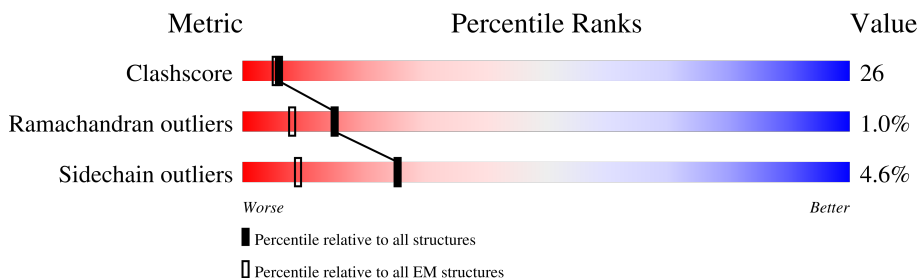
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 7.50 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.



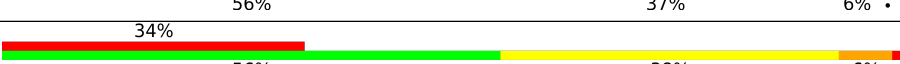
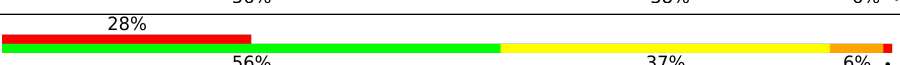
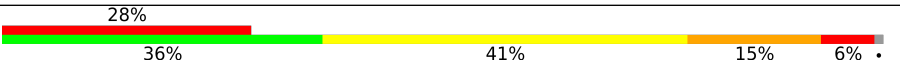
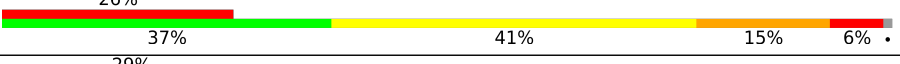
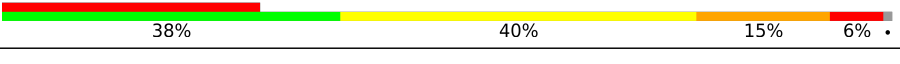
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	436 (7.00 - 8.00)

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

Mol	Chain	Length	Quality of chain
1	A	441	 6% 70% 20% 9%
1	E	441	 9% 71% 19% 9%
1	I	441	 1% 71% 19% 9%
1	M	441	 10% 71% 19% 9%

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
2	B	420	
2	F	420	
2	J	420	
2	N	420	
3	C	218	
3	G	218	
3	K	218	
3	O	218	
4	D	214	
4	H	214	
4	L	214	
4	P	214	

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 35528 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 E1.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	400	Total	C	N	O	S	0	0
			3063	1940	511	592	20		
1	E	400	Total	C	N	O	S	0	0
			3063	1940	511	592	20		
1	I	400	Total	C	N	O	S	0	0
			3063	1940	511	592	20		
1	M	400	Total	C	N	O	S	0	0
			3063	1940	511	592	20		

- Molecule 2 is a protein called E2.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	325	Total	C	N	O	S	0	0
			2550	1601	471	462	16		
2	F	325	Total	C	N	O	S	0	0
			2550	1601	471	462	16		
2	J	325	Total	C	N	O	S	0	0
			2550	1601	471	462	16		
2	N	325	Total	C	N	O	S	0	0
			2550	1601	471	462	16		

- Molecule 3 is a protein called EEEV-5 antibody heavy chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	218	Total	C	N	O	S	0	0
			1671	1066	272	326	7		
3	G	218	Total	C	N	O	S	0	0
			1671	1066	272	326	7		
3	K	218	Total	C	N	O	S	0	0
			1671	1066	272	326	7		
3	O	218	Total	C	N	O	S	0	0
			1671	1066	272	326	7		

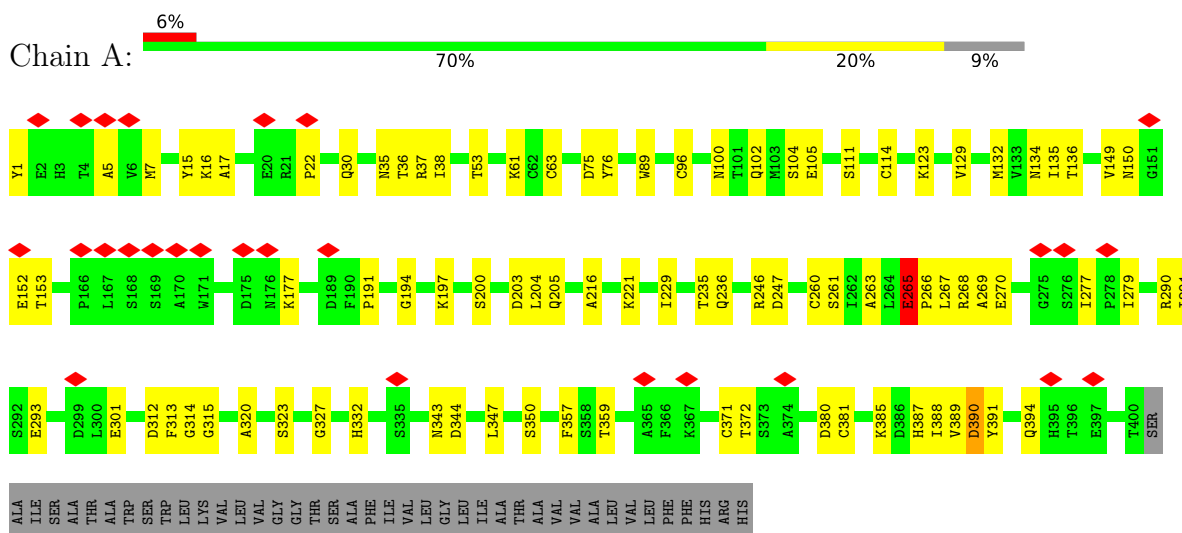
- Molecule 4 is a protein called EEEV-5 antibody light chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	D	211	Total	C	N	O	S	0	0
			1598	999	270	322	7		
4	H	211	Total	C	N	O	S	0	0
			1598	999	270	322	7		
4	L	211	Total	C	N	O	S	0	0
			1598	999	270	322	7		
4	P	211	Total	C	N	O	S	0	0
			1598	999	270	322	7		

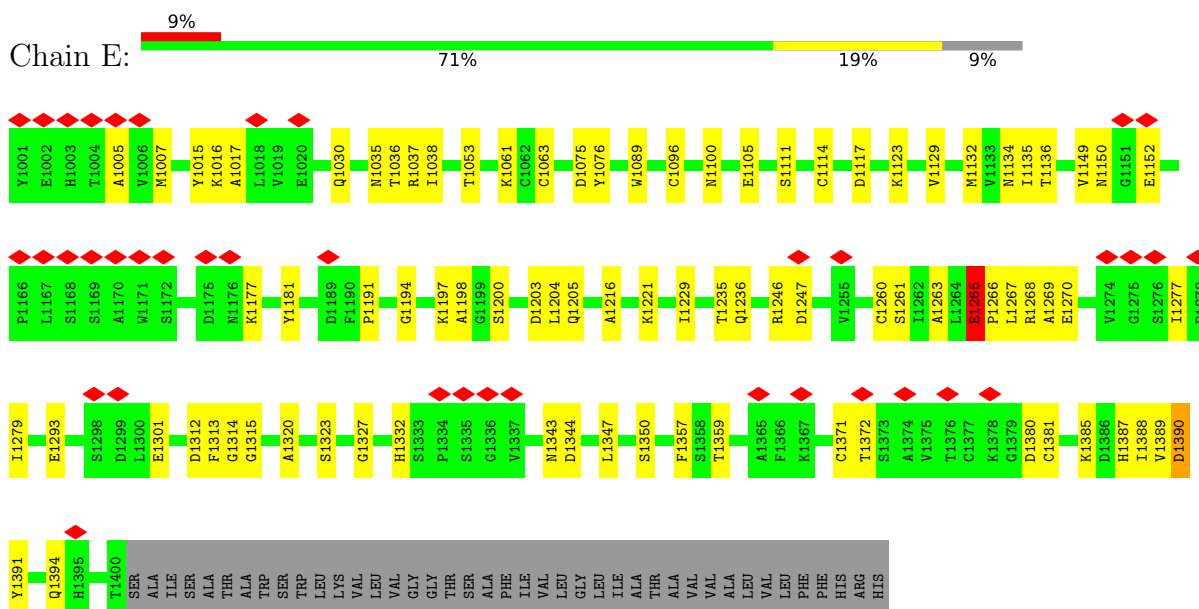
3 Residue-property plots

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

• Molecule 1: E1

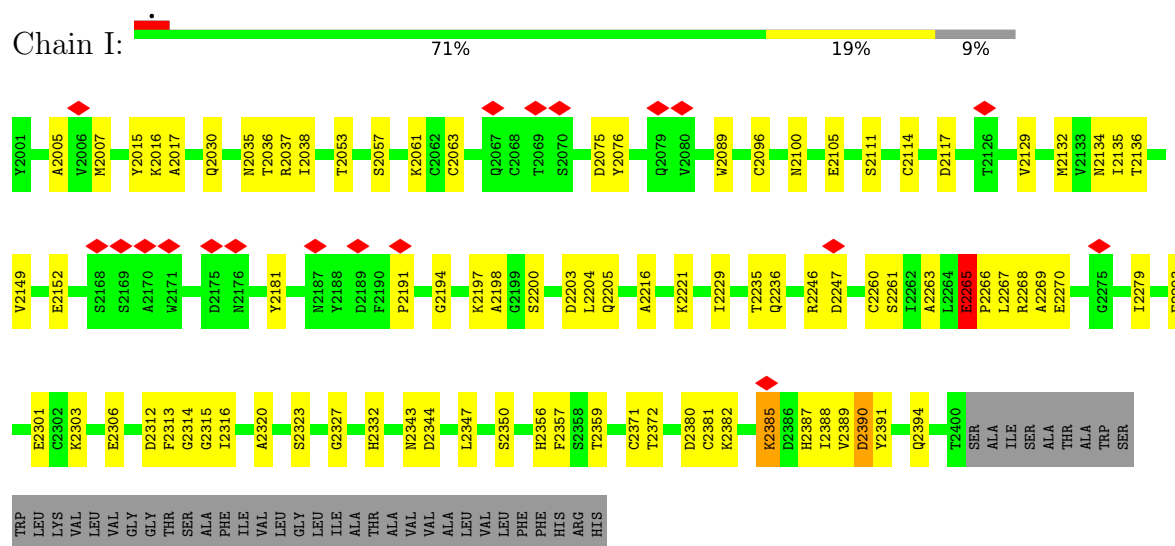


• Molecule 1: E1



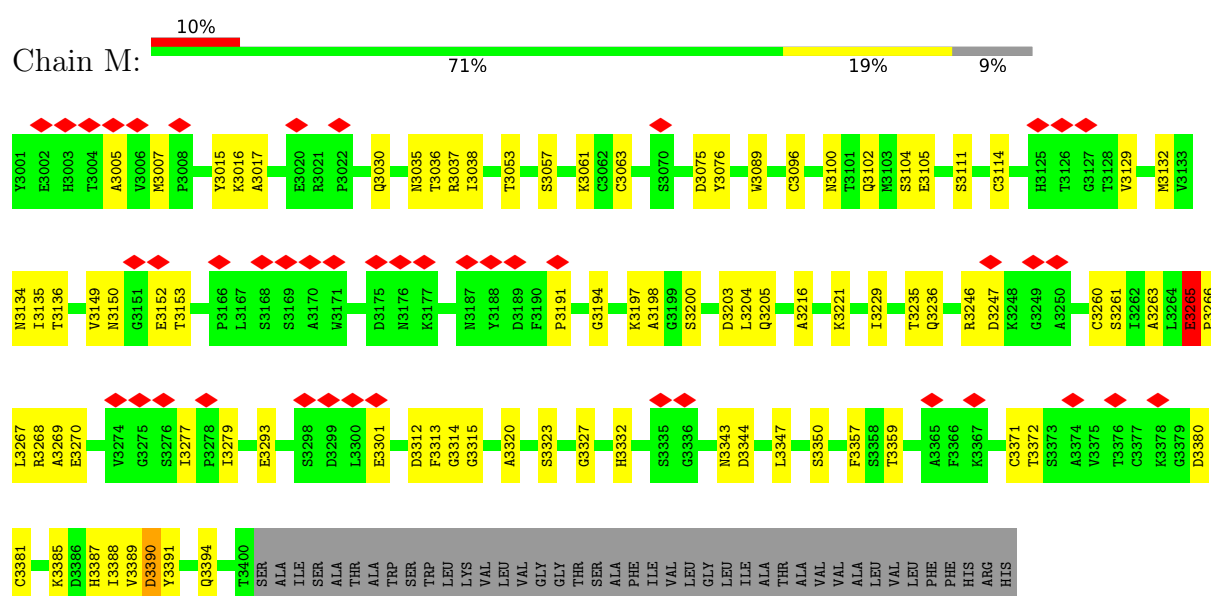
• Molecule 1: E1

Chain I:



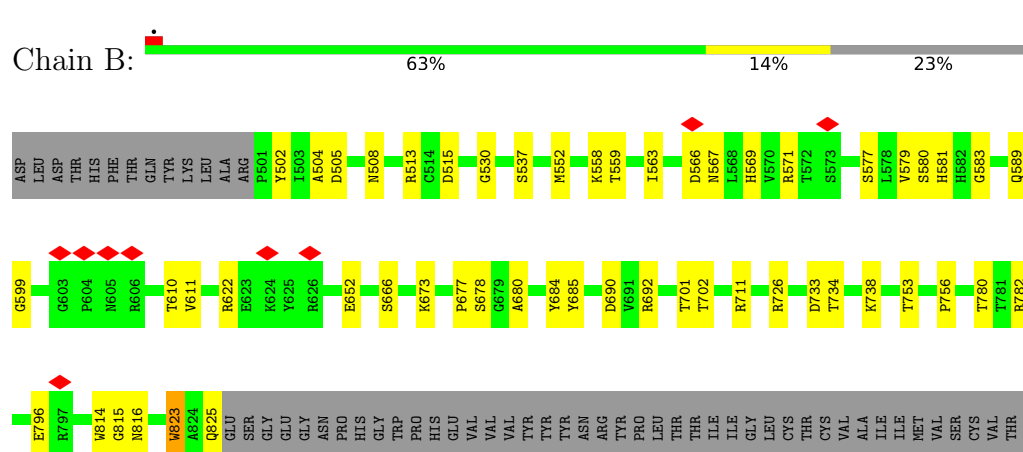
• Molecule 1: E1

Chain M:



• Molecule 2: E2

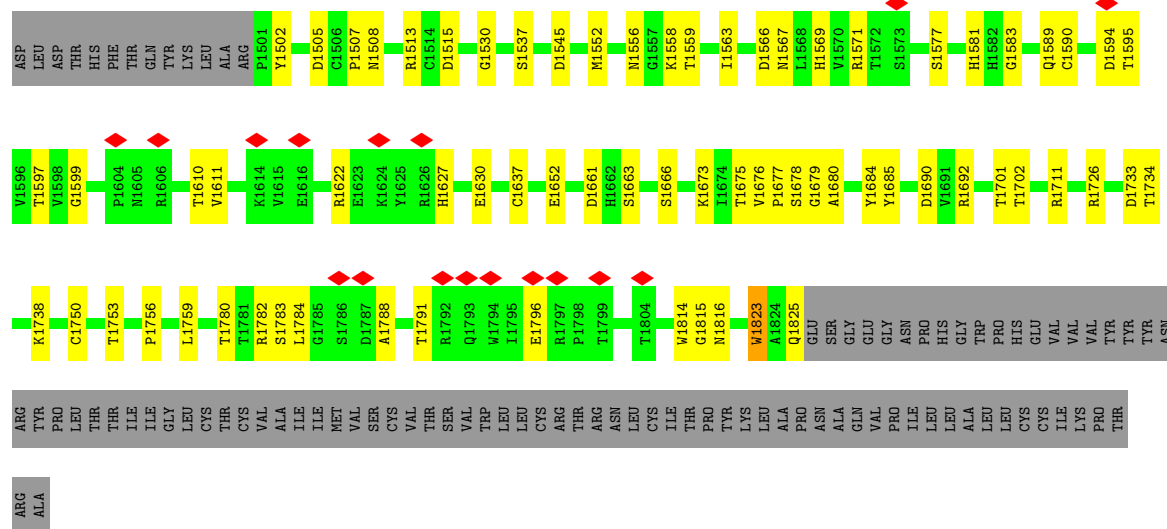
Chain B:



ARG THR ARG ASP THR ARG
ASN THR LEU CYS
TLE THR PRO THR
LYS LEU ALA
PRO ASN
ALA VAL
Gln VAL
PRO THR
TLE LEU
LEU ALA
LEU LEU
CYS CYS
TLE LYS
PRO LYS
THR ARG
ALA

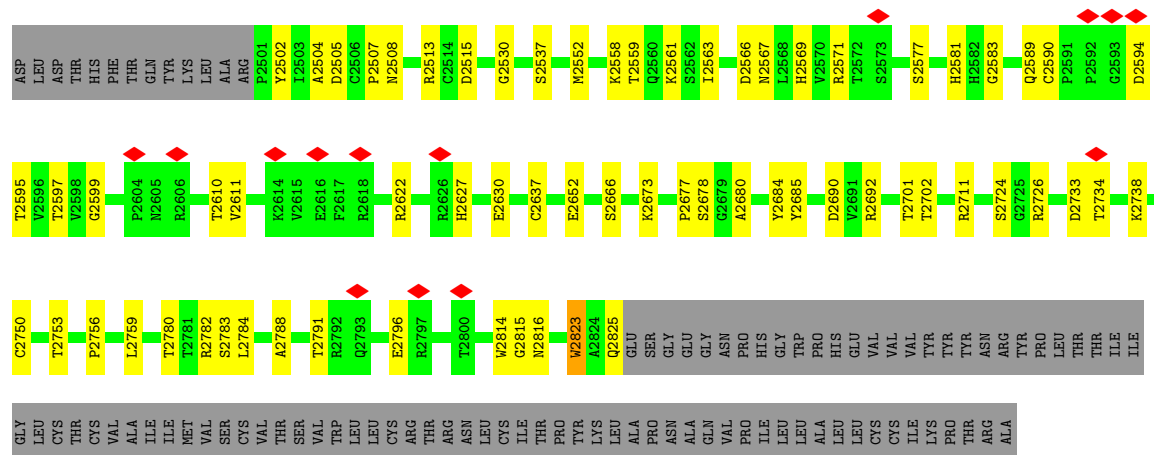
• Molecule 2: E2

Chain F:  60% 17% 23%



• Molecule 2: E2

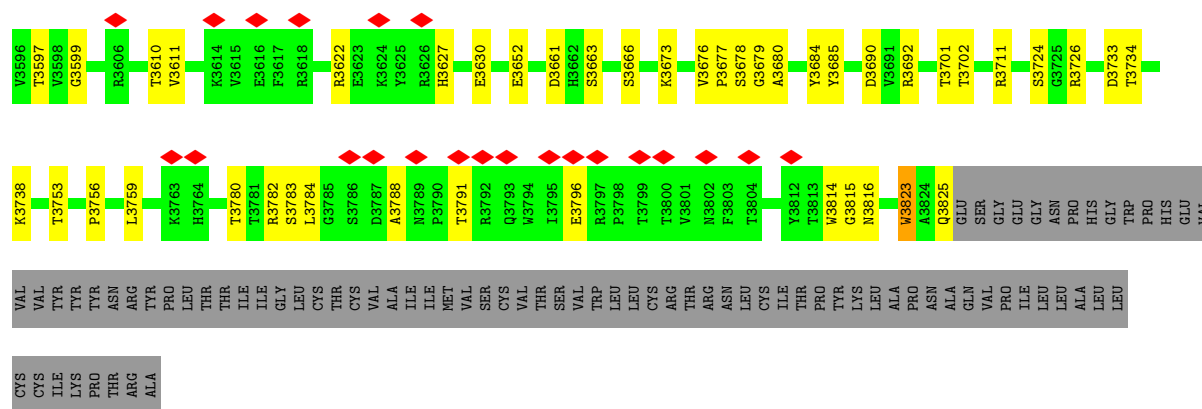
Chain J:  61% 16% 23%



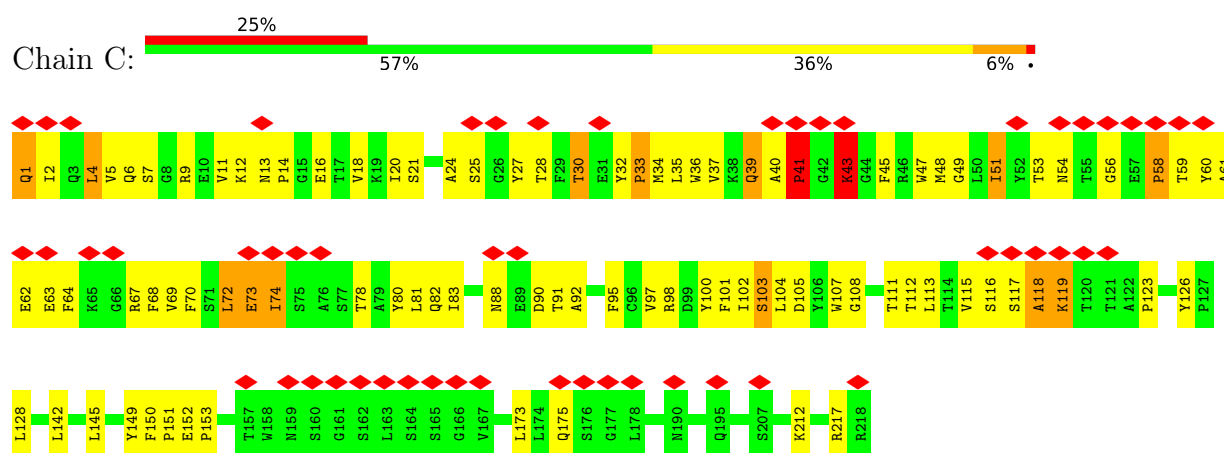
• Molecule 2: E2

Chain N:  6% 61% 23%

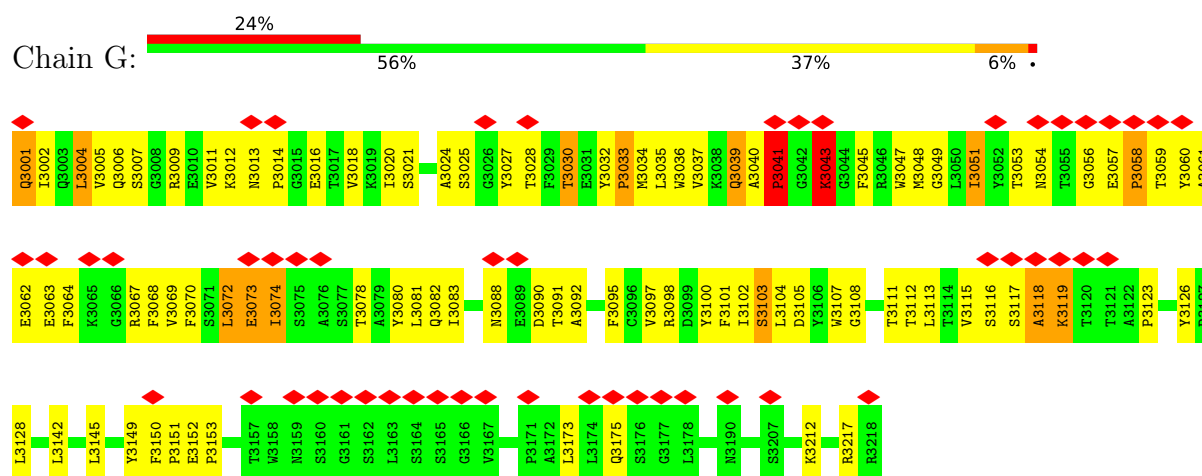




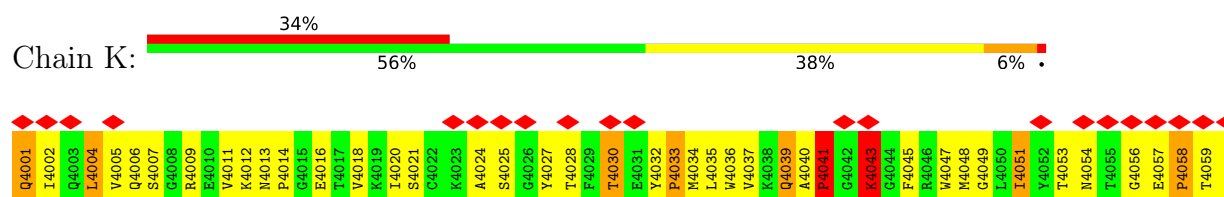
- Molecule 3: EEEV-5 antibody heavy chain

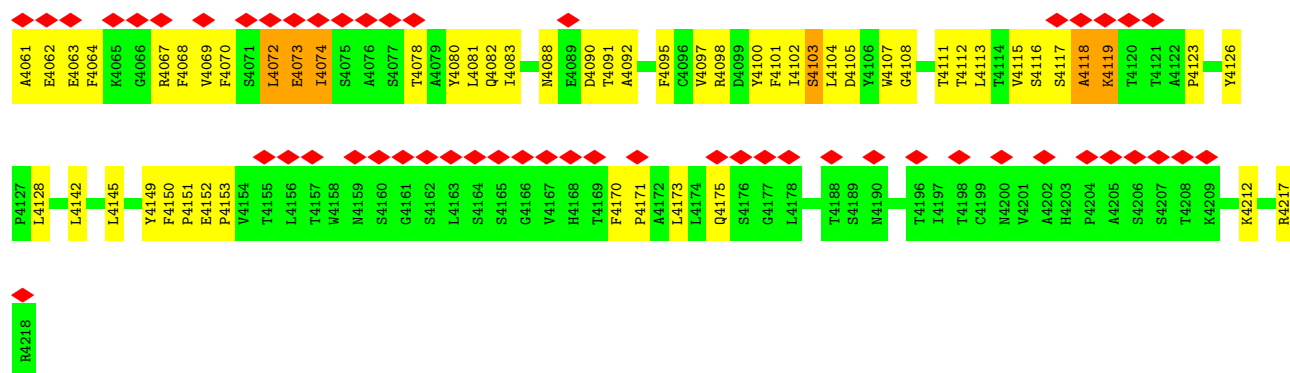


- Molecule 3: EEEV-5 antibody heavy chain

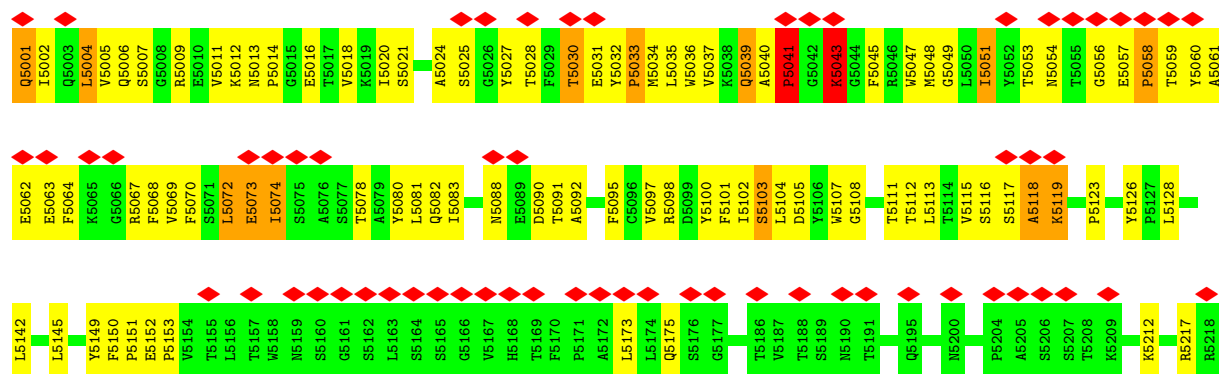


- Molecule 3: EEEV-5 antibody heavy chain

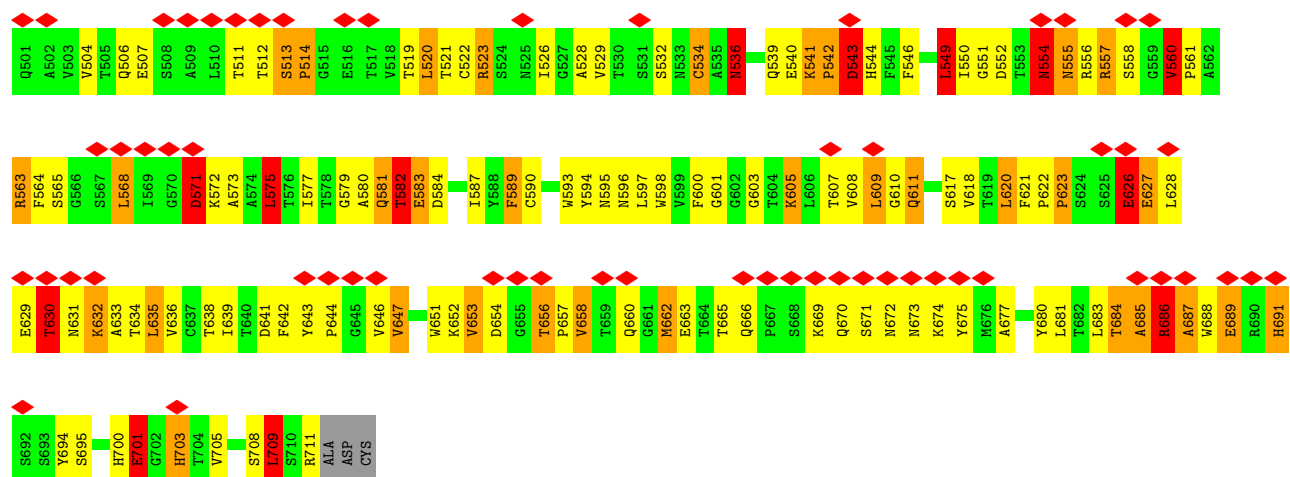




• Molecule 3: EEEV-5 antibody heavy chain

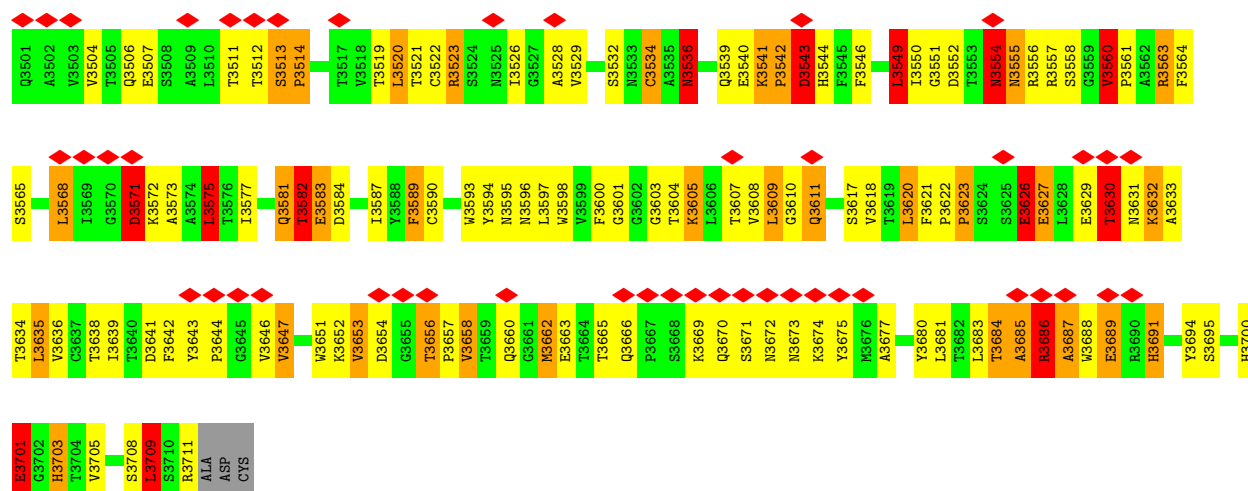


• Molecule 4: EEEV-5 antibody light chain

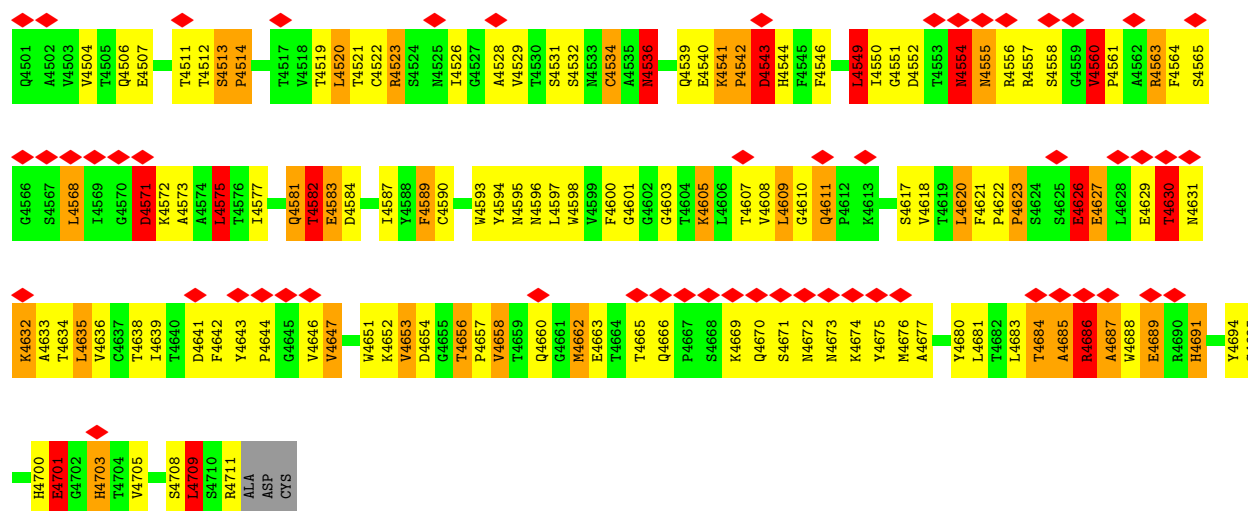


• Molecule 4: EEEV-5 antibody light chain

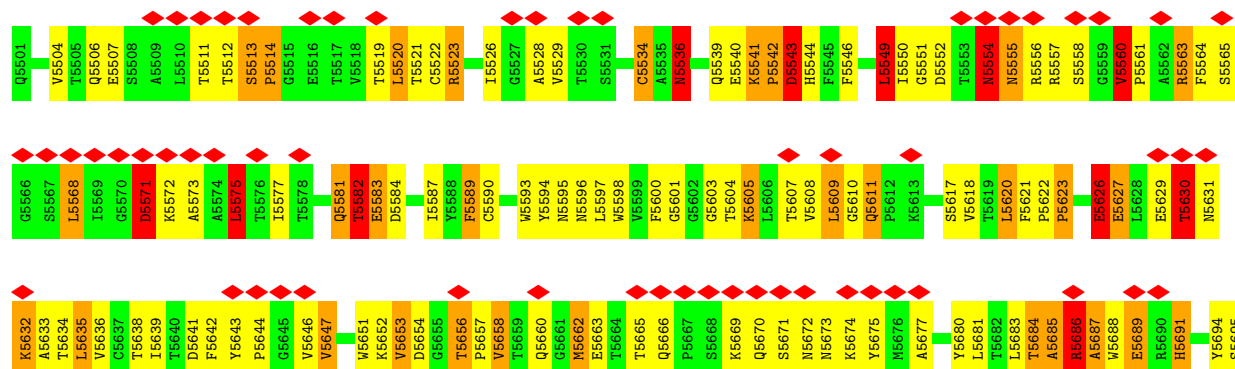


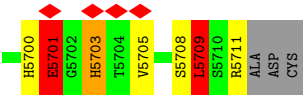


• Molecule 4: EEV-5 antibody light chain



• Molecule 4: EEV-5 antibody light chain





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	6583	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	31	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	5.851	Depositor
Minimum map value	-6.792	Depositor
Average map value	0.054	Depositor
Map value standard deviation	0.754	Depositor
Recommended contour level	0.7	Depositor
Map size (Å)	907.2, 907.2, 907.2	wwPDB
Map dimensions	560, 560, 560	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.62, 1.62, 1.62	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	0.44	0/3147	0.63	1/4294 (0.0%)
1	E	0.44	0/3147	0.63	1/4294 (0.0%)
1	I	0.44	0/3147	0.63	1/4294 (0.0%)
1	M	0.44	0/3147	0.63	1/4294 (0.0%)
2	B	0.43	0/2624	0.64	2/3571 (0.1%)
2	F	0.43	0/2624	0.64	2/3571 (0.1%)
2	J	0.43	0/2624	0.64	2/3571 (0.1%)
2	N	0.43	0/2624	0.64	2/3571 (0.1%)
3	C	0.84	5/1714 (0.3%)	1.15	12/2340 (0.5%)
3	G	0.83	5/1714 (0.3%)	1.15	12/2340 (0.5%)
3	K	0.83	5/1714 (0.3%)	1.15	12/2340 (0.5%)
3	O	0.83	5/1714 (0.3%)	1.15	12/2340 (0.5%)
4	D	1.18	4/1634 (0.2%)	1.94	57/2232 (2.6%)
4	H	1.18	4/1634 (0.2%)	1.94	56/2232 (2.5%)
4	L	1.18	4/1634 (0.2%)	1.94	56/2232 (2.5%)
4	P	1.18	4/1634 (0.2%)	1.94	55/2232 (2.5%)
All	All	0.71	36/36476 (0.1%)	1.09	284/49748 (0.6%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1
1	E	0	1
1	I	0	1
1	M	0	1
All	All	0	4

All (36) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	K	4058	PRO	N-CD	17.46	1.72	1.47
3	G	3058	PRO	N-CD	17.43	1.72	1.47
3	C	58	PRO	N-CD	17.42	1.72	1.47
3	O	5058	PRO	N-CD	17.36	1.72	1.47
3	C	41	PRO	N-CD	14.06	1.67	1.47
3	O	5041	PRO	N-CD	14.02	1.67	1.47
3	G	3041	PRO	N-CD	14.01	1.67	1.47
3	K	4041	PRO	N-CD	14.00	1.67	1.47
4	D	514	PRO	N-CD	13.22	1.66	1.47
4	L	4514	PRO	N-CD	13.21	1.66	1.47
4	H	3514	PRO	N-CD	13.18	1.66	1.47
4	P	5514	PRO	N-CD	13.16	1.66	1.47
3	C	14	PRO	N-CD	9.57	1.61	1.47
3	O	5014	PRO	N-CD	9.57	1.61	1.47
3	G	3014	PRO	N-CD	9.55	1.61	1.47
3	K	4014	PRO	N-CD	9.53	1.61	1.47
4	D	544	HIS	CG-CD2	9.36	1.46	1.35
4	P	5544	HIS	CG-CD2	9.30	1.46	1.35
4	H	3544	HIS	CG-CD2	9.30	1.46	1.35
4	L	4544	HIS	CG-CD2	9.24	1.46	1.35
4	H	3542	PRO	N-CD	7.07	1.57	1.47
4	D	542	PRO	N-CD	7.04	1.57	1.47
4	P	5542	PRO	N-CD	7.03	1.57	1.47
4	L	4542	PRO	N-CD	7.00	1.57	1.47
3	C	33	PRO	N-CD	6.25	1.56	1.47
3	O	5033	PRO	N-CD	6.25	1.56	1.47
3	K	4033	PRO	N-CD	6.24	1.56	1.47
3	G	3033	PRO	N-CD	6.22	1.56	1.47
4	H	3544	HIS	CD2-NE2	-5.20	1.32	1.37
4	L	4544	HIS	CD2-NE2	-5.19	1.32	1.37
3	C	108	GLY	C-N	5.16	1.41	1.33
4	D	544	HIS	CD2-NE2	-5.15	1.32	1.37
4	P	5544	HIS	CD2-NE2	-5.15	1.32	1.37
3	G	3108	GLY	C-N	5.14	1.41	1.33
3	O	5108	GLY	C-N	5.12	1.41	1.33
3	K	4108	GLY	C-N	5.10	1.41	1.33

All (284) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	H	3701	GLU	CB-CG-CD	12.67	134.14	112.60
4	P	5701	GLU	CB-CG-CD	12.66	134.12	112.60
4	D	701	GLU	CB-CG-CD	12.65	134.11	112.60

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	L	4701	GLU	CB-CG-CD	12.65	134.10	112.60
4	L	4658	VAL	N-CA-C	-9.04	100.00	110.21
4	P	5658	VAL	N-CA-C	-9.04	100.00	110.21
4	D	658	VAL	N-CA-C	-9.00	100.04	110.21
4	H	3658	VAL	N-CA-C	-8.98	100.06	110.21
4	H	3703	HIS	CA-CB-CG	-8.56	105.24	113.80
4	D	703	HIS	CA-CB-CG	-8.52	105.28	113.80
4	L	4703	HIS	CA-CB-CG	-8.52	105.28	113.80
4	P	5703	HIS	CA-CB-CG	-8.52	105.28	113.80
4	H	3575	LEU	CA-C-O	-8.08	111.66	120.30
4	L	4575	LEU	CA-C-O	-8.07	111.66	120.30
4	D	575	LEU	CA-C-O	-8.07	111.67	120.30
4	P	5575	LEU	CA-C-O	-8.04	111.70	120.30
4	D	674	LYS	CA-C-O	-7.82	111.72	121.88
4	L	4674	LYS	CA-C-O	-7.82	111.72	121.88
4	P	5674	LYS	CA-C-O	-7.81	111.73	121.88
4	H	3674	LYS	CA-C-O	-7.79	111.75	121.88
4	P	5658	VAL	CB-CA-C	7.78	120.16	111.45
4	D	658	VAL	CB-CA-C	7.76	120.14	111.45
4	H	3658	VAL	CB-CA-C	7.76	120.14	111.45
4	L	4658	VAL	CB-CA-C	7.75	120.13	111.45
4	L	4627	GLU	CB-CG-CD	7.50	125.35	112.60
4	D	627	GLU	CB-CG-CD	7.50	125.34	112.60
4	H	3627	GLU	CB-CG-CD	7.49	125.34	112.60
4	P	5627	GLU	CB-CG-CD	7.49	125.34	112.60
4	H	3589	PHE	CA-C-O	-7.27	113.00	120.71
4	P	5589	PHE	CA-C-O	-7.26	113.01	120.71
4	D	589	PHE	CA-C-O	-7.26	113.02	120.71
4	L	4589	PHE	CA-C-O	-7.25	113.03	120.71
4	P	5541	LYS	CA-C-O	-7.02	113.60	120.97
4	H	3541	LYS	CA-C-O	-6.99	113.63	120.97
4	L	4541	LYS	CA-C-O	-6.97	113.65	120.97
4	D	541	LYS	CA-C-O	-6.92	113.71	120.97
4	D	701	GLU	N-CA-CB	6.88	122.11	110.49
4	P	5701	GLU	N-CA-CB	6.85	122.07	110.49
4	H	3701	GLU	N-CA-CB	6.85	122.06	110.49
1	E	1265	GLU	N-CA-C	-6.84	94.68	109.81
4	L	4701	GLU	N-CA-CB	6.84	122.06	110.49
1	A	265	GLU	N-CA-C	-6.83	94.72	109.81
1	I	2265	GLU	N-CA-C	-6.82	94.74	109.81
1	M	3265	GLU	N-CA-C	-6.82	94.74	109.81
4	H	3687	ALA	N-CA-C	-6.82	103.85	111.28

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	L	4687	ALA	N-CA-C	-6.81	103.86	111.28
4	D	687	ALA	N-CA-C	-6.80	103.87	111.28
4	P	5687	ALA	N-CA-C	-6.78	103.89	111.28
4	D	634	THR	CA-CB-OG1	-6.72	99.51	109.60
4	H	3634	THR	CA-CB-OG1	-6.72	99.53	109.60
4	L	4634	THR	CA-CB-OG1	-6.71	99.54	109.60
4	P	5634	THR	CA-CB-OG1	-6.71	99.54	109.60
4	H	3686	ARG	N-CA-C	6.64	118.31	111.14
4	L	4686	ARG	N-CA-C	6.63	118.30	111.14
3	O	5004	LEU	N-CA-C	-6.62	97.62	108.41
3	K	4004	LEU	N-CA-C	-6.62	97.62	108.41
4	P	5686	ARG	N-CA-C	6.61	118.28	111.14
4	D	686	ARG	N-CA-C	6.60	118.27	111.14
3	G	3004	LEU	N-CA-C	-6.60	97.65	108.41
3	C	4	LEU	N-CA-C	-6.60	97.66	108.41
3	O	5043	LYS	N-CA-C	6.53	124.72	110.80
3	K	4043	LYS	N-CA-C	6.53	124.70	110.80
3	C	43	LYS	N-CA-C	6.52	124.69	110.80
3	G	3043	LYS	N-CA-C	6.52	124.69	110.80
4	D	541	LYS	N-CA-C	-6.51	101.87	110.40
4	H	3541	LYS	N-CA-C	-6.51	101.87	110.40
4	P	5541	LYS	N-CA-C	-6.50	101.88	110.40
4	L	4541	LYS	N-CA-C	-6.49	101.89	110.40
3	G	3030	THR	N-CA-C	6.47	120.43	112.54
3	K	4030	THR	N-CA-C	6.47	120.43	112.54
3	O	5030	THR	N-CA-C	6.45	120.41	112.54
3	C	30	THR	N-CA-C	6.44	120.39	112.54
4	P	5582	THR	CA-C-O	6.42	127.36	120.10
4	D	582	THR	CA-C-O	6.42	127.35	120.10
4	L	4582	THR	CA-C-O	6.40	127.33	120.10
4	H	3582	THR	CA-C-O	6.39	127.33	120.10
4	D	560	VAL	N-CA-C	-6.18	101.15	107.89
4	L	4560	VAL	N-CA-C	-6.17	101.17	107.89
4	P	5560	VAL	N-CA-C	-6.16	101.18	107.89
4	D	635	LEU	CA-CB-CG	6.11	137.70	116.30
4	H	3560	VAL	N-CA-C	-6.11	101.23	107.89
4	P	5635	LEU	CA-CB-CG	6.10	137.66	116.30
4	H	3635	LEU	CA-CB-CG	6.10	137.64	116.30
4	L	4635	LEU	CA-CB-CG	6.10	137.63	116.30
4	H	3677	ALA	O-C-N	6.07	129.47	123.46
4	L	4677	ALA	O-C-N	6.06	129.46	123.46
4	D	677	ALA	O-C-N	6.04	129.44	123.46

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	P	5677	ALA	O-C-N	6.04	129.43	123.46
4	P	5600	PHE	CA-C-O	-5.97	114.23	121.28
4	D	600	PHE	CA-C-O	-5.95	114.26	121.28
4	L	4600	PHE	CA-C-O	-5.95	114.26	121.28
4	H	3600	PHE	CA-C-O	-5.94	114.27	121.28
4	D	536	ASN	CA-C-O	-5.92	114.42	121.11
4	H	3536	ASN	CA-C-O	-5.91	114.43	121.11
4	L	4536	ASN	CA-C-O	-5.90	114.44	121.11
4	P	5685	ALA	CA-C-N	5.89	128.46	120.44
4	P	5685	ALA	C-N-CA	5.89	128.46	120.44
4	H	3685	ALA	CA-C-N	5.88	128.44	120.44
4	H	3685	ALA	C-N-CA	5.88	128.44	120.44
4	P	5536	ASN	CA-C-O	-5.88	114.46	121.11
4	P	5511	THR	CA-C-O	-5.88	114.02	120.36
4	D	685	ALA	CA-C-N	5.87	128.43	120.44
4	D	685	ALA	C-N-CA	5.87	128.43	120.44
4	L	4685	ALA	CA-C-N	5.86	128.40	120.44
4	L	4685	ALA	C-N-CA	5.86	128.40	120.44
4	D	511	THR	CA-C-O	-5.85	114.04	120.36
4	L	4511	THR	CA-C-O	-5.84	114.06	120.36
4	H	3511	THR	CA-C-O	-5.82	114.08	120.36
3	K	4034	MET	N-CA-C	5.81	118.37	108.90
3	C	34	MET	N-CA-C	5.79	118.34	108.90
3	G	3034	MET	N-CA-C	5.79	118.34	108.90
4	H	3554	ASN	CA-C-O	-5.79	113.49	119.51
3	O	5034	MET	N-CA-C	5.78	118.33	108.90
2	F	1685	TYR	CA-CB-CG	5.78	124.30	113.90
2	B	685	TYR	CA-CB-CG	5.77	124.29	113.90
2	N	3685	TYR	CA-CB-CG	5.77	124.29	113.90
4	P	5554	ASN	CA-C-O	-5.76	113.52	119.51
2	J	2685	TYR	CA-CB-CG	5.75	124.26	113.90
4	D	554	ASN	CA-C-O	-5.75	113.53	119.51
4	L	4554	ASN	CA-C-O	-5.75	113.53	119.51
4	D	641	ASP	CA-C-O	-5.73	114.89	121.54
4	P	5641	ASP	CA-C-O	-5.73	114.89	121.54
4	L	4641	ASP	CA-C-O	-5.73	114.89	121.54
4	H	3641	ASP	CA-C-O	-5.69	114.94	121.54
3	K	4039	GLN	N-CA-C	-5.68	98.07	108.02
4	P	5611	GLN	CA-C-N	-5.68	114.10	119.89
4	P	5611	GLN	C-N-CA	-5.68	114.10	119.89
4	D	677	ALA	CA-C-O	-5.68	114.85	121.10
4	H	3611	GLN	CA-C-N	-5.68	114.10	119.89

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	H	3611	GLN	C-N-CA	-5.68	114.10	119.89
3	G	3039	GLN	N-CA-C	-5.66	98.11	108.02
4	L	4611	GLN	CA-C-N	-5.66	114.11	119.89
4	L	4611	GLN	C-N-CA	-5.66	114.11	119.89
3	O	5039	GLN	N-CA-C	-5.66	98.11	108.02
3	C	39	GLN	N-CA-C	-5.66	98.11	108.02
4	D	611	GLN	CA-C-N	-5.66	114.13	119.90
4	D	611	GLN	C-N-CA	-5.66	114.13	119.90
4	L	4677	ALA	CA-C-O	-5.65	114.89	121.10
4	P	5677	ALA	CA-C-O	-5.60	114.94	121.10
4	H	3677	ALA	CA-C-O	-5.59	114.95	121.10
4	D	634	THR	CA-CB-CG2	5.59	120.00	110.50
4	L	4647	VAL	N-CA-CB	5.59	120.67	112.35
4	D	647	VAL	N-CA-CB	5.58	120.67	112.35
4	H	3647	VAL	N-CA-CB	5.57	120.66	112.35
4	P	5634	THR	CA-CB-CG2	5.57	119.97	110.50
4	P	5647	VAL	N-CA-CB	5.57	120.65	112.35
4	H	3634	THR	CA-CB-CG2	5.55	119.94	110.50
4	L	4634	THR	CA-CB-CG2	5.55	119.94	110.50
4	P	5607	THR	CA-C-O	-5.53	114.36	120.38
4	H	3607	THR	CA-C-O	-5.52	114.36	120.38
4	L	4607	THR	CA-C-O	-5.52	114.36	120.38
4	H	3563	ARG	N-CA-C	-5.51	106.40	113.01
4	L	4656	THR	CA-CB-OG1	-5.51	101.33	109.60
4	D	656	THR	CA-CB-OG1	-5.51	101.34	109.60
3	C	111	THR	N-CA-C	-5.50	99.31	108.34
3	K	4111	THR	N-CA-C	-5.50	99.32	108.34
4	H	3701	GLU	CA-C-N	5.50	132.19	121.41
4	H	3701	GLU	C-N-CA	5.50	132.19	121.41
4	D	701	GLU	CA-C-N	5.49	132.18	121.41
4	D	701	GLU	C-N-CA	5.49	132.18	121.41
4	P	5701	GLU	CA-C-N	5.49	132.18	121.41
4	P	5701	GLU	C-N-CA	5.49	132.18	121.41
4	H	3656	THR	CA-CB-OG1	-5.49	101.36	109.60
4	L	4701	GLU	CA-C-N	5.49	132.17	121.41
4	L	4701	GLU	C-N-CA	5.49	132.17	121.41
4	P	5656	THR	CA-CB-OG1	-5.49	101.37	109.60
4	D	607	THR	CA-C-O	-5.49	114.40	120.38
3	O	5111	THR	N-CA-C	-5.49	99.34	108.34
4	L	4563	ARG	N-CA-C	-5.48	106.43	113.01
4	D	563	ARG	N-CA-C	-5.47	106.44	113.01
3	G	3111	THR	N-CA-C	-5.47	99.36	108.34

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	P	5563	ARG	N-CA-C	-5.46	106.45	113.01
4	L	4653	VAL	O-C-N	5.45	129.17	122.95
4	D	653	VAL	O-C-N	5.45	129.16	122.95
4	H	3653	VAL	O-C-N	5.45	129.16	122.95
4	P	5653	VAL	O-C-N	5.42	129.13	122.95
4	L	4617	SER	O-C-N	5.42	129.96	123.13
4	D	617	SER	O-C-N	5.40	129.94	123.13
4	H	3617	SER	O-C-N	5.39	129.92	123.13
4	P	5617	SER	O-C-N	5.38	129.91	123.13
4	H	3529	VAL	CA-C-O	-5.35	114.74	121.11
4	P	5534	CYS	CA-C-O	-5.34	115.78	122.03
4	P	5529	VAL	CA-C-O	-5.34	114.76	121.11
4	D	534	CYS	CA-C-O	-5.33	115.79	122.03
4	D	529	VAL	CA-C-O	-5.33	114.77	121.11
4	L	4534	CYS	CA-C-O	-5.33	115.80	122.03
4	H	3534	CYS	CA-C-O	-5.32	115.80	122.03
4	H	3543	ASP	CA-C-O	-5.32	112.90	120.51
4	D	543	ASP	CA-C-O	-5.32	112.90	120.51
4	L	4543	ASP	CA-C-O	-5.30	112.93	120.51
4	L	4529	VAL	CA-C-O	-5.30	114.81	121.11
4	P	5543	ASP	CA-C-O	-5.29	112.94	120.51
4	P	5555	ASN	CA-C-O	-5.27	114.72	120.36
4	D	557	ARG	CA-C-O	-5.26	116.09	121.87
4	H	3555	ASN	CA-C-O	-5.24	114.75	120.36
4	L	4555	ASN	CA-C-O	-5.23	114.76	120.36
3	C	40	ALA	CA-C-N	5.20	126.34	119.84
3	C	40	ALA	C-N-CA	5.20	126.34	119.84
4	D	555	ASN	CA-C-O	-5.20	114.79	120.36
4	L	4623	PRO	CA-C-O	-5.19	115.42	121.34
4	D	675	TYR	O-C-N	5.19	130.05	122.94
4	D	646	VAL	CA-C-O	-5.19	114.78	120.43
4	P	5630	THR	CA-CB-CG2	5.18	119.31	110.50
3	O	5040	ALA	CA-C-N	5.18	126.32	119.84
3	O	5040	ALA	C-N-CA	5.18	126.32	119.84
4	P	5571	ASP	CA-C-N	-5.18	113.82	122.21
4	P	5571	ASP	C-N-CA	-5.18	113.82	122.21
3	C	74	ILE	CA-C-O	5.18	127.25	120.78
4	D	571	ASP	CA-C-N	-5.18	113.82	122.21
4	D	571	ASP	C-N-CA	-5.18	113.82	122.21
4	D	630	THR	CA-CB-CG2	5.17	119.30	110.50
4	H	3571	ASP	CA-C-N	-5.17	113.83	122.21
4	H	3571	ASP	C-N-CA	-5.17	113.83	122.21

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	P	5513	SER	O-C-N	5.17	126.59	121.57
4	D	513	SER	O-C-N	5.17	126.58	121.57
3	G	3074	ILE	CA-C-O	5.17	127.24	120.78
4	L	4571	ASP	CA-C-N	-5.17	113.84	122.21
4	L	4571	ASP	C-N-CA	-5.17	113.84	122.21
4	H	3630	THR	CA-CB-CG2	5.17	119.28	110.50
4	L	4630	THR	CA-CB-CG2	5.17	119.28	110.50
4	P	5675	TYR	O-C-N	5.17	130.02	122.94
3	K	4074	ILE	CA-C-O	5.16	127.23	120.78
4	H	3675	TYR	O-C-N	5.16	130.01	122.94
3	O	5074	ILE	CA-C-O	5.16	127.23	120.78
4	H	3646	VAL	CA-C-O	-5.16	114.81	120.43
4	P	5646	VAL	CA-C-O	-5.16	114.81	120.43
4	L	4646	VAL	CA-C-O	-5.15	114.81	120.43
3	G	3040	ALA	CA-C-N	5.15	126.28	119.84
3	G	3040	ALA	C-N-CA	5.15	126.28	119.84
4	P	5623	PRO	CA-C-O	-5.14	115.47	121.34
4	L	4675	TYR	O-C-N	5.14	129.98	122.94
4	H	3623	PRO	CA-C-O	-5.13	115.49	121.34
4	D	568	LEU	N-CA-C	-5.13	100.54	108.90
3	K	4040	ALA	CA-C-N	5.13	126.25	119.84
3	K	4040	ALA	C-N-CA	5.13	126.25	119.84
4	P	5549	LEU	CA-C-N	5.13	130.84	122.69
4	P	5549	LEU	C-N-CA	5.13	130.84	122.69
4	L	4568	LEU	N-CA-C	-5.12	100.55	108.90
4	H	3568	LEU	N-CA-C	-5.12	100.56	108.90
4	H	3513	SER	O-C-N	5.12	126.53	121.57
4	P	5568	LEU	N-CA-C	-5.11	100.56	108.90
4	D	549	LEU	CA-C-N	5.11	130.81	122.69
4	D	549	LEU	C-N-CA	5.11	130.81	122.69
4	D	623	PRO	CA-C-O	-5.11	115.51	121.34
4	P	5709	LEU	CB-CA-C	5.11	118.91	109.71
4	L	4549	LEU	CA-C-N	5.10	130.80	122.69
4	L	4549	LEU	C-N-CA	5.10	130.80	122.69
4	D	709	LEU	CB-CA-C	5.10	118.89	109.71
4	L	4513	SER	O-C-N	5.09	126.51	121.57
4	L	4709	LEU	CB-CA-C	5.09	118.87	109.71
4	H	3549	LEU	CA-C-N	5.09	130.78	122.69
4	H	3549	LEU	C-N-CA	5.09	130.78	122.69
3	G	3059	THR	N-CA-C	-5.08	101.40	109.59
3	K	4001	GLN	CA-C-O	-5.08	112.16	120.80
3	C	59	THR	N-CA-C	-5.08	101.41	109.59

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	K	4059	THR	N-CA-C	-5.08	101.41	109.59
4	P	5623	PRO	N-CA-C	-5.08	103.22	111.14
4	D	557	ARG	N-CA-C	-5.08	103.78	110.43
3	O	5001	GLN	CA-C-O	-5.08	112.17	120.80
4	D	647	VAL	CA-CB-CG1	5.08	119.03	110.40
3	K	4056	GLY	O-C-N	-5.08	116.51	122.50
3	O	5059	THR	N-CA-C	-5.08	101.42	109.59
4	H	3709	LEU	CB-CA-C	5.07	118.84	109.71
3	C	1	GLN	CA-C-O	-5.07	112.18	120.80
3	G	3056	GLY	O-C-N	-5.07	116.52	122.50
4	D	623	PRO	N-CA-C	-5.07	103.23	111.14
4	L	4623	PRO	N-CA-C	-5.07	103.23	111.14
2	J	2823	TRP	CA-CB-CG	5.07	123.23	113.60
4	P	5647	VAL	CA-CB-CG1	5.06	119.01	110.40
3	O	5056	GLY	O-C-N	-5.06	116.53	122.50
4	H	3623	PRO	N-CA-C	-5.06	103.25	111.14
4	L	4647	VAL	CA-CB-CG1	5.06	119.00	110.40
2	N	3823	TRP	CA-CB-CG	5.06	123.21	113.60
3	C	56	GLY	O-C-N	-5.05	116.54	122.50
4	L	4626	GLU	CB-CG-CD	5.05	121.19	112.60
3	G	3001	GLN	CA-C-O	-5.05	112.22	120.80
4	L	4560	VAL	O-C-N	5.05	125.95	121.41
2	B	823	TRP	CA-CB-CG	5.05	123.19	113.60
4	H	3647	VAL	CA-CB-CG1	5.05	118.98	110.40
4	H	3560	VAL	O-C-N	5.04	125.95	121.41
4	H	3626	GLU	CB-CG-CD	5.03	121.15	112.60
2	F	1823	TRP	CA-CB-CG	5.03	123.16	113.60
4	P	5626	GLU	CB-CG-CD	5.03	121.15	112.60
4	D	626	GLU	CB-CG-CD	5.02	121.13	112.60

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	385	LYS	Peptide
1	E	1385	LYS	Peptide
1	I	2385	LYS	Peptide
1	M	3385	LYS	Peptide

5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3063	0	2950	85	0
1	E	3063	0	2947	66	0
1	I	3063	0	2945	76	0
1	M	3063	0	2947	58	0
2	B	2550	0	2491	60	0
2	F	2550	0	2489	102	0
2	J	2550	0	2493	98	0
2	N	2550	0	2493	74	0
3	C	1671	0	1641	210	0
3	G	1671	0	1638	217	0
3	K	1671	0	1638	218	0
3	O	1671	0	1638	226	0
4	D	1598	0	1524	200	0
4	H	1598	0	1523	225	0
4	L	1598	0	1525	226	0
4	P	1598	0	1526	198	0
All	All	35528	0	34408	1843	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 26.

All (1843) 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)
3:K:4118:ALA:HB3	3:K:4150:PHE:CE2	1.17	1.66
3:G:3118:ALA:HB3	3:G:3150:PHE:CE2	1.17	1.66
3:O:5118:ALA:HB3	3:O:5150:PHE:CE2	1.17	1.66
3:C:118:ALA:HB3	3:C:150:PHE:CE2	1.17	1.65
3:C:32:TYR:HE1	3:C:100:TYR:CD1	1.00	1.64
3:O:5032:TYR:HE1	3:O:5100:TYR:CD1	1.00	1.63
3:K:4032:TYR:HE1	3:K:4100:TYR:CD1	1.00	1.63
3:G:3032:TYR:HE1	3:G:3100:TYR:CD1	1.00	1.60
3:G:3032:TYR:CE1	3:G:3100:TYR:CD1	1.86	1.58
3:K:4032:TYR:CE1	3:K:4100:TYR:CD1	1.86	1.56
3:O:5032:TYR:CE1	3:O:5100:TYR:CD1	1.86	1.56

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:32:TYR:CE1	3:C:100:TYR:CD1	1.86	1.56
3:C:35:LEU:CD1	3:C:104:LEU:HD21	1.36	1.55
2:F:1679:GLY:CA	4:H:3596:ASN:HD22	1.07	1.54
3:G:3045:PHE:CZ	4:H:3546:PHE:CZ	1.96	1.54
3:K:4045:PHE:CZ	4:L:4546:PHE:HZ	1.25	1.54
3:C:45:PHE:CZ	4:D:546:PHE:CZ	1.96	1.53
3:G:3035:LEU:CD1	3:G:3104:LEU:HD21	1.36	1.53
3:C:45:PHE:CZ	4:D:546:PHE:HZ	1.25	1.52
3:K:4035:LEU:HD13	3:K:4104:LEU:CD2	1.36	1.52
3:K:4035:LEU:CD1	3:K:4104:LEU:HD21	1.36	1.52
2:J:2678:SER:CB	4:L:4595:ASN:HB2	1.37	1.52
3:O:5045:PHE:CZ	4:P:5546:PHE:CZ	1.96	1.52
3:G:3045:PHE:CZ	4:H:3546:PHE:HZ	1.25	1.52
2:J:2678:SER:HB2	4:L:4595:ASN:CB	1.38	1.52
3:G:3118:ALA:CB	3:G:3150:PHE:CE2	1.93	1.51
3:K:4045:PHE:CZ	4:L:4546:PHE:CZ	1.96	1.51
3:C:118:ALA:CB	3:C:150:PHE:CE2	1.92	1.51
3:O:5045:PHE:CZ	4:P:5546:PHE:HZ	1.25	1.51
3:O:5035:LEU:CD1	3:O:5104:LEU:HD21	1.36	1.51
3:O:5118:ALA:CB	3:O:5150:PHE:CE2	1.92	1.50
3:C:35:LEU:HD13	3:C:104:LEU:CD2	1.36	1.50
3:K:4118:ALA:CB	3:K:4150:PHE:CE2	1.92	1.49
3:O:5035:LEU:HD13	3:O:5104:LEU:CD2	1.36	1.49
3:G:3035:LEU:HD13	3:G:3104:LEU:CD2	1.36	1.48
3:C:58:PRO:CD	3:C:58:PRO:N	1.72	1.45
3:G:3102:ILE:CB	4:H:3552:ASP:HB2	1.49	1.43
2:F:1679:GLY:HA3	4:H:3596:ASN:ND2	1.26	1.42
3:O:5102:ILE:CB	4:P:5552:ASP:HB2	1.49	1.42
3:C:102:ILE:CB	4:D:552:ASP:HB2	1.49	1.40
3:K:4102:ILE:CB	4:L:4552:ASP:HB2	1.49	1.40
2:B:677:PRO:O	4:D:594:TYR:C	1.63	1.39
2:J:2559:THR:CB	4:L:4532:SER:CB	2.01	1.39
2:J:2677:PRO:C	4:L:4595:ASN:HD22	1.32	1.38
3:K:4078:THR:HG21	3:K:4080:TYR:CZ	1.60	1.37
3:O:5058:PRO:N	3:O:5058:PRO:CD	1.72	1.37
3:C:78:THR:HG21	3:C:80:TYR:CZ	1.59	1.37
3:G:3045:PHE:CE2	4:H:3546:PHE:CZ	2.14	1.36
2:J:2677:PRO:CB	4:L:4595:ASN:ND2	1.87	1.36
2:B:559:THR:CG2	4:D:532:SER:HB2	1.52	1.36
3:C:45:PHE:CE2	4:D:546:PHE:CZ	2.14	1.36
3:G:3078:THR:HG21	3:G:3080:TYR:CZ	1.59	1.35

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:K:4045:PHE:CE2	4:L:4546:PHE:CZ	2.13	1.35
3:O:5045:PHE:CE2	4:P:5546:PHE:CZ	2.13	1.35
2:J:2559:THR:CG2	4:L:4532:SER:HB2	1.54	1.34
2:B:559:THR:HG21	4:D:532:SER:CB	1.57	1.34
3:O:5078:THR:HG21	3:O:5080:TYR:CZ	1.59	1.34
3:G:3058:PRO:CD	3:G:3058:PRO:N	1.72	1.34
3:C:32:TYR:OH	3:C:100:TYR:CZ	1.69	1.33
2:F:1559:THR:CG2	4:H:3532:SER:HA	1.60	1.32
2:J:2559:THR:HG21	4:L:4532:SER:CB	1.58	1.32
1:A:1:TYR:N	1:I:2385:LYS:CD	1.80	1.31
2:J:2559:THR:CB	4:L:4532:SER:HB3	1.56	1.31
3:K:4032:TYR:OH	3:K:4100:TYR:CZ	1.69	1.31
2:B:559:THR:CG2	4:D:532:SER:CB	2.08	1.30
3:K:4032:TYR:OH	3:K:4100:TYR:CE1	1.84	1.30
3:O:5032:TYR:OH	3:O:5100:TYR:CZ	1.69	1.30
2:F:1559:THR:HG21	4:H:3532:SER:CA	1.62	1.30
3:O:5002:ILE:CD1	3:O:5098:ARG:NH1	1.95	1.30
3:G:3002:ILE:CD1	3:G:3098:ARG:NH1	1.95	1.29
3:C:32:TYR:OH	3:C:100:TYR:CE1	1.84	1.29
3:K:4002:ILE:CD1	3:K:4098:ARG:NH1	1.95	1.29
3:K:4058:PRO:CD	3:K:4058:PRO:N	1.72	1.28
3:O:5032:TYR:OH	3:O:5100:TYR:CE1	1.84	1.28
2:J:2559:THR:OG1	4:L:4532:SER:HB3	1.12	1.28
2:J:2678:SER:OG	4:L:4596:ASN:ND2	1.63	1.27
3:C:2:ILE:CD1	3:C:98:ARG:NH1	1.95	1.27
3:O:5045:PHE:HZ	4:P:5546:PHE:CZ	1.43	1.26
3:G:3032:TYR:OH	3:G:3100:TYR:CZ	1.69	1.26
3:C:32:TYR:CE1	3:C:100:TYR:CG	2.24	1.25
3:C:102:ILE:HB	4:D:552:ASP:CB	1.66	1.25
3:G:3032:TYR:CE1	3:G:3100:TYR:CG	2.24	1.25
3:G:3102:ILE:HB	4:H:3552:ASP:CB	1.66	1.24
3:O:5102:ILE:HB	4:P:5552:ASP:CB	1.66	1.24
3:K:4032:TYR:CE1	3:K:4100:TYR:CG	2.24	1.24
3:O:5032:TYR:CE1	3:O:5100:TYR:CG	2.24	1.24
3:G:3045:PHE:HZ	4:H:3546:PHE:CZ	1.43	1.24
3:K:4102:ILE:HB	4:L:4552:ASP:CB	1.66	1.24
2:N:3678:SER:HB2	4:P:5595:ASN:O	1.36	1.24
3:O:5021:SER:OG	3:O:5080:TYR:HE2	1.21	1.24
3:K:4021:SER:OG	3:K:4080:TYR:HE2	1.21	1.23
3:C:21:SER:OG	3:C:80:TYR:CE2	1.92	1.23
3:G:3021:SER:OG	3:G:3080:TYR:CE2	1.92	1.23

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1:TYR:H1	1:I:2385:LYS:CD	1.46	1.21
3:C:45:PHE:HZ	4:D:546:PHE:CZ	1.43	1.21
3:K:4021:SER:OG	3:K:4080:TYR:CE2	1.92	1.21
3:C:21:SER:OG	3:C:80:TYR:HE2	1.21	1.21
3:G:3032:TYR:OH	3:G:3100:TYR:CE1	1.84	1.20
3:C:217:ARG:NH2	4:D:622:PRO:HD2	1.55	1.20
2:F:1677:PRO:O	4:H:3594:TYR:HA	1.40	1.19
3:K:4045:PHE:HZ	4:L:4546:PHE:CZ	1.43	1.19
2:J:2559:THR:CG2	4:L:4532:SER:CB	2.11	1.19
3:O:5217:ARG:NH2	4:P:5622:PRO:HD2	1.55	1.19
2:F:1545:ASP:OD2	3:G:3100:TYR:HE1	1.24	1.19
3:G:3217:ARG:NH2	4:H:3622:PRO:HD2	1.55	1.18
3:C:78:THR:CG2	3:C:80:TYR:CZ	2.26	1.18
3:K:4217:ARG:NH2	4:L:4622:PRO:HD2	1.55	1.18
3:K:4078:THR:CG2	3:K:4080:TYR:CZ	2.26	1.17
3:K:4102:ILE:HG22	4:L:4534:CYS:HB3	1.25	1.17
3:O:5078:THR:CG2	3:O:5080:TYR:CZ	2.26	1.17
3:G:3078:THR:CG2	3:G:3080:TYR:CZ	2.26	1.17
4:D:514:PRO:CG	4:D:609:LEU:O	1.93	1.17
4:H:3514:PRO:CG	4:H:3609:LEU:O	1.93	1.17
3:K:4032:TYR:HE1	3:K:4100:TYR:CG	1.61	1.17
3:O:5032:TYR:HE1	3:O:5100:TYR:CG	1.61	1.17
1:A:1:TYR:H1	1:I:2385:LYS:HD2	1.01	1.16
3:C:32:TYR:HE1	3:C:100:TYR:CG	1.61	1.16
2:F:1679:GLY:CA	4:H:3596:ASN:ND2	1.91	1.16
4:L:4514:PRO:CG	4:L:4609:LEU:O	1.93	1.16
4:P:5514:PRO:CG	4:P:5609:LEU:O	1.93	1.16
3:G:3021:SER:OG	3:G:3080:TYR:HE2	1.21	1.16
4:D:514:PRO:HG3	4:D:609:LEU:O	1.45	1.15
3:G:3102:ILE:HG22	4:H:3534:CYS:HB3	1.25	1.15
4:L:4514:PRO:HG3	4:L:4609:LEU:O	1.45	1.15
1:A:1:TYR:N	1:I:2385:LYS:HD3	1.44	1.15
1:A:123:LYS:HE2	1:E:1150:ASN:HD22	1.06	1.14
2:B:678:SER:HA	4:D:594:TYR:O	1.47	1.14
4:P:5514:PRO:HG3	4:P:5609:LEU:O	1.45	1.14
4:H:3514:PRO:HG3	4:H:3609:LEU:O	1.45	1.14
3:O:5102:ILE:HG22	4:P:5534:CYS:HB3	1.25	1.14
3:G:3032:TYR:HE1	3:G:3100:TYR:CG	1.61	1.13
1:A:150:ASN:HD22	1:E:1123:LYS:HE2	1.06	1.13
3:G:3002:ILE:HD11	3:G:3098:ARG:HH12	1.12	1.13
3:C:2:ILE:HD11	3:C:98:ARG:HH12	1.12	1.13

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:J:2559:THR:OG1	4:L:4532:SER:CB	1.93	1.13
2:J:2677:PRO:HB3	4:L:4595:ASN:ND2	1.54	1.12
3:O:5021:SER:OG	3:O:5080:TYR:CE2	1.91	1.12
3:G:3035:LEU:CD2	3:G:3037:VAL:HG23	1.80	1.11
3:O:5002:ILE:HD11	3:O:5098:ARG:HH12	1.12	1.11
3:O:5035:LEU:CD2	3:O:5037:VAL:HG23	1.80	1.11
3:K:4102:ILE:HG13	4:L:4552:ASP:CG	1.76	1.11
3:C:102:ILE:HG13	4:D:552:ASP:CG	1.76	1.11
2:N:3677:PRO:O	4:P:5596:ASN:N	1.84	1.11
3:O:5035:LEU:CD2	3:O:5037:VAL:CG2	2.29	1.11
3:C:35:LEU:CD2	3:C:37:VAL:HG23	1.80	1.11
2:F:1679:GLY:N	4:H:3595:ASN:CB	2.13	1.11
3:G:3035:LEU:CD2	3:G:3037:VAL:CG2	2.29	1.10
2:F:1680:ALA:H	4:H:3595:ASN:HB3	1.08	1.10
3:G:3002:ILE:HD11	3:G:3098:ARG:NH1	1.62	1.10
3:K:4035:LEU:CD2	3:K:4037:VAL:HG23	1.80	1.10
2:F:1559:THR:CG2	4:H:3532:SER:CA	2.24	1.10
3:G:3102:ILE:HG13	4:H:3552:ASP:CG	1.75	1.09
3:O:5102:ILE:HG13	4:P:5552:ASP:CG	1.75	1.09
3:C:35:LEU:CD2	3:C:37:VAL:CG2	2.29	1.09
3:C:118:ALA:HB3	3:C:150:PHE:CZ	1.88	1.09
3:G:3118:ALA:HB3	3:G:3150:PHE:CZ	1.88	1.09
2:J:2677:PRO:CA	4:L:4595:ASN:ND2	2.14	1.09
3:K:4035:LEU:CD2	3:K:4037:VAL:CG2	2.29	1.09
3:O:5118:ALA:HB3	3:O:5150:PHE:CZ	1.88	1.09
2:F:1679:GLY:N	4:H:3595:ASN:HB2	1.33	1.09
3:K:4118:ALA:HB3	3:K:4150:PHE:CZ	1.88	1.09
3:O:5002:ILE:HD11	3:O:5098:ARG:NH1	1.62	1.08
3:C:102:ILE:HG22	4:D:534:CYS:HB3	1.25	1.08
2:F:1559:THR:HG23	4:H:3532:SER:HB3	1.11	1.08
3:K:4002:ILE:HD11	3:K:4098:ARG:NH1	1.62	1.08
2:F:1675:THR:CB	4:H:3526:ILE:HG21	1.84	1.07
2:F:1675:THR:HB	4:H:3526:ILE:CG2	1.84	1.07
3:G:3102:ILE:HG21	4:H:3552:ASP:OD1	1.55	1.07
3:C:2:ILE:HD11	3:C:98:ARG:NH1	1.62	1.06
2:F:1677:PRO:O	4:H:3594:TYR:CA	2.01	1.06
2:F:1678:SER:HB2	4:H:3593:TRP:NE1	1.61	1.06
3:C:102:ILE:CB	4:D:552:ASP:CB	2.30	1.06
2:J:2559:THR:HG21	4:L:4532:SER:HB2	1.09	1.06
2:J:2677:PRO:C	4:L:4595:ASN:ND2	2.13	1.06
3:O:5039:GLN:NE2	3:O:5045:PHE:CE1	2.24	1.06

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:39:GLN:NE2	3:C:45:PHE:CE1	2.24	1.06
3:G:3039:GLN:NE2	3:G:3045:PHE:CE1	2.24	1.05
3:K:4102:ILE:HG21	4:L:4552:ASP:OD1	1.55	1.05
2:B:677:PRO:O	4:D:594:TYR:O	1.72	1.05
3:K:4039:GLN:NE2	3:K:4045:PHE:CE1	2.24	1.05
2:J:2678:SER:CB	4:L:4595:ASN:CB	2.12	1.04
4:L:4514:PRO:HD3	4:L:4609:LEU:CB	1.87	1.04
4:H:3514:PRO:HD3	4:H:3609:LEU:CB	1.87	1.04
1:A:22:PRO:HB3	1:I:2382:LYS:CB	1.88	1.04
3:O:5102:ILE:HG21	4:P:5552:ASP:OD1	1.55	1.04
3:C:102:ILE:HG21	4:D:552:ASP:OD1	1.55	1.03
4:P:5514:PRO:HD3	4:P:5609:LEU:CB	1.87	1.03
2:F:1559:THR:CG2	4:H:3532:SER:CB	2.36	1.03
2:J:2559:THR:CB	4:L:4532:SER:HB2	1.76	1.03
3:C:45:PHE:CE2	4:D:546:PHE:CE1	2.46	1.03
3:G:3045:PHE:CE2	4:H:3546:PHE:CE1	2.46	1.03
3:K:4045:PHE:CE2	4:L:4546:PHE:CE1	2.46	1.03
3:O:5045:PHE:CE2	4:P:5546:PHE:CE1	2.46	1.03
4:D:514:PRO:HD3	4:D:609:LEU:CB	1.87	1.02
2:F:1559:THR:HG23	4:H:3532:SER:CB	1.89	1.02
2:B:559:THR:HG21	4:D:532:SER:HB2	1.12	1.02
3:O:5102:ILE:CB	4:P:5552:ASP:CB	2.30	1.02
3:K:4045:PHE:CZ	4:L:4546:PHE:CE1	2.48	1.02
3:O:5045:PHE:CZ	4:P:5546:PHE:CE1	2.48	1.02
2:J:2677:PRO:CA	4:L:4595:ASN:HD22	1.73	1.02
2:F:1680:ALA:H	4:H:3595:ASN:CB	1.73	1.01
3:K:4102:ILE:CB	4:L:4552:ASP:CB	2.30	1.01
3:G:3045:PHE:CZ	4:H:3546:PHE:CE1	2.48	1.01
3:K:4217:ARG:HH21	4:L:4622:PRO:HD2	1.18	1.01
2:F:1559:THR:CG2	4:H:3532:SER:HB3	1.88	1.01
3:K:4002:ILE:HD11	3:K:4098:ARG:HH12	1.12	1.01
3:C:45:PHE:CZ	4:D:546:PHE:CE1	2.48	1.01
2:F:1675:THR:HB	4:H:3526:ILE:HG21	1.39	1.00
1:A:152:GLU:OE2	1:E:1177:LYS:NZ	1.95	1.00
3:C:35:LEU:HD21	3:C:37:VAL:HG22	1.43	1.00
3:G:3035:LEU:HD21	3:G:3037:VAL:HG22	1.43	1.00
2:J:2678:SER:OG	4:L:4596:ASN:CG	2.05	1.00
3:O:5032:TYR:CZ	3:O:5100:TYR:CE1	2.50	0.99
3:C:32:TYR:CZ	3:C:100:TYR:CE1	2.50	0.99
3:K:4035:LEU:HD21	3:K:4037:VAL:HG22	1.43	0.99
3:K:4032:TYR:CZ	3:K:4100:TYR:CE1	2.50	0.99

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:150:ASN:ND2	1:E:1123:LYS:HE2	1.77	0.99
3:C:217:ARG:HH21	4:D:622:PRO:HD2	1.18	0.98
3:G:3011:VAL:HG11	3:G:3151:PRO:CB	1.93	0.98
3:O:5097:VAL:HG11	3:O:5104:LEU:HD23	1.45	0.98
3:K:4011:VAL:HG11	3:K:4151:PRO:CB	1.93	0.98
1:A:123:LYS:HE2	1:E:1150:ASN:ND2	1.77	0.98
1:A:177:LYS:NZ	1:E:1152:GLU:OE2	1.95	0.98
3:C:97:VAL:HG11	3:C:104:LEU:HD23	1.45	0.98
2:F:1545:ASP:OD2	3:G:3100:TYR:CE1	2.16	0.98
4:P:5563:ARG:NH2	4:P:5584:ASP:OD1	1.96	0.98
2:B:559:THR:HG23	4:D:532:SER:HB2	1.40	0.98
3:C:11:VAL:HG11	3:C:151:PRO:CB	1.93	0.98
3:G:3102:ILE:CG2	4:H:3534:CYS:HB3	1.94	0.98
4:L:4563:ARG:NH2	4:L:4584:ASP:OD1	1.96	0.98
3:O:5011:VAL:HG11	3:O:5151:PRO:CB	1.93	0.98
3:O:5102:ILE:CG2	4:P:5534:CYS:HB3	1.94	0.97
3:G:3032:TYR:CE1	3:G:3100:TYR:CE1	2.53	0.97
2:F:1680:ALA:N	4:H:3595:ASN:HB3	1.77	0.97
3:G:3032:TYR:CZ	3:G:3100:TYR:CE1	2.50	0.97
3:C:32:TYR:CE1	3:C:100:TYR:CE1	2.53	0.97
3:K:4097:VAL:HG11	3:K:4104:LEU:HD23	1.45	0.97
3:K:4102:ILE:CG2	4:L:4534:CYS:HB3	1.94	0.97
2:N:3678:SER:HB2	4:P:5595:ASN:C	1.89	0.97
3:O:5035:LEU:HD21	3:O:5037:VAL:HG22	1.43	0.97
4:D:563:ARG:NH2	4:D:584:ASP:OD1	1.96	0.97
4:H:3631:ASN:HA	4:H:3685:ALA:HB2	1.47	0.97
4:P:5513:SER:OG	4:P:5609:LEU:HD22	1.65	0.97
3:C:45:PHE:HE2	4:D:546:PHE:CZ	1.80	0.96
3:O:5032:TYR:CE1	3:O:5100:TYR:CE1	2.53	0.96
3:C:11:VAL:HG21	3:C:152:GLU:H	1.29	0.96
4:D:631:ASN:HA	4:D:685:ALA:HB2	1.47	0.96
4:L:4513:SER:OG	4:L:4609:LEU:HD22	1.65	0.96
3:C:102:ILE:CG2	4:D:534:CYS:HB3	1.94	0.96
3:G:3097:VAL:HG11	3:G:3104:LEU:HD23	1.45	0.96
3:C:32:TYR:HE1	3:C:100:TYR:HD1	1.13	0.96
4:H:3563:ARG:NH2	4:H:3584:ASP:OD1	1.96	0.96
3:G:3102:ILE:CB	4:H:3552:ASP:CB	2.30	0.96
4:D:513:SER:OG	4:D:609:LEU:HD22	1.65	0.96
4:H:3513:SER:OG	4:H:3609:LEU:HD22	1.65	0.95
2:N:3677:PRO:O	4:P:5594:TYR:O	1.83	0.95
2:N:3677:PRO:O	4:P:5595:ASN:C	1.87	0.95

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:O:5011:VAL:HG21	3:O:5152:GLU:H	1.29	0.95
1:A:22:PRO:HB3	1:I:2382:LYS:HB3	1.46	0.95
2:B:559:THR:CG2	4:D:532:SER:HB3	1.96	0.95
3:K:4032:TYR:CE1	3:K:4100:TYR:CE1	2.53	0.95
3:O:5217:ARG:HH21	4:P:5622:PRO:HD2	1.18	0.95
2:N:3547:VAL:CG1	3:O:5031:GLU:OE1	2.15	0.95
4:L:4631:ASN:HA	4:L:4685:ALA:HB2	1.47	0.95
3:G:3035:LEU:HD22	3:G:3037:VAL:HG23	1.48	0.94
4:P:5631:ASN:HA	4:P:5685:ALA:HB2	1.47	0.94
3:G:3032:TYR:HE1	3:G:3100:TYR:HD1	1.13	0.94
2:J:2559:THR:HB	4:L:4532:SER:CB	1.98	0.94
2:J:2677:PRO:HB3	4:L:4595:ASN:HD21	1.13	0.94
3:C:102:ILE:HG23	4:D:534:CYS:SG	2.07	0.94
3:G:3118:ALA:HB1	3:G:3150:PHE:CE2	2.03	0.94
3:K:4102:ILE:HG23	4:L:4534:CYS:SG	2.07	0.94
3:G:3011:VAL:HG21	3:G:3152:GLU:H	1.29	0.94
3:G:3102:ILE:HG23	4:H:3534:CYS:SG	2.07	0.94
4:H:3694:TYR:HB2	4:H:3709:LEU:HD22	1.50	0.94
4:P:5694:TYR:HB2	4:P:5709:LEU:HD22	1.50	0.94
3:K:4011:VAL:HG21	3:K:4152:GLU:H	1.29	0.94
3:O:5097:VAL:CG1	3:O:5104:LEU:HD23	1.98	0.94
3:O:5102:ILE:HG23	4:P:5534:CYS:SG	2.07	0.94
3:O:5118:ALA:HB1	3:O:5150:PHE:CE2	2.03	0.94
3:G:3217:ARG:HH21	4:H:3622:PRO:HD2	1.18	0.94
3:O:5035:LEU:HD22	3:O:5037:VAL:HG23	1.48	0.93
4:L:4694:TYR:HB2	4:L:4709:LEU:HD22	1.50	0.93
3:C:35:LEU:HD22	3:C:37:VAL:HG23	1.48	0.93
3:O:5032:TYR:CZ	3:O:5100:TYR:CD1	2.56	0.93
2:B:559:THR:HG21	4:D:532:SER:CA	1.97	0.93
4:D:694:TYR:HB2	4:D:709:LEU:HD22	1.50	0.93
3:C:97:VAL:CG1	3:C:104:LEU:HD23	1.98	0.93
3:G:3032:TYR:CZ	3:G:3100:TYR:CD1	2.56	0.93
2:J:2678:SER:OG	4:L:4596:ASN:CB	2.16	0.93
3:C:32:TYR:CZ	3:C:100:TYR:CD1	2.56	0.93
2:F:1678:SER:CB	4:H:3593:TRP:NE1	2.31	0.93
3:O:5118:ALA:CB	3:O:5150:PHE:CZ	2.51	0.93
3:K:4032:TYR:CZ	3:K:4100:TYR:CD1	2.56	0.92
3:K:4035:LEU:HD22	3:K:4037:VAL:HG23	1.48	0.92
3:O:5078:THR:HG21	3:O:5080:TYR:OH	1.69	0.92
2:J:2559:THR:HG21	4:L:4532:SER:OG	1.67	0.92
3:C:118:ALA:HB1	3:C:150:PHE:CE2	2.03	0.92

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:G:3097:VAL:CG1	3:G:3104:LEU:HD23	1.98	0.92
3:K:4078:THR:HG21	3:K:4080:TYR:OH	1.69	0.92
2:N:3678:SER:OG	4:P:5596:ASN:CA	1.99	0.92
3:K:4097:VAL:CG1	3:K:4104:LEU:HD23	1.98	0.92
1:A:150:ASN:HD22	1:E:1123:LYS:CE	1.83	0.92
3:C:78:THR:HG21	3:C:80:TYR:OH	1.69	0.91
3:G:3118:ALA:CB	3:G:3150:PHE:CZ	2.51	0.91
3:K:4035:LEU:HD21	3:K:4037:VAL:CG2	1.98	0.91
3:G:3045:PHE:HE2	4:H:3546:PHE:CZ	1.80	0.91
3:K:4118:ALA:CB	3:K:4150:PHE:CZ	2.51	0.91
3:K:4118:ALA:HB1	3:K:4150:PHE:CE2	2.03	0.90
3:K:4011:VAL:HG11	3:K:4151:PRO:HB3	1.53	0.90
2:N:3678:SER:CB	4:P:5595:ASN:O	2.17	0.90
3:G:3011:VAL:HG11	3:G:3151:PRO:HB3	1.53	0.90
3:G:3078:THR:HG21	3:G:3080:TYR:OH	1.69	0.90
2:B:559:THR:HG23	4:D:532:SER:CB	1.90	0.90
3:C:11:VAL:HG21	3:C:152:GLU:N	1.87	0.90
3:K:4045:PHE:HE2	4:L:4546:PHE:CZ	1.80	0.90
3:C:11:VAL:HG11	3:C:151:PRO:HB3	1.53	0.90
4:D:552:ASP:HB3	4:D:555:ASN:ND2	1.87	0.90
2:F:1679:GLY:H	4:H:3595:ASN:HB2	1.12	0.90
1:A:123:LYS:CE	1:E:1150:ASN:HD22	1.83	0.90
4:L:4552:ASP:HB3	4:L:4555:ASN:ND2	1.87	0.90
2:J:2678:SER:HG	4:L:4596:ASN:ND2	1.56	0.89
4:H:3552:ASP:HB3	4:H:3555:ASN:ND2	1.87	0.89
3:O:5011:VAL:HG11	3:O:5151:PRO:HB3	1.53	0.89
4:P:5694:TYR:HB2	4:P:5709:LEU:CD2	2.03	0.89
3:K:4011:VAL:HG21	3:K:4152:GLU:N	1.87	0.89
4:P:5552:ASP:HB3	4:P:5555:ASN:ND2	1.87	0.89
3:G:3173:LEU:HD12	4:H:3665:THR:HG22	1.54	0.89
4:D:554:ASN:HD22	4:D:554:ASN:C	1.81	0.88
3:O:5035:LEU:HD21	3:O:5037:VAL:CG2	1.98	0.88
4:L:4694:TYR:HB2	4:L:4709:LEU:CD2	2.03	0.88
3:C:173:LEU:HD12	4:D:665:THR:HG22	1.54	0.88
4:H:3554:ASN:C	4:H:3554:ASN:HD22	1.81	0.88
3:O:5011:VAL:HG21	3:O:5152:GLU:N	1.87	0.88
4:H:3694:TYR:HB2	4:H:3709:LEU:CD2	2.03	0.88
2:F:1675:THR:OG1	4:H:3526:ILE:HG21	1.74	0.88
3:G:3011:VAL:HG21	3:G:3152:GLU:N	1.87	0.88
4:D:694:TYR:HB2	4:D:709:LEU:CD2	2.03	0.88
3:O:5032:TYR:HE1	3:O:5100:TYR:HD1	1.13	0.87

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:O:5173:LEU:HD12	4:P:5665:THR:HG22	1.54	0.87
3:C:35:LEU:HD21	3:C:37:VAL:CG2	1.98	0.87
3:O:5045:PHE:HE2	4:P:5546:PHE:CZ	1.80	0.87
2:J:2678:SER:OG	4:L:4596:ASN:N	2.08	0.87
3:C:11:VAL:CB	3:C:151:PRO:HB2	2.05	0.87
3:K:4173:LEU:HD12	4:L:4665:THR:HG22	1.54	0.86
3:K:4032:TYR:HE1	3:K:4100:TYR:HD1	1.13	0.86
2:N:3547:VAL:HG11	3:O:5031:GLU:OE1	1.75	0.86
4:P:5554:ASN:C	4:P:5554:ASN:HD22	1.81	0.86
3:G:3035:LEU:HD21	3:G:3037:VAL:CG2	1.98	0.86
3:C:118:ALA:CB	3:C:150:PHE:CZ	2.51	0.86
3:O:5011:VAL:CB	3:O:5151:PRO:HB2	2.05	0.86
3:G:3011:VAL:CB	3:G:3151:PRO:HB2	2.05	0.85
3:G:3039:GLN:NE2	3:G:3045:PHE:CZ	2.45	0.85
3:O:5035:LEU:HD22	3:O:5037:VAL:CG2	2.05	0.85
3:O:5070:PHE:HE1	3:O:5081:LEU:HD13	1.40	0.85
4:H:3513:SER:HA	4:H:3609:LEU:HB2	1.58	0.85
3:K:4011:VAL:CB	3:K:4151:PRO:HB2	2.05	0.85
2:F:1559:THR:HG21	4:H:3532:SER:HA	0.87	0.85
3:K:4039:GLN:NE2	3:K:4045:PHE:CZ	2.44	0.85
3:C:39:GLN:NE2	3:C:45:PHE:CZ	2.45	0.84
4:L:4582:THR:OG1	4:L:4610:GLY:HA3	1.78	0.84
3:G:3070:PHE:HE1	3:G:3081:LEU:HD13	1.40	0.84
3:K:4175:GLN:HG3	4:L:4663:GLU:OE2	1.78	0.84
3:G:3102:ILE:HG21	4:H:3552:ASP:CG	2.03	0.84
1:A:1:TYR:H2	1:I:2385:LYS:CD	1.50	0.84
4:H:3582:THR:OG1	4:H:3610:GLY:HA3	1.78	0.84
3:O:5175:GLN:HG3	4:P:5663:GLU:OE2	1.78	0.84
4:D:582:THR:OG1	4:D:610:GLY:HA3	1.78	0.84
3:O:5039:GLN:NE2	3:O:5045:PHE:CZ	2.45	0.84
3:O:5078:THR:CG2	3:O:5080:TYR:CE1	2.61	0.84
1:A:291:ILE:HG23	1:I:2316:ILE:HD13	1.58	0.83
3:C:70:PHE:HE1	3:C:81:LEU:HD13	1.40	0.83
4:D:513:SER:HA	4:D:609:LEU:HB2	1.58	0.83
3:O:5037:VAL:HG21	3:O:5107:TRP:CH2	2.13	0.83
4:P:5513:SER:HA	4:P:5609:LEU:HB2	1.59	0.83
3:K:4011:VAL:HG11	3:K:4151:PRO:HB2	1.60	0.83
3:C:175:GLN:HG3	4:D:663:GLU:OE2	1.78	0.83
3:K:4078:THR:CG2	3:K:4080:TYR:CE1	2.61	0.83
4:L:4513:SER:HA	4:L:4609:LEU:HB2	1.59	0.83
3:O:5102:ILE:HG21	4:P:5552:ASP:CG	2.03	0.83

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:653:VAL:HG23	4:D:658:VAL:HG21	1.60	0.83
3:G:3035:LEU:HD22	3:G:3037:VAL:CG2	2.05	0.83
2:F:1679:GLY:HA2	4:H:3596:ASN:HD22	1.39	0.83
3:G:3078:THR:CG2	3:G:3080:TYR:CE1	2.61	0.83
4:P:5582:THR:OG1	4:P:5610:GLY:HA3	1.78	0.83
3:C:78:THR:CG2	3:C:80:TYR:CE1	2.61	0.83
3:K:4070:PHE:HE1	3:K:4081:LEU:HD13	1.40	0.83
3:K:4102:ILE:HG21	4:L:4552:ASP:CG	2.03	0.83
3:C:37:VAL:HG21	3:C:107:TRP:CH2	2.13	0.83
3:C:11:VAL:HG11	3:C:151:PRO:HB2	1.60	0.83
3:K:4078:THR:HG21	3:K:4080:TYR:CE2	2.14	0.83
3:G:3037:VAL:HG21	3:G:3107:TRP:CH2	2.13	0.82
3:K:4030:THR:HG23	3:K:4054:ASN:HD22	1.44	0.82
4:L:4554:ASN:HD22	4:L:4554:ASN:C	1.81	0.82
4:P:5683:LEU:HD11	4:P:5694:TYR:HE2	1.44	0.82
3:G:3175:GLN:HG3	4:H:3663:GLU:OE2	1.78	0.82
1:A:1:TYR:H2	1:I:2385:LYS:HD3	1.04	0.82
3:C:91:THR:HG22	3:C:115:VAL:H	1.43	0.82
3:K:4037:VAL:HG21	3:K:4107:TRP:CH2	2.13	0.82
4:P:5653:VAL:HG23	4:P:5658:VAL:HG21	1.60	0.82
3:C:102:ILE:HG21	4:D:552:ASP:CG	2.03	0.82
3:O:5102:ILE:HG22	3:O:5102:ILE:O	1.78	0.82
3:C:98:ARG:NH2	3:C:105:ASP:OD2	2.13	0.82
3:C:102:ILE:CG2	4:D:534:CYS:SG	2.68	0.82
3:G:3091:THR:HG22	3:G:3115:VAL:H	1.43	0.82
4:L:4653:VAL:HG23	4:L:4658:VAL:HG21	1.60	0.82
2:F:1676:VAL:HB	4:H:3595:ASN:HD22	1.44	0.82
3:O:5011:VAL:HG11	3:O:5151:PRO:HB2	1.60	0.81
3:K:4102:ILE:HG13	4:L:4552:ASP:OD2	1.80	0.81
3:C:78:THR:HG21	3:C:80:TYR:CE2	2.14	0.81
3:G:3011:VAL:HG11	3:G:3151:PRO:HB2	1.60	0.81
3:G:3011:VAL:HG21	3:G:3151:PRO:HB2	1.62	0.81
3:K:4091:THR:HG22	3:K:4115:VAL:H	1.43	0.81
3:K:4102:ILE:CG2	4:L:4534:CYS:SG	2.68	0.81
3:O:5011:VAL:HG21	3:O:5151:PRO:HB2	1.62	0.81
3:O:5102:ILE:HG13	4:P:5552:ASP:OD2	1.80	0.81
4:P:5514:PRO:HD3	4:P:5609:LEU:HB2	1.62	0.81
3:G:3102:ILE:CG2	4:H:3534:CYS:SG	2.68	0.81
4:H:3653:VAL:HG23	4:H:3658:VAL:HG21	1.60	0.81
4:D:683:LEU:HD11	4:D:694:TYR:HE2	1.44	0.81
3:G:3102:ILE:HG22	3:G:3102:ILE:O	1.78	0.81

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:O:5091:THR:HG22	3:O:5115:VAL:H	1.43	0.81
3:C:102:ILE:HG13	4:D:552:ASP:OD2	1.80	0.81
4:D:514:PRO:HD3	4:D:609:LEU:HB2	1.62	0.81
3:K:4102:ILE:HG22	3:K:4102:ILE:O	1.79	0.81
4:L:4683:LEU:HD11	4:L:4694:TYR:HE2	1.44	0.81
3:O:5078:THR:HG21	3:O:5080:TYR:CE2	2.14	0.81
3:O:5102:ILE:CG2	4:P:5534:CYS:SG	2.68	0.81
2:B:677:PRO:O	4:D:595:ASN:N	2.05	0.81
3:C:102:ILE:HG22	3:C:102:ILE:O	1.78	0.80
2:F:1679:GLY:HA3	4:H:3596:ASN:CG	2.05	0.80
3:G:3098:ARG:NH2	3:G:3105:ASP:OD2	2.13	0.80
4:H:3683:LEU:HD11	4:H:3694:TYR:HE2	1.44	0.80
3:O:5030:THR:HG23	3:O:5054:ASN:HD22	1.44	0.80
3:G:3078:THR:HG21	3:G:3080:TYR:CE2	2.14	0.80
3:G:3102:ILE:HG13	4:H:3552:ASP:OD2	1.80	0.80
3:G:3030:THR:HG23	3:G:3054:ASN:HD22	1.44	0.80
2:J:2559:THR:HB	4:L:4532:SER:HB2	1.60	0.80
3:K:4011:VAL:HG21	3:K:4151:PRO:HB2	1.62	0.80
3:C:30:THR:HG23	3:C:54:ASN:HD22	1.44	0.80
3:G:3102:ILE:CG2	4:H:3552:ASP:HA	2.12	0.80
2:J:2678:SER:HB3	4:L:4595:ASN:CB	2.10	0.80
3:K:4102:ILE:CG2	4:L:4552:ASP:HA	2.12	0.80
3:G:3102:ILE:CG1	4:H:3552:ASP:HB2	2.12	0.80
1:I:2389:VAL:O	2:J:2823:TRP:N	2.13	0.80
3:O:5098:ARG:NH2	3:O:5105:ASP:OD2	2.13	0.80
2:J:2678:SER:HB2	4:L:4595:ASN:CA	2.12	0.80
4:L:4514:PRO:HD3	4:L:4609:LEU:HB2	1.62	0.80
3:C:11:VAL:HG21	3:C:151:PRO:HB2	1.62	0.80
3:C:102:ILE:CG2	4:D:552:ASP:HA	2.12	0.80
4:H:3514:PRO:HD3	4:H:3609:LEU:HB2	1.62	0.80
3:O:5102:ILE:CG2	4:P:5534:CYS:CB	2.60	0.80
3:O:5102:ILE:CG1	4:P:5552:ASP:CG	2.55	0.80
3:O:5102:ILE:CG2	4:P:5552:ASP:HA	2.12	0.79
3:K:4102:ILE:CG2	4:L:4534:CYS:CB	2.60	0.79
3:O:5020:ILE:HD11	3:O:5113:LEU:HD11	1.65	0.79
1:E:1389:VAL:O	2:F:1823:TRP:N	2.13	0.79
3:K:4035:LEU:HD22	3:K:4037:VAL:CG2	2.05	0.79
3:K:4102:ILE:CG1	4:L:4552:ASP:CG	2.56	0.79
3:C:102:ILE:CG1	4:D:552:ASP:HB2	2.12	0.79
4:H:3695:SER:HB2	4:H:3708:SER:OG	1.83	0.79
4:P:5695:SER:HB2	4:P:5708:SER:OG	1.83	0.79

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:G:3002:ILE:HD12	3:G:3098:ARG:NH1	1.98	0.79
1:A:389:VAL:O	2:B:823:TRP:N	2.13	0.79
3:C:102:ILE:CG2	4:D:534:CYS:CB	2.60	0.79
3:K:4020:ILE:HD11	3:K:4113:LEU:HD11	1.65	0.79
3:O:5102:ILE:CG1	4:P:5552:ASP:HB2	2.12	0.79
1:M:3389:VAL:O	2:N:3823:TRP:N	2.13	0.79
3:K:4098:ARG:NH2	3:K:4105:ASP:OD2	2.13	0.78
3:K:4102:ILE:CG1	4:L:4552:ASP:HB2	2.12	0.78
3:C:102:ILE:CG1	4:D:552:ASP:CG	2.56	0.78
3:G:3021:SER:OG	3:G:3080:TYR:CD2	2.37	0.78
3:K:4048:MET:HG2	3:K:4064:PHE:CZ	2.19	0.78
3:C:35:LEU:HD22	3:C:37:VAL:CG2	2.05	0.78
4:D:519:THR:C	4:D:520:LEU:HD23	2.09	0.78
4:L:4519:THR:C	4:L:4520:LEU:HD23	2.09	0.78
3:G:3102:ILE:CG2	4:H:3534:CYS:CB	2.60	0.78
3:O:5048:MET:HG2	3:O:5064:PHE:CZ	2.19	0.78
3:O:5102:ILE:CG2	4:P:5552:ASP:CB	2.62	0.78
3:G:3048:MET:HG2	3:G:3064:PHE:CZ	2.19	0.78
4:L:4695:SER:HB2	4:L:4708:SER:OG	1.83	0.78
3:C:48:MET:HG2	3:C:64:PHE:CZ	2.19	0.77
3:O:5021:SER:OG	3:O:5080:TYR:CD2	2.37	0.77
4:P:5542:PRO:O	4:P:5543:ASP:HB2	1.83	0.77
4:D:695:SER:HB2	4:D:708:SER:OG	1.83	0.77
3:K:4011:VAL:CG1	3:K:4151:PRO:HB2	2.14	0.77
4:P:5519:THR:C	4:P:5520:LEU:HD23	2.09	0.77
2:F:1677:PRO:O	4:H:3594:TYR:C	2.05	0.77
3:G:3070:PHE:CE1	3:G:3081:LEU:HD13	2.19	0.77
4:H:3519:THR:C	4:H:3520:LEU:HD23	2.09	0.77
4:L:4520:LEU:HD23	4:L:4520:LEU:N	1.99	0.77
4:H:3542:PRO:O	4:H:3543:ASP:HB2	1.83	0.77
3:K:4070:PHE:CE1	3:K:4081:LEU:HD13	2.19	0.77
4:D:514:PRO:HD3	4:D:609:LEU:CA	2.15	0.77
3:G:3011:VAL:CG1	3:G:3151:PRO:HB2	2.14	0.77
3:C:11:VAL:CG1	3:C:151:PRO:HB2	2.14	0.77
3:C:20:ILE:HD11	3:C:113:LEU:HD11	1.65	0.77
3:C:21:SER:OG	3:C:80:TYR:CD2	2.37	0.77
3:C:78:THR:HG22	3:C:80:TYR:CE1	2.20	0.77
4:D:520:LEU:HD23	4:D:520:LEU:N	1.99	0.77
3:G:3102:ILE:CG2	4:H:3552:ASP:CB	2.62	0.77
3:K:4045:PHE:CE1	4:L:4589:PHE:CE2	2.73	0.77
3:O:5078:THR:HG22	3:O:5080:TYR:CE1	2.20	0.77

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:P:5520:LEU:HD23	4:P:5520:LEU:N	1.99	0.77
4:L:4685:ALA:O	4:L:4688:TRP:HB3	1.85	0.77
4:H:3520:LEU:HD23	4:H:3520:LEU:N	1.99	0.77
2:J:2677:PRO:CB	4:L:4595:ASN:HD21	1.71	0.77
3:K:4102:ILE:CG2	4:L:4552:ASP:CB	2.62	0.77
2:N:3543:LYS:NZ	3:O:5100:TYR:CE1	2.53	0.77
4:D:542:PRO:O	4:D:543:ASP:HB2	1.83	0.77
2:J:2756:PRO:O	2:J:2814:TRP:NE1	2.18	0.77
3:O:5045:PHE:CE1	4:P:5589:PHE:CE2	2.73	0.77
2:N:3684:TYR:OH	2:N:3701:THR:OG1	2.03	0.76
3:O:5011:VAL:CG1	3:O:5151:PRO:HB2	2.14	0.76
3:O:5070:PHE:CE1	3:O:5081:LEU:HD13	2.19	0.76
3:G:3020:ILE:HD11	3:G:3113:LEU:HD11	1.65	0.76
4:P:5514:PRO:HD3	4:P:5609:LEU:CA	2.15	0.76
2:B:692:ARG:O	2:B:711:ARG:NH2	2.19	0.76
3:C:102:ILE:CG2	4:D:552:ASP:CB	2.62	0.76
2:F:1692:ARG:O	2:F:1711:ARG:NH2	2.19	0.76
2:J:2677:PRO:HB2	4:L:4595:ASN:ND2	1.96	0.76
4:H:3514:PRO:HD3	4:H:3609:LEU:CA	2.15	0.76
4:L:4514:PRO:HD3	4:L:4609:LEU:CA	2.15	0.76
3:C:70:PHE:CE1	3:C:81:LEU:HD13	2.19	0.76
3:G:3078:THR:HG22	3:G:3080:TYR:CE1	2.20	0.76
3:O:5011:VAL:CG2	3:O:5151:PRO:HB2	2.16	0.76
2:J:2595:THR:OG1	2:J:2611:VAL:O	2.04	0.76
4:P:5685:ALA:O	4:P:5688:TRP:HB3	1.85	0.76
1:I:291:ILE:HG23	1:I:2316:ILE:CD1	2.16	0.76
3:C:11:VAL:CG2	3:C:151:PRO:HB2	2.16	0.76
3:C:45:PHE:CE1	4:D:589:PHE:CE2	2.73	0.76
4:D:514:PRO:CD	4:D:609:LEU:O	2.34	0.76
4:H:3685:ALA:O	4:H:3688:TRP:HB3	1.85	0.76
2:B:684:TYR:OH	2:B:701:THR:OG1	2.03	0.76
3:G:3021:SER:CB	3:G:3080:TYR:CE2	2.69	0.76
2:N:3678:SER:OG	4:P:5596:ASN:HA	1.54	0.76
2:B:756:PRO:O	2:B:814:TRP:NE1	2.18	0.76
2:N:3692:ARG:O	2:N:3711:ARG:NH2	2.19	0.76
4:P:5514:PRO:CD	4:P:5609:LEU:O	2.34	0.76
4:D:685:ALA:O	4:D:688:TRP:HB3	1.85	0.75
3:G:3002:ILE:HD13	3:G:3098:ARG:NH1	2.00	0.75
3:G:3045:PHE:CE1	4:H:3589:PHE:CE2	2.73	0.75
4:H:3514:PRO:CD	4:H:3609:LEU:O	2.34	0.75
3:C:2:ILE:HD13	3:C:98:ARG:NH1	2.00	0.75

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:G:3102:ILE:CG1	4:H:3552:ASP:CG	2.56	0.75
3:K:4102:ILE:HG22	4:L:4534:CYS:CB	2.13	0.75
2:N:3753:THR:OG1	2:N:3816:ASN:ND2	2.20	0.75
3:C:21:SER:CB	3:C:80:TYR:CE2	2.69	0.75
2:J:2753:THR:OG1	2:J:2816:ASN:ND2	2.20	0.75
3:K:4002:ILE:HD12	3:K:4098:ARG:NH1	1.98	0.75
4:L:4514:PRO:CD	4:L:4609:LEU:O	2.34	0.75
2:N:3756:PRO:O	2:N:3814:TRP:NE1	2.19	0.75
4:P:5631:ASN:CA	4:P:5685:ALA:HB2	2.17	0.75
2:F:1595:THR:OG1	2:F:1611:VAL:O	2.04	0.75
4:L:4542:PRO:O	4:L:4543:ASP:HB2	1.84	0.75
2:B:678:SER:CA	4:D:594:TYR:O	2.32	0.75
2:F:1756:PRO:O	2:F:1814:TRP:NE1	2.18	0.75
3:K:4078:THR:HG22	3:K:4080:TYR:CE1	2.20	0.75
3:G:3011:VAL:CG2	3:G:3151:PRO:HB2	2.16	0.75
3:G:3102:ILE:HG21	4:H:3552:ASP:HA	1.69	0.75
4:H:3514:PRO:CD	4:H:3609:LEU:CB	2.65	0.75
2:J:2692:ARG:O	2:J:2711:ARG:NH2	2.19	0.75
3:O:5021:SER:CB	3:O:5080:TYR:CE2	2.69	0.75
3:G:3097:VAL:CG2	3:G:3107:TRP:CE3	2.70	0.75
3:K:4021:SER:CB	3:K:4080:TYR:CE2	2.69	0.75
2:N:3595:THR:OG1	2:N:3611:VAL:O	2.04	0.75
3:G:3097:VAL:HG11	3:G:3104:LEU:CD2	2.16	0.75
4:H:3631:ASN:CA	4:H:3685:ALA:HB2	2.17	0.75
3:K:4002:ILE:HD13	3:K:4098:ARG:NH1	2.00	0.75
2:B:595:THR:OG1	2:B:611:VAL:O	2.04	0.74
4:D:514:PRO:CD	4:D:609:LEU:CB	2.65	0.74
2:F:1753:THR:OG1	2:F:1816:ASN:ND2	2.20	0.74
3:O:5002:ILE:HD12	3:O:5098:ARG:NH1	1.98	0.74
3:K:4097:VAL:CG2	3:K:4107:TRP:CE3	2.70	0.74
4:L:4514:PRO:CD	4:L:4609:LEU:CB	2.65	0.74
2:B:753:THR:OG1	2:B:816:ASN:ND2	2.20	0.74
3:C:97:VAL:HG11	3:C:104:LEU:CD2	2.16	0.74
4:D:631:ASN:CA	4:D:685:ALA:HB2	2.17	0.74
4:H:3552:ASP:HB3	4:H:3555:ASN:HD22	1.51	0.74
3:K:4011:VAL:CG2	3:K:4151:PRO:HB2	2.16	0.74
3:K:4217:ARG:NH2	4:L:4622:PRO:CD	2.45	0.74
3:O:5097:VAL:HG11	3:O:5104:LEU:CD2	2.16	0.74
1:A:30:GLN:OE1	1:A:136:THR:OG1	2.06	0.74
3:C:102:ILE:HG23	4:D:534:CYS:HG	1.51	0.74
1:E:1030:GLN:OE1	1:E:1136:THR:OG1	2.06	0.74

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:O:5097:VAL:CG2	3:O:5107:TRP:CE3	2.70	0.74
4:D:552:ASP:HB3	4:D:555:ASN:HD22	1.51	0.74
3:G:3024:ALA:HB1	3:G:3027:TYR:CE1	2.22	0.74
2:J:2678:SER:CB	4:L:4595:ASN:HB3	2.18	0.74
3:K:4102:ILE:HG21	4:L:4552:ASP:HA	1.69	0.74
4:L:4552:ASP:HB3	4:L:4555:ASN:HD22	1.51	0.74
3:C:97:VAL:CG2	3:C:107:TRP:CE3	2.70	0.74
3:O:5024:ALA:HB1	3:O:5027:TYR:CE1	2.22	0.74
3:C:24:ALA:HB1	3:C:27:TYR:CE1	2.22	0.74
3:K:4024:ALA:HB1	3:K:4027:TYR:CE1	2.22	0.74
3:K:4097:VAL:HG11	3:K:4104:LEU:CD2	2.16	0.74
1:M:3030:GLN:OE1	1:M:3136:THR:OG1	2.06	0.74
3:C:97:VAL:HG21	3:C:107:TRP:CE3	2.23	0.74
3:G:3126:TYR:CE2	4:H:3627:GLU:HG3	2.23	0.74
3:K:4097:VAL:HG21	3:K:4107:TRP:CE3	2.23	0.74
3:K:4126:TYR:CE2	4:L:4627:GLU:HG3	2.23	0.73
2:F:1684:TYR:OH	2:F:1701:THR:OG1	2.03	0.73
2:N:3547:VAL:CG1	3:O:5031:GLU:CD	2.61	0.73
3:O:5097:VAL:HG21	3:O:5107:TRP:CE3	2.23	0.73
3:C:102:ILE:HG21	4:D:552:ASP:HA	1.69	0.73
3:C:217:ARG:NH2	4:D:622:PRO:CD	2.45	0.73
3:G:3097:VAL:HG21	3:G:3107:TRP:CE3	2.23	0.73
3:G:3102:ILE:HG22	4:H:3534:CYS:CB	2.13	0.73
3:C:39:GLN:CD	3:C:45:PHE:CZ	2.66	0.73
3:G:3039:GLN:CD	3:G:3045:PHE:CZ	2.66	0.73
3:C:126:TYR:CE2	4:D:627:GLU:HG3	2.23	0.73
3:G:3011:VAL:CG1	3:G:3151:PRO:CB	2.67	0.73
3:O:5102:ILE:HG21	4:P:5552:ASP:HA	1.69	0.73
3:O:5011:VAL:CG1	3:O:5151:PRO:CB	2.67	0.73
3:K:4039:GLN:CD	3:K:4045:PHE:CZ	2.66	0.73
3:O:5039:GLN:CD	3:O:5045:PHE:CZ	2.66	0.73
3:O:5126:TYR:CE2	4:P:5627:GLU:HG3	2.23	0.73
2:J:2678:SER:HG	4:L:4596:ASN:CG	1.92	0.73
4:L:4631:ASN:CA	4:L:4685:ALA:HB2	2.17	0.73
3:C:2:ILE:HD12	3:C:98:ARG:NH1	1.98	0.72
3:G:3217:ARG:NH2	4:H:3622:PRO:CD	2.45	0.72
1:I:2030:GLN:OE1	1:I:2136:THR:OG1	2.06	0.72
3:O:5002:ILE:HD13	3:O:5098:ARG:NH1	2.00	0.72
3:G:3102:ILE:HB	4:H:3552:ASP:HB2	0.75	0.72
2:N:3543:LYS:NZ	3:O:5100:TYR:HE1	1.87	0.72
4:P:5514:PRO:CD	4:P:5609:LEU:CB	2.65	0.72

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:622:ARG:NH2	2:B:815:GLY:O	2.23	0.72
2:F:1622:ARG:NH2	2:F:1815:GLY:O	2.23	0.72
2:N:3622:ARG:NH2	2:N:3815:GLY:O	2.23	0.72
1:A:291:ILE:HG12	1:I:2306:GLU:HB2	1.71	0.72
2:J:2622:ARG:NH2	2:J:2815:GLY:O	2.23	0.72
3:C:118:ALA:CB	3:C:150:PHE:HE2	1.65	0.72
4:P:5552:ASP:HB3	4:P:5555:ASN:HD22	1.51	0.72
1:A:22:PRO:CB	1:I:2382:LYS:HB3	2.18	0.72
3:K:4011:VAL:CG1	3:K:4151:PRO:CB	2.67	0.72
2:F:1783:SER:OG	2:F:1788:ALA:O	2.06	0.71
1:E:1076:TYR:OH	1:E:1105:GLU:OE1	2.08	0.71
2:J:2684:TYR:OH	2:J:2701:THR:OG1	2.04	0.71
3:O:5217:ARG:NH2	4:P:5622:PRO:CD	2.45	0.71
1:A:290:ARG:HH22	1:I:2356:HIS:CE1	2.08	0.71
2:F:1558:LYS:CG	4:H:3532:SER:CB	2.68	0.71
3:K:4102:ILE:HB	4:L:4552:ASP:HB2	0.75	0.71
3:G:3102:ILE:CG2	4:H:3552:ASP:CA	2.69	0.71
3:K:4002:ILE:HD12	3:K:4098:ARG:CZ	2.21	0.71
3:O:5102:ILE:CG2	4:P:5552:ASP:CA	2.69	0.71
1:M:3076:TYR:OH	1:M:3105:GLU:OE1	2.08	0.71
1:A:76:TYR:OH	1:A:105:GLU:OE1	2.08	0.70
3:C:11:VAL:CG1	3:C:151:PRO:CB	2.67	0.70
2:N:3783:SER:OG	2:N:3788:ALA:O	2.06	0.70
3:C:102:ILE:CG2	4:D:552:ASP:CA	2.69	0.70
3:K:4102:ILE:CG2	4:L:4552:ASP:CA	2.69	0.70
4:P:5593:TRP:CH2	4:P:5596:ASN:C	2.70	0.70
3:K:4002:ILE:CD1	3:K:4098:ARG:CZ	2.70	0.70
3:K:4030:THR:HG23	3:K:4054:ASN:ND2	2.07	0.70
3:O:5002:ILE:HD12	3:O:5098:ARG:CZ	2.21	0.70
3:O:5030:THR:HG23	3:O:5054:ASN:ND2	2.07	0.70
4:H:3542:PRO:HB3	4:H:3669:LYS:HD3	1.74	0.70
4:H:3593:TRP:CH2	4:H:3596:ASN:C	2.70	0.70
4:L:4593:TRP:CH2	4:L:4596:ASN:C	2.70	0.70
4:D:542:PRO:HB3	4:D:669:LYS:HD3	1.74	0.70
4:L:4542:PRO:HB3	4:L:4669:LYS:HD3	1.74	0.70
3:G:3002:ILE:HD12	3:G:3098:ARG:CZ	2.21	0.70
3:G:3030:THR:HG23	3:G:3054:ASN:ND2	2.07	0.69
3:K:4060:TYR:OH	3:K:4069:VAL:HA	1.92	0.69
3:C:2:ILE:CD1	3:C:98:ARG:CZ	2.70	0.69
3:G:3060:TYR:OH	3:G:3069:VAL:HA	1.92	0.69
1:A:111:SER:N	1:A:114:CYS:SG	2.66	0.69

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:2076:TYR:OH	1:I:2105:GLU:OE1	2.08	0.69
2:B:558:LYS:HE3	4:D:595:ASN:OD1	1.93	0.69
3:C:30:THR:HG23	3:C:54:ASN:ND2	2.07	0.69
3:C:60:TYR:OH	3:C:69:VAL:HA	1.92	0.69
2:J:2678:SER:HB3	4:L:4595:ASN:HB3	1.73	0.69
1:M:3111:SER:N	1:M:3114:CYS:SG	2.66	0.69
3:O:5102:ILE:HG22	4:P:5534:CYS:CB	2.13	0.69
4:D:557:ARG:HD2	4:D:558:SER:O	1.92	0.69
4:D:593:TRP:CH2	4:D:596:ASN:C	2.70	0.69
1:E:1111:SER:N	1:E:1114:CYS:SG	2.65	0.69
3:C:2:ILE:HD12	3:C:98:ARG:CZ	2.21	0.69
1:M:3359:THR:O	1:M:3394:GLN:NE2	2.26	0.69
2:B:552:MET:N	2:B:563:ILE:O	2.26	0.69
3:C:78:THR:HG22	3:C:80:TYR:CZ	2.25	0.69
3:K:4118:ALA:CB	3:K:4150:PHE:HE2	1.65	0.69
4:L:4557:ARG:HD2	4:L:4558:SER:O	1.92	0.69
3:O:5060:TYR:OH	3:O:5069:VAL:HA	1.92	0.69
2:J:2678:SER:OG	4:L:4596:ASN:HB3	1.94	0.69
3:C:102:ILE:HB	4:D:552:ASP:HB2	0.75	0.68
3:G:3002:ILE:CD1	3:G:3098:ARG:CZ	2.70	0.68
3:G:3102:ILE:HG21	4:H:3552:ASP:CB	2.24	0.68
1:A:359:THR:O	1:A:394:GLN:NE2	2.26	0.68
3:O:5102:ILE:HB	4:P:5552:ASP:HB2	0.75	0.68
4:P:5542:PRO:HB3	4:P:5669:LYS:HD3	1.74	0.68
3:K:4102:ILE:HG21	4:L:4552:ASP:CB	2.23	0.68
1:E:1359:THR:O	1:E:1394:GLN:NE2	2.26	0.68
1:I:2391:TYR:OH	2:J:2784:LEU:HD11	1.94	0.68
2:N:3677:PRO:O	4:P:5594:TYR:C	2.35	0.68
4:H:3557:ARG:HD2	4:H:3558:SER:O	1.92	0.68
1:I:2111:SER:N	1:I:2114:CYS:SG	2.66	0.68
4:P:5683:LEU:HD11	4:P:5694:TYR:CE2	2.29	0.68
2:B:783:SER:OG	2:B:788:ALA:O	2.06	0.68
3:C:102:ILE:HG21	4:D:552:ASP:CB	2.23	0.68
1:I:2359:THR:O	1:I:2394:GLN:NE2	2.26	0.68
2:N:3552:MET:N	2:N:3563:ILE:O	2.26	0.68
4:P:5557:ARG:HD2	4:P:5558:SER:O	1.92	0.68
3:G:3118:ALA:CB	3:G:3150:PHE:HE2	1.65	0.68
2:J:2552:MET:N	2:J:2563:ILE:O	2.26	0.68
2:J:2783:SER:OG	2:J:2788:ALA:O	2.06	0.68
3:O:5102:ILE:HG21	4:P:5552:ASP:CB	2.24	0.68
1:A:391:TYR:OH	2:B:784:LEU:HD11	1.94	0.68

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:1391:TYR:OH	2:F:1784:LEU:HD11	1.94	0.68
2:F:1679:GLY:N	4:H:3594:TYR:O	2.18	0.67
4:D:683:LEU:HD11	4:D:694:TYR:CE2	2.29	0.67
2:F:1676:VAL:CB	4:H:3595:ASN:HD22	2.00	0.67
3:G:3078:THR:HG22	3:G:3080:TYR:CZ	2.25	0.67
2:F:1552:MET:N	2:F:1563:ILE:O	2.26	0.67
2:J:2559:THR:CG2	4:L:4532:SER:OG	2.35	0.67
2:B:558:LYS:CE	4:D:595:ASN:OD1	2.43	0.67
2:F:1558:LYS:CG	4:H:3532:SER:HB3	2.25	0.67
3:O:5128:LEU:HB3	4:P:5621:PHE:CD2	2.30	0.67
4:D:672:ASN:O	4:D:673:ASN:HB2	1.95	0.67
2:F:1679:GLY:HA3	4:H:3596:ASN:HD22	0.50	0.67
3:G:3041:PRO:HD3	3:G:3092:ALA:HA	1.77	0.67
3:C:128:LEU:HB3	4:D:621:PHE:CD2	2.30	0.67
3:O:5041:PRO:HD3	3:O:5092:ALA:HA	1.77	0.67
1:A:22:PRO:HB3	1:I:2382:LYS:HB2	1.73	0.66
1:M:3391:TYR:OH	2:N:3784:LEU:HD11	1.94	0.66
3:C:73:GLU:OE1	3:C:80:TYR:CZ	2.49	0.66
3:G:3128:LEU:HB3	4:H:3621:PHE:CD2	2.30	0.66
3:O:5073:GLU:OE1	3:O:5080:TYR:CZ	2.49	0.66
4:P:5672:ASN:O	4:P:5673:ASN:HB2	1.95	0.66
3:C:41:PRO:HD3	3:C:92:ALA:HA	1.77	0.66
3:K:4073:GLU:OE1	3:K:4080:TYR:CZ	2.49	0.66
4:P:5506:GLN:CD	4:P:5590:CYS:SG	2.79	0.66
3:G:3073:GLU:OE1	3:G:3080:TYR:CZ	2.49	0.66
3:K:4128:LEU:HB3	4:L:4621:PHE:CD2	2.30	0.66
3:O:5002:ILE:CD1	3:O:5098:ARG:CZ	2.70	0.66
4:H:3672:ASN:O	4:H:3673:ASN:HB2	1.95	0.65
3:G:3006:GLN:HE22	3:G:3095:PHE:HA	1.61	0.65
3:O:5102:ILE:CG1	4:P:5552:ASP:CB	2.73	0.65
4:D:506:GLN:CD	4:D:590:CYS:SG	2.79	0.65
4:L:4683:LEU:HD11	4:L:4694:TYR:CE2	2.29	0.65
4:P:5631:ASN:HA	4:P:5685:ALA:CB	2.25	0.65
3:K:4041:PRO:HD3	3:K:4092:ALA:HA	1.77	0.65
4:L:4672:ASN:O	4:L:4673:ASN:HB2	1.95	0.65
3:G:3102:ILE:CG1	4:H:3552:ASP:CB	2.73	0.65
4:L:4506:GLN:CD	4:L:4590:CYS:SG	2.79	0.65
3:O:5006:GLN:HE22	3:O:5095:PHE:HA	1.62	0.65
4:L:4610:GLY:O	4:L:4611:GLN:HG3	1.97	0.65
4:D:610:GLY:O	4:D:611:GLN:HG3	1.97	0.65
2:F:1558:LYS:HG2	4:H:3532:SER:HB3	1.79	0.65

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:H:3506:GLN:CD	4:H:3590:CYS:SG	2.79	0.65
3:K:4006:GLN:HE22	3:K:4095:PHE:HA	1.62	0.65
3:K:4021:SER:OG	3:K:4080:TYR:CD2	2.37	0.65
4:H:3631:ASN:HA	4:H:3685:ALA:CB	2.25	0.64
4:H:3581:GLN:HB3	4:H:3583:GLU:HG2	1.80	0.64
3:K:4078:THR:HG22	3:K:4080:TYR:CZ	2.25	0.64
4:D:513:SER:OG	4:D:609:LEU:CD2	2.44	0.64
3:O:5073:GLU:OE1	3:O:5080:TYR:CE1	2.51	0.64
4:L:4564:PHE:CE1	4:L:4577:ILE:HG12	2.33	0.64
3:C:73:GLU:OE1	3:C:80:TYR:CE1	2.51	0.64
4:D:514:PRO:HD3	4:D:609:LEU:HB3	1.79	0.64
3:G:3073:GLU:OE1	3:G:3080:TYR:CE1	2.51	0.64
2:N:3678:SER:CB	4:P:5595:ASN:C	2.66	0.64
4:P:5513:SER:OG	4:P:5609:LEU:CD2	2.44	0.64
3:C:6:GLN:HE22	3:C:95:PHE:HA	1.62	0.64
4:D:514:PRO:HD3	4:D:609:LEU:C	2.23	0.64
4:H:3610:GLY:O	4:H:3611:GLN:HG3	1.97	0.64
3:K:4073:GLU:OE1	3:K:4080:TYR:CE1	2.51	0.64
4:P:5514:PRO:HD3	4:P:5609:LEU:HB3	1.79	0.64
4:D:652:LYS:HG2	4:D:657:PRO:HA	1.79	0.64
4:H:3514:PRO:HD3	4:H:3609:LEU:C	2.23	0.64
4:H:3564:PHE:CE1	4:H:3577:ILE:HG12	2.33	0.64
3:K:4030:THR:CG2	3:K:4030:THR:O	2.46	0.64
4:L:4652:LYS:HG2	4:L:4657:PRO:HA	1.79	0.64
4:P:5568:LEU:HD23	4:P:5573:ALA:HA	1.80	0.64
4:P:5581:GLN:HB3	4:P:5583:GLU:HG2	1.80	0.64
4:P:5610:GLY:O	4:P:5611:GLN:HG3	1.97	0.64
1:A:123:LYS:CE	1:E:1150:ASN:ND2	2.52	0.64
2:B:559:THR:OG1	4:D:532:SER:HB3	1.98	0.64
4:H:3652:LYS:HG2	4:H:3657:PRO:HA	1.79	0.64
4:H:3683:LEU:HD11	4:H:3694:TYR:CE2	2.29	0.64
2:J:2678:SER:N	4:L:4595:ASN:HD22	1.91	0.64
3:O:5030:THR:O	3:O:5030:THR:CG2	2.46	0.64
3:O:5118:ALA:CB	3:O:5150:PHE:HE2	1.65	0.64
4:H:3514:PRO:HD3	4:H:3609:LEU:HB3	1.79	0.63
2:J:2678:SER:CB	4:L:4596:ASN:ND2	2.55	0.63
4:P:5564:PHE:CE1	4:P:5577:ILE:HG12	2.33	0.63
4:P:5652:LYS:HG2	4:P:5657:PRO:HA	1.79	0.63
3:C:30:THR:O	3:C:30:THR:CG2	2.46	0.63
4:D:564:PHE:CE1	4:D:577:ILE:HG12	2.33	0.63
4:H:3647:VAL:HG12	4:H:3700:HIS:HB2	1.81	0.63

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:J:2678:SER:CA	4:L:4595:ASN:HB2	2.26	0.63
4:L:4568:LEU:HD23	4:L:4573:ALA:HA	1.80	0.63
4:L:4581:GLN:HB3	4:L:4583:GLU:HG2	1.79	0.63
4:L:4514:PRO:HD3	4:L:4609:LEU:C	2.23	0.63
4:P:5647:VAL:HG12	4:P:5700:HIS:HB2	1.81	0.63
2:F:1679:GLY:HA2	4:H:3596:ASN:ND2	1.99	0.63
3:K:4072:LEU:HD13	3:K:4074:ILE:HG13	1.81	0.63
1:A:150:ASN:ND2	1:E:1123:LYS:CE	2.52	0.63
3:G:3072:LEU:HD13	3:G:3074:ILE:HG13	1.81	0.63
4:L:4561:PRO:HG2	4:L:4563:ARG:NH1	2.14	0.63
1:A:291:ILE:CG2	1:I:2316:ILE:HD13	2.28	0.63
3:C:102:ILE:CG1	4:D:552:ASP:CB	2.73	0.63
3:G:3030:THR:CG2	3:G:3030:THR:O	2.46	0.63
4:H:3568:LEU:HD23	4:H:3573:ALA:HA	1.80	0.63
4:D:568:LEU:HD23	4:D:573:ALA:HA	1.80	0.62
4:D:631:ASN:HA	4:D:685:ALA:CB	2.25	0.62
4:D:581:GLN:HB3	4:D:583:GLU:HG2	1.80	0.62
3:K:4032:TYR:CE1	3:K:4100:TYR:HD1	1.97	0.62
4:D:561:PRO:HG2	4:D:563:ARG:NH1	2.14	0.62
4:P:5514:PRO:HD3	4:P:5609:LEU:C	2.23	0.62
4:P:5561:PRO:HG2	4:P:5563:ARG:NH1	2.14	0.62
4:D:514:PRO:HD3	4:D:609:LEU:O	2.00	0.62
4:L:4513:SER:OG	4:L:4609:LEU:CD2	2.44	0.62
4:L:4647:VAL:HG12	4:L:4700:HIS:HB2	1.81	0.62
3:O:5035:LEU:HG	3:O:5047:TRP:CD1	2.34	0.62
4:D:647:VAL:HG12	4:D:700:HIS:HB2	1.81	0.62
3:G:3035:LEU:HG	3:G:3047:TRP:CD1	2.35	0.62
3:K:4035:LEU:HG	3:K:4047:TRP:CD1	2.34	0.62
4:L:4514:PRO:HD3	4:L:4609:LEU:O	2.00	0.62
4:H:3631:ASN:C	4:H:3685:ALA:HB2	2.25	0.62
3:O:5072:LEU:HD13	3:O:5074:ILE:HG13	1.81	0.62
3:C:72:LEU:HD13	3:C:74:ILE:HG13	1.81	0.62
1:A:53:THR:OG1	1:A:236:GLN:OE1	2.18	0.62
3:C:35:LEU:HG	3:C:47:TRP:CD1	2.34	0.61
4:D:514:PRO:CD	4:D:609:LEU:HB3	2.30	0.61
2:B:505:ASP:O	2:B:726:ARG:NH1	2.32	0.61
3:C:11:VAL:HG23	3:C:152:GLU:O	2.00	0.61
4:D:631:ASN:C	4:D:685:ALA:HB2	2.25	0.61
4:H:3561:PRO:HG2	4:H:3563:ARG:NH1	2.14	0.61
4:L:4514:PRO:CD	4:L:4609:LEU:HB3	2.30	0.61
3:G:3009:ARG:HG2	3:G:3112:THR:H	1.65	0.61

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:G:3118:ALA:CB	3:G:3150:PHE:CD2	2.77	0.61
4:P:5514:PRO:CD	4:P:5609:LEU:HB3	2.31	0.61
3:C:9:ARG:HG2	3:C:112:THR:H	1.65	0.61
2:N:3505:ASP:O	2:N:3726:ARG:NH1	2.32	0.61
2:N:3679:GLY:N	4:P:5596:ASN:ND2	2.45	0.61
2:F:1505:ASP:O	2:F:1726:ARG:NH1	2.32	0.61
4:H:3514:PRO:HD3	4:H:3609:LEU:O	2.00	0.61
4:P:5631:ASN:C	4:P:5685:ALA:HB2	2.25	0.61
4:H:3662:MET:HA	4:H:3680:TYR:O	2.01	0.61
3:O:5011:VAL:HG23	3:O:5152:GLU:O	2.00	0.61
3:C:2:ILE:CD1	3:C:98:ARG:HH12	1.83	0.61
1:E:1198:ALA:HB3	2:J:2759:LEU:HD11	1.81	0.61
1:I:2198:ALA:HB3	2:N:3759:LEU:HD11	1.81	0.61
4:D:662:MET:HA	4:D:680:TYR:O	2.01	0.61
4:H:3513:SER:OG	4:H:3609:LEU:CD2	2.44	0.61
3:G:3011:VAL:HG23	3:G:3152:GLU:O	2.00	0.61
3:O:5118:ALA:HB1	3:O:5150:PHE:CD2	2.36	0.61
4:P:5662:MET:HA	4:P:5680:TYR:O	2.01	0.61
2:J:2505:ASP:O	2:J:2726:ARG:NH1	2.32	0.61
2:F:1581:HIS:NE2	2:F:1583:GLY:O	2.34	0.60
3:G:3145:LEU:HD13	4:H:3680:TYR:HE2	1.66	0.60
3:K:4118:ALA:CB	3:K:4150:PHE:CD2	2.77	0.60
3:C:97:VAL:HG21	3:C:107:TRP:CZ3	2.36	0.60
1:E:1053:THR:OG1	1:E:1236:GLN:OE1	2.18	0.60
1:I:2053:THR:OG1	1:I:2236:GLN:OE1	2.18	0.60
1:M:3053:THR:OG1	1:M:3236:GLN:OE1	2.18	0.60
3:O:5145:LEU:HD13	4:P:5680:TYR:HE2	1.67	0.60
3:C:9:ARG:O	3:C:153:PRO:HD3	2.02	0.60
3:G:3097:VAL:HG21	3:G:3107:TRP:CZ3	2.36	0.60
4:L:4631:ASN:C	4:L:4685:ALA:HB2	2.25	0.60
2:F:1759:LEU:HD11	1:M:3198:ALA:HB3	1.81	0.60
3:K:4011:VAL:HG23	3:K:4152:GLU:O	2.00	0.60
3:O:5009:ARG:HG2	3:O:5112:THR:H	1.66	0.60
3:K:4009:ARG:HG2	3:K:4112:THR:H	1.66	0.60
3:C:118:ALA:HB1	3:C:150:PHE:CD2	2.36	0.60
2:F:1558:LYS:HG2	4:H:3532:SER:CB	2.31	0.60
4:H:3514:PRO:CD	4:H:3609:LEU:HB3	2.31	0.60
3:G:3021:SER:HA	3:G:3080:TYR:CD2	2.37	0.60
3:G:3118:ALA:HB1	3:G:3150:PHE:CD2	2.36	0.60
3:C:73:GLU:CD	3:C:80:TYR:CE1	2.80	0.60
3:G:3073:GLU:CD	3:G:3080:TYR:CE1	2.80	0.60

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:L:4554:ASN:C	4:L:4554:ASN:ND2	2.54	0.60
4:L:4631:ASN:HA	4:L:4685:ALA:CB	2.25	0.60
4:L:4662:MET:HA	4:L:4680:TYR:O	2.01	0.60
4:D:541:LYS:HE2	4:D:583:GLU:O	2.02	0.59
3:G:3118:ALA:HB3	3:G:3150:PHE:HE2	0.78	0.59
4:H:3554:ASN:C	4:H:3554:ASN:ND2	2.54	0.59
3:C:145:LEU:HD13	4:D:680:TYR:HE2	1.66	0.59
2:J:2581:HIS:NE2	2:J:2583:GLY:O	2.34	0.59
3:K:4073:GLU:CD	3:K:4080:TYR:CE1	2.80	0.59
3:O:5097:VAL:HG21	3:O:5107:TRP:CZ3	2.36	0.59
2:N:3677:PRO:C	4:P:5596:ASN:N	2.54	0.59
3:O:5009:ARG:O	3:O:5153:PRO:HD3	2.02	0.59
3:G:3009:ARG:O	3:G:3153:PRO:HD3	2.02	0.59
3:O:5073:GLU:CD	3:O:5080:TYR:CE1	2.80	0.59
3:O:5102:ILE:CG2	3:O:5102:ILE:O	2.51	0.59
4:P:5514:PRO:HD3	4:P:5609:LEU:O	2.00	0.59
2:B:581:HIS:NE2	2:B:583:GLY:O	2.34	0.59
4:H:3528:ALA:HA	4:H:3571:ASP:HB2	1.85	0.59
4:P:5686:ARG:HG3	4:P:5686:ARG:HH11	1.67	0.59
4:H:3686:ARG:HG3	4:H:3686:ARG:HH11	1.67	0.59
4:H:3689:GLU:HA	4:H:3711:ARG:NH2	2.18	0.59
3:K:4145:LEU:HD13	4:L:4680:TYR:HE2	1.67	0.59
3:K:4009:ARG:O	3:K:4153:PRO:HD3	2.02	0.59
3:K:4021:SER:HA	3:K:4080:TYR:CD2	2.37	0.59
3:K:4102:ILE:HG21	4:L:4552:ASP:CA	2.31	0.59
3:K:4102:ILE:CG2	4:L:4552:ASP:CG	2.75	0.59
1:M:3197:LYS:O	1:M:3200:SER:OG	2.18	0.59
3:O:5118:ALA:HB3	3:O:5150:PHE:HE2	0.78	0.59
2:B:559:THR:HG23	4:D:532:SER:HB3	1.69	0.59
3:K:4097:VAL:HG21	3:K:4107:TRP:CZ3	2.36	0.59
4:D:528:ALA:HA	4:D:571:ASP:HB2	1.85	0.59
4:H:3541:LYS:HE2	4:H:3583:GLU:O	2.02	0.59
1:M:3057:SER:OG	2:N:3724:SER:O	2.16	0.59
2:N:3581:HIS:NE2	2:N:3583:GLY:O	2.34	0.59
4:P:5689:GLU:HA	4:P:5711:ARG:NH2	2.18	0.59
4:P:5700:HIS:O	4:P:5701:GLU:C	2.46	0.59
1:A:291:ILE:HG21	1:I:2306:GLU:HB3	1.84	0.58
1:M:3038:ILE:HD12	1:M:3269:ALA:HB3	1.85	0.58
4:P:5541:LYS:HE2	4:P:5583:GLU:O	2.02	0.58
4:D:686:ARG:HH11	4:D:686:ARG:HG3	1.67	0.58
3:K:4118:ALA:HB1	3:K:4150:PHE:CD2	2.36	0.58

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:L:4689:GLU:HA	4:L:4711:ARG:NH2	2.18	0.58
3:C:21:SER:HA	3:C:80:TYR:CD2	2.37	0.58
3:K:4102:ILE:CG1	4:L:4552:ASP:CB	2.73	0.58
3:O:5021:SER:HA	3:O:5080:TYR:CD2	2.37	0.58
4:P:5514:PRO:CD	4:P:5609:LEU:HB2	2.31	0.58
1:A:291:ILE:HG12	1:I:2306:GLU:CB	2.32	0.58
4:D:689:GLU:HA	4:D:711:ARG:NH2	2.18	0.58
3:G:3102:ILE:CG2	4:H:3552:ASP:CG	2.75	0.58
4:L:4686:ARG:HH11	4:L:4686:ARG:HG3	1.67	0.58
3:G:3102:ILE:CG2	3:G:3102:ILE:O	2.51	0.58
4:P:5528:ALA:HA	4:P:5571:ASP:HB2	1.85	0.58
2:F:1569:HIS:N	2:F:1599:GLY:O	2.37	0.58
4:L:4541:LYS:HE2	4:L:4583:GLU:O	2.02	0.58
4:H:3688:TRP:CZ2	4:H:3711:ARG:HG3	2.39	0.58
1:E:1038:ILE:HD12	1:E:1269:ALA:HB3	1.85	0.58
4:L:4528:ALA:HA	4:L:4571:ASP:HB2	1.85	0.58
3:O:5102:ILE:HG21	4:P:5552:ASP:CA	2.31	0.58
3:O:5118:ALA:CB	3:O:5150:PHE:CD2	2.77	0.58
1:A:38:ILE:HD12	1:A:269:ALA:HB3	1.85	0.58
3:O:5045:PHE:HE1	4:P:5589:PHE:CE2	2.22	0.58
1:E:1387:HIS:CD2	2:F:1825:GLN:HE21	2.22	0.58
2:F:1678:SER:HB2	4:H:3593:TRP:HE1	1.61	0.58
2:F:1679:GLY:HA3	4:H:3596:ASN:CB	2.34	0.58
1:M:3387:HIS:CD2	2:N:3825:GLN:HE21	2.22	0.58
2:B:569:HIS:N	2:B:599:GLY:O	2.37	0.57
3:C:102:ILE:CB	4:D:552:ASP:CG	2.77	0.57
3:C:118:ALA:HB3	3:C:150:PHE:HE2	0.78	0.57
4:D:514:PRO:CD	4:D:609:LEU:HB2	2.31	0.57
3:K:4118:ALA:HB3	3:K:4150:PHE:HE2	0.78	0.57
1:A:197:LYS:O	1:A:200:SER:OG	2.18	0.57
3:C:102:ILE:HG21	4:D:552:ASP:CA	2.31	0.57
4:D:611:GLN:HG3	4:D:611:GLN:O	2.04	0.57
4:D:700:HIS:O	4:D:701:GLU:C	2.46	0.57
3:G:3102:ILE:HG13	4:H:3552:ASP:CB	2.34	0.57
4:L:4688:TRP:CZ2	4:L:4711:ARG:HG3	2.39	0.57
3:O:5078:THR:HG22	3:O:5080:TYR:CZ	2.25	0.57
3:C:61:ALA:HB3	3:C:64:PHE:HD2	1.70	0.57
3:G:3145:LEU:CD1	4:H:3680:TYR:HE2	2.17	0.57
2:J:2677:PRO:CA	4:L:4595:ASN:HD21	2.02	0.57
3:K:4145:LEU:CD1	4:L:4680:TYR:HE2	2.17	0.57
1:M:3391:TYR:CZ	2:N:3784:LEU:HD11	2.40	0.57

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:O:5145:LEU:CD1	4:P:5680:TYR:HE2	2.17	0.57
4:H:3700:HIS:O	4:H:3701:GLU:C	2.46	0.57
3:K:4061:ALA:HB3	3:K:4064:PHE:HD2	1.70	0.57
4:L:4700:HIS:O	4:L:4701:GLU:C	2.46	0.57
3:O:5102:ILE:CG2	4:P:5552:ASP:CG	2.75	0.57
1:A:391:TYR:CZ	2:B:784:LEU:HD11	2.40	0.57
3:G:3078:THR:CG2	3:G:3080:TYR:CE2	2.84	0.57
3:G:3102:ILE:HG21	4:H:3552:ASP:CA	2.31	0.57
1:I:2391:TYR:CZ	2:J:2784:LEU:HD11	2.39	0.57
4:L:4611:GLN:HG3	4:L:4611:GLN:O	2.05	0.57
3:O:5102:ILE:CB	4:P:5552:ASP:CG	2.77	0.57
2:F:1577:SER:O	2:F:1589:GLN:N	2.37	0.57
3:K:4102:ILE:CB	4:L:4552:ASP:CG	2.77	0.57
1:A:387:HIS:CD2	2:B:825:GLN:HE21	2.22	0.57
3:G:3117:SER:O	3:G:3118:ALA:HB2	2.05	0.57
2:N:3530:GLY:O	2:N:3590:CYS:N	2.38	0.57
2:N:3577:SER:O	2:N:3589:GLN:N	2.37	0.57
3:O:5100:TYR:CE2	3:O:5101:PHE:CZ	2.93	0.57
1:E:1391:TYR:CZ	2:F:1784:LEU:HD11	2.40	0.56
3:G:3032:TYR:CE1	3:G:3100:TYR:HD1	1.97	0.56
1:I:2038:ILE:HD12	1:I:2269:ALA:HB3	1.85	0.56
4:L:4684:THR:O	4:L:4685:ALA:C	2.48	0.56
4:P:5688:TRP:CZ2	4:P:5711:ARG:HG3	2.39	0.56
3:C:45:PHE:HE1	4:D:589:PHE:CE2	2.22	0.56
2:F:1530:GLY:O	2:F:1590:CYS:N	2.38	0.56
3:G:3061:ALA:HB3	3:G:3064:PHE:HD2	1.70	0.56
4:P:5684:THR:O	4:P:5685:ALA:C	2.48	0.56
4:D:688:TRP:CZ2	4:D:711:ARG:HG3	2.39	0.56
4:H:3557:ARG:HE	4:H:3560:VAL:HG23	1.70	0.56
4:H:3653:VAL:HG23	4:H:3658:VAL:CG2	2.35	0.56
4:P:5557:ARG:HE	4:P:5560:VAL:HG23	1.70	0.56
4:P:5611:GLN:HG3	4:P:5611:GLN:O	2.05	0.56
4:P:5653:VAL:HG23	4:P:5658:VAL:CG2	2.35	0.56
3:C:100:TYR:CE2	3:C:101:PHE:CZ	2.93	0.56
3:K:4045:PHE:HE1	4:L:4589:PHE:CE2	2.22	0.56
3:K:4100:TYR:CE2	3:K:4101:PHE:CZ	2.93	0.56
3:O:5035:LEU:HD23	3:O:5037:VAL:HG23	1.82	0.56
3:C:145:LEU:CD1	4:D:680:TYR:HE2	2.17	0.56
4:D:684:THR:O	4:D:685:ALA:C	2.48	0.56
3:G:3100:TYR:CE2	3:G:3101:PHE:CZ	2.93	0.56
4:H:3611:GLN:HG3	4:H:3611:GLN:O	2.05	0.56

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:2057:SER:OG	2:J:2724:SER:O	2.16	0.56
2:J:2561:LYS:HE2	4:L:4531:SER:CB	2.36	0.56
2:F:1678:SER:HB2	4:H:3593:TRP:CD1	2.36	0.56
4:P:5620:LEU:HD23	4:P:5636:VAL:O	2.06	0.56
4:H:3514:PRO:CD	4:H:3609:LEU:HB2	2.31	0.56
2:N:3678:SER:N	4:P:5596:ASN:HD22	2.04	0.56
3:O:5032:TYR:CE1	3:O:5100:TYR:CB	2.89	0.56
3:O:5061:ALA:HB3	3:O:5064:PHE:HD2	1.70	0.56
3:C:32:TYR:CE1	3:C:100:TYR:CB	2.89	0.56
3:K:4011:VAL:HB	3:K:4151:PRO:HB2	1.87	0.56
3:K:4045:PHE:CE1	4:L:4589:PHE:CZ	2.94	0.56
3:O:5045:PHE:CE1	4:P:5589:PHE:CZ	2.94	0.56
3:C:102:ILE:HG22	4:D:534:CYS:CB	2.13	0.56
4:D:620:LEU:HD23	4:D:636:VAL:O	2.06	0.56
1:I:2387:HIS:CD2	2:J:2825:GLN:HE21	2.22	0.56
4:L:4514:PRO:HD3	4:L:4609:LEU:HB3	1.79	0.56
1:A:194:GLY:N	1:A:205:GLN:OE1	2.39	0.55
1:A:221:LYS:O	1:A:235:THR:OG1	2.19	0.55
2:B:559:THR:HG21	4:D:532:SER:HA	1.87	0.55
4:H:3620:LEU:HD23	4:H:3636:VAL:O	2.06	0.55
2:J:2530:GLY:O	2:J:2590:CYS:N	2.38	0.55
2:N:3569:HIS:N	2:N:3599:GLY:O	2.37	0.55
1:A:291:ILE:CG2	1:I:2316:ILE:CD1	2.84	0.55
3:C:32:TYR:CE1	3:C:100:TYR:HD1	1.97	0.55
3:C:102:ILE:CG2	4:D:552:ASP:CG	2.75	0.55
4:D:557:ARG:HE	4:D:560:VAL:HG23	1.70	0.55
3:G:3037:VAL:HG21	3:G:3107:TRP:HH2	1.70	0.55
4:L:4689:GLU:HA	4:L:4711:ARG:HH21	1.72	0.55
4:P:5689:GLU:HA	4:P:5711:ARG:HE	1.72	0.55
4:L:4514:PRO:CD	4:L:4609:LEU:HB2	2.31	0.55
4:L:4620:LEU:HD23	4:L:4636:VAL:O	2.06	0.55
3:C:78:THR:CG2	3:C:80:TYR:CE2	2.84	0.55
4:D:620:LEU:HD21	4:D:651:TRP:HH2	1.72	0.55
4:L:4557:ARG:HE	4:L:4560:VAL:HG23	1.70	0.55
1:M:3194:GLY:N	1:M:3205:GLN:OE1	2.39	0.55
3:O:5117:SER:O	3:O:5118:ALA:HB2	2.05	0.55
4:P:5653:VAL:CG2	4:P:5658:VAL:HG21	2.35	0.55
3:C:126:TYR:CZ	4:D:627:GLU:HG3	2.41	0.55
2:F:1679:GLY:HA3	4:H:3596:ASN:HB3	1.88	0.55
2:F:1679:GLY:N	4:H:3596:ASN:ND2	2.51	0.55
3:G:3045:PHE:CE1	4:H:3589:PHE:CZ	2.94	0.55

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:G:3126:TYR:CZ	4:H:3627:GLU:HG3	2.41	0.55
2:J:2507:PRO:HB3	2:N:3630:GLU:HB2	1.89	0.55
4:L:4653:VAL:CG2	4:L:4658:VAL:HG21	2.35	0.55
3:G:3102:ILE:CB	4:H:3552:ASP:CG	2.77	0.55
2:N:3543:LYS:HZ3	3:O:5100:TYR:HE1	1.53	0.55
3:C:45:PHE:CE1	4:D:589:PHE:CZ	2.94	0.55
4:D:565:SER:O	4:D:575:LEU:HD23	2.07	0.55
1:E:1194:GLY:N	1:E:1205:GLN:OE1	2.39	0.55
2:J:2569:HIS:N	2:J:2599:GLY:O	2.37	0.55
4:L:4620:LEU:HD21	4:L:4651:TRP:HH2	1.72	0.55
2:B:530:GLY:O	2:B:590:CYS:N	2.38	0.55
2:F:1508:ASN:OD1	2:F:1610:THR:OG1	2.11	0.55
2:J:2502:TYR:N	2:J:2537:SER:O	2.40	0.55
2:J:2577:SER:O	2:J:2589:GLN:N	2.37	0.55
3:K:4117:SER:O	3:K:4118:ALA:HB2	2.05	0.55
2:N:3508:ASN:OD1	2:N:3610:THR:OG1	2.11	0.55
3:O:5126:TYR:CZ	4:P:5627:GLU:HG3	2.41	0.55
4:D:507:GLU:OE2	4:D:521:THR:OG1	2.23	0.55
3:G:3045:PHE:HE1	4:H:3589:PHE:CE2	2.22	0.55
4:H:3684:THR:O	4:H:3685:ALA:C	2.48	0.55
4:L:4507:GLU:OE2	4:L:4521:THR:OG1	2.23	0.55
4:L:4565:SER:O	4:L:4575:LEU:HD23	2.07	0.55
3:O:5045:PHE:HZ	4:P:5546:PHE:HZ	0.62	0.55
4:D:689:GLU:HA	4:D:711:ARG:HH21	1.72	0.55
1:I:2194:GLY:N	1:I:2205:GLN:OE1	2.39	0.55
3:K:4030:THR:CG2	3:K:4054:ASN:HD22	2.17	0.55
3:K:4126:TYR:CZ	4:L:4627:GLU:HG3	2.41	0.55
2:B:502:TYR:N	2:B:537:SER:O	2.40	0.54
4:D:653:VAL:HG23	4:D:658:VAL:CG2	2.35	0.54
4:H:3689:GLU:HA	4:H:3711:ARG:HE	1.72	0.54
3:K:4035:LEU:HD23	3:K:4037:VAL:HG23	1.82	0.54
3:O:5102:ILE:HG22	4:P:5552:ASP:HA	1.89	0.54
3:K:4037:VAL:HG21	3:K:4107:TRP:HH2	1.70	0.54
4:P:5565:SER:O	4:P:5575:LEU:HD23	2.07	0.54
2:F:1594:ASP:OD2	2:J:2627:HIS:HB2	2.08	0.54
4:H:3620:LEU:HD21	4:H:3651:TRP:HH2	1.72	0.54
3:C:117:SER:O	3:C:118:ALA:HB2	2.05	0.54
4:D:689:GLU:HA	4:D:711:ARG:HE	1.72	0.54
4:L:4689:GLU:HA	4:L:4711:ARG:HE	1.72	0.54
2:B:652:GLU:OE2	2:B:738:LYS:NZ	2.41	0.54
2:F:1677:PRO:HD2	2:F:1680:ALA:HB3	1.90	0.54

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:1630:GLU:HB2	2:N:3507:PRO:HB3	1.89	0.54
3:K:4102:ILE:CG2	3:K:4102:ILE:O	2.51	0.54
1:M:3371:CYS:O	1:M:3372:THR:OG1	2.25	0.54
2:N:3502:TYR:N	2:N:3537:SER:O	2.40	0.54
2:N:3652:GLU:OE2	2:N:3738:LYS:NZ	2.41	0.54
4:H:3689:GLU:HA	4:H:3711:ARG:HH21	1.72	0.54
3:K:4032:TYR:CE1	3:K:4100:TYR:CB	2.89	0.54
3:C:37:VAL:HG21	3:C:107:TRP:HH2	1.70	0.54
1:E:1061:LYS:NZ	1:E:1063:CYS:O	2.41	0.54
2:F:1502:TYR:N	2:F:1537:SER:O	2.40	0.54
2:J:2652:GLU:OE2	2:J:2738:LYS:NZ	2.41	0.54
2:J:2678:SER:OG	4:L:4596:ASN:CA	2.56	0.54
1:E:1221:LYS:O	1:E:1235:THR:OG1	2.19	0.54
3:G:3217:ARG:HH21	4:H:3622:PRO:CD	2.08	0.54
4:H:3565:SER:O	4:H:3575:LEU:HD23	2.07	0.54
4:H:3689:GLU:HA	4:H:3711:ARG:NE	2.23	0.54
3:K:4078:THR:CG2	3:K:4080:TYR:CE2	2.84	0.54
1:M:3061:LYS:NZ	1:M:3063:CYS:O	2.41	0.54
4:P:5554:ASN:C	4:P:5554:ASN:ND2	2.54	0.54
3:G:3035:LEU:HD23	3:G:3037:VAL:HG23	1.82	0.54
3:C:35:LEU:HD23	3:C:37:VAL:HG23	1.82	0.53
3:C:39:GLN:CD	3:C:45:PHE:CE1	2.87	0.53
4:D:654:ASP:OD2	4:D:691:HIS:HB3	2.08	0.53
2:F:1675:THR:CB	4:H:3526:ILE:CG2	2.57	0.53
4:L:4654:ASP:OD2	4:L:4691:HIS:HB3	2.08	0.53
2:B:690:ASP:OD2	2:B:702:THR:N	2.41	0.53
3:C:102:ILE:HG22	4:D:552:ASP:HA	1.89	0.53
2:F:1627:HIS:HB2	2:N:3594:ASP:OD2	2.08	0.53
3:G:3128:LEU:HB3	4:H:3621:PHE:CG	2.44	0.53
4:H:3654:ASP:OD2	4:H:3691:HIS:HB3	2.08	0.53
3:O:5128:LEU:HB3	4:P:5621:PHE:CG	2.44	0.53
4:P:5620:LEU:HD21	4:P:5651:TRP:HH2	1.72	0.53
4:P:5689:GLU:HA	4:P:5711:ARG:HH21	1.72	0.53
1:A:61:LYS:NZ	1:A:63:CYS:O	2.41	0.53
2:F:1652:GLU:OE2	2:F:1738:LYS:NZ	2.41	0.53
1:I:2061:LYS:NZ	1:I:2063:CYS:O	2.41	0.53
3:K:4011:VAL:CG2	3:K:4152:GLU:HB2	2.39	0.53
4:L:4689:GLU:HA	4:L:4711:ARG:NE	2.23	0.53
2:N:3678:SER:CA	4:P:5595:ASN:C	2.80	0.53
3:C:11:VAL:CG2	3:C:152:GLU:HB2	2.38	0.53
3:C:128:LEU:HB3	4:D:621:PHE:CG	2.44	0.53

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:2197:LYS:O	1:I:2200:SER:OG	2.18	0.53
2:J:2690:ASP:OD2	2:J:2702:THR:N	2.42	0.53
4:P:5654:ASP:OD2	4:P:5691:HIS:HB3	2.08	0.53
4:D:554:ASN:C	4:D:554:ASN:ND2	2.54	0.53
2:F:1680:ALA:N	4:H:3595:ASN:CB	2.52	0.53
2:J:2594:ASP:OD2	2:N:3627:HIS:HB2	2.08	0.53
3:C:102:ILE:CG2	3:C:102:ILE:O	2.51	0.53
3:K:4128:LEU:HB3	4:L:4621:PHE:CG	2.44	0.53
4:L:4653:VAL:HG23	4:L:4658:VAL:CG2	2.35	0.53
4:D:504:VAL:CG1	4:D:522:CYS:SG	2.97	0.53
3:K:4033:PRO:HA	3:K:4053:THR:HG23	1.91	0.53
3:O:5011:VAL:HB	3:O:5151:PRO:HB2	1.87	0.53
4:D:683:LEU:HD22	4:D:687:ALA:HB1	1.91	0.53
1:E:1035:ASN:OD1	1:E:1036:THR:N	2.42	0.53
3:G:3011:VAL:CG2	3:G:3152:GLU:HB2	2.38	0.53
3:G:3039:GLN:CD	3:G:3045:PHE:CE1	2.86	0.53
1:I:2221:LYS:O	1:I:2235:THR:OG1	2.19	0.53
3:K:4030:THR:O	3:K:4030:THR:HG22	2.09	0.53
3:O:5033:PRO:HB2	3:O:5051:ILE:O	2.09	0.53
1:A:343:ASN:OD1	1:A:344:ASP:N	2.42	0.53
3:C:33:PRO:HB2	3:C:51:ILE:O	2.09	0.53
4:D:689:GLU:HA	4:D:711:ARG:NE	2.23	0.53
2:F:1690:ASP:OD2	2:F:1702:THR:N	2.41	0.53
3:G:3030:THR:CG2	3:G:3054:ASN:HD22	2.17	0.53
3:G:3102:ILE:HG22	4:H:3552:ASP:HA	1.89	0.53
4:H:3514:PRO:HG2	4:H:3609:LEU:O	2.03	0.53
3:K:4039:GLN:CD	3:K:4045:PHE:CE1	2.87	0.53
3:C:30:THR:CG2	3:C:54:ASN:HD22	2.17	0.53
3:G:3032:TYR:CZ	3:G:3100:TYR:CZ	2.84	0.53
3:O:5102:ILE:HG13	4:P:5552:ASP:CB	2.34	0.53
4:P:5504:VAL:CG1	4:P:5522:CYS:SG	2.97	0.53
3:C:33:PRO:HA	3:C:53:THR:HG23	1.91	0.52
1:E:1005:ALA:N	1:E:1279:ILE:O	2.42	0.52
2:F:1507:PRO:HB3	2:J:2630:GLU:HB2	1.89	0.52
3:G:3032:TYR:CE1	3:G:3100:TYR:CB	2.89	0.52
4:H:3653:VAL:CG2	4:H:3658:VAL:HG21	2.35	0.52
1:I:2035:ASN:OD1	1:I:2036:THR:N	2.42	0.52
1:I:2343:ASN:OD1	1:I:2344:ASP:N	2.42	0.52
4:L:4504:VAL:CG1	4:L:4522:CYS:SG	2.97	0.52
4:L:4683:LEU:HD22	4:L:4687:ALA:HB1	1.91	0.52
1:M:3035:ASN:OD1	1:M:3036:THR:N	2.42	0.52

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M:3260:CYS:H	2:N:3782:ARG:HH22	1.58	0.52
3:O:5033:PRO:HA	3:O:5053:THR:HG23	1.91	0.52
1:A:35:ASN:OD1	1:A:36:THR:N	2.42	0.52
1:E:1343:ASN:OD1	1:E:1344:ASP:N	2.42	0.52
4:H:3504:VAL:CG1	4:H:3522:CYS:SG	2.97	0.52
4:H:3507:GLU:OE2	4:H:3521:THR:OG1	2.23	0.52
2:J:2677:PRO:CB	4:L:4595:ASN:HD22	1.89	0.52
2:N:3677:PRO:HD2	2:N:3680:ALA:HB3	1.90	0.52
2:N:3690:ASP:OD2	2:N:3702:THR:N	2.42	0.52
3:O:5030:THR:CG2	3:O:5054:ASN:HD22	2.17	0.52
2:B:577:SER:O	2:B:589:GLN:N	2.37	0.52
4:H:3683:LEU:HD22	4:H:3687:ALA:HB1	1.91	0.52
1:I:2005:ALA:N	1:I:2279:ILE:O	2.42	0.52
2:J:2561:LYS:HE2	4:L:4531:SER:OG	2.09	0.52
1:M:3315:GLY:O	1:M:3357:PHE:N	2.42	0.52
1:M:3343:ASN:OD1	1:M:3344:ASP:N	2.42	0.52
2:J:2677:PRO:HD2	2:J:2680:ALA:HB3	1.90	0.52
3:C:30:THR:O	3:C:30:THR:HG22	2.09	0.52
3:G:3033:PRO:HA	3:G:3053:THR:HG23	1.91	0.52
3:G:3212:LYS:CE	4:H:3626:GLU:OE1	2.58	0.52
3:K:4033:PRO:HB2	3:K:4051:ILE:O	2.09	0.52
3:K:4102:ILE:HG22	4:L:4552:ASP:HA	1.89	0.52
4:P:5683:LEU:HD22	4:P:5687:ALA:HB1	1.91	0.52
2:J:2678:SER:HB2	4:L:4595:ASN:HB2	0.59	0.52
3:K:4097:VAL:CG2	3:K:4107:TRP:CD2	2.93	0.52
1:M:3005:ALA:N	1:M:3279:ILE:O	2.42	0.52
3:O:5011:VAL:CG2	3:O:5152:GLU:HB2	2.39	0.52
2:B:677:PRO:HD2	2:B:680:ALA:HB3	1.90	0.52
3:K:4212:LYS:CE	4:L:4626:GLU:OE1	2.58	0.52
4:P:5689:GLU:HA	4:P:5711:ARG:NE	2.23	0.52
3:C:212:LYS:CE	4:D:626:GLU:OE1	2.58	0.52
3:K:4107:TRP:HB2	4:L:4546:PHE:CB	2.40	0.52
3:O:5030:THR:O	3:O:5030:THR:HG22	2.09	0.52
3:C:35:LEU:HD23	3:C:36:TRP:N	2.25	0.51
3:G:3030:THR:O	3:G:3030:THR:HG22	2.09	0.51
2:J:2733:ASP:OD1	2:J:2734:THR:N	2.44	0.51
3:K:4035:LEU:HD23	3:K:4036:TRP:N	2.25	0.51
3:O:5097:VAL:CG2	3:O:5107:TRP:CD2	2.93	0.51
3:C:97:VAL:CG2	3:C:107:TRP:CD2	2.93	0.51
3:C:107:TRP:HB2	4:D:546:PHE:CB	2.40	0.51
3:G:3033:PRO:HB2	3:G:3051:ILE:O	2.09	0.51

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:L:4630:THR:HG22	4:L:4632:LYS:HB2	1.91	0.51
1:E:1260:CYS:H	2:F:1782:ARG:HH22	1.58	0.51
3:G:3097:VAL:CG2	3:G:3107:TRP:CD2	2.93	0.51
3:O:5078:THR:CG2	3:O:5080:TYR:OH	2.48	0.51
2:N:3547:VAL:HG13	3:O:5031:GLU:CD	2.35	0.51
2:N:3733:ASP:OD1	2:N:3734:THR:N	2.44	0.51
3:O:5212:LYS:CE	4:P:5626:GLU:OE1	2.58	0.51
4:P:5630:THR:HG22	4:P:5632:LYS:HB2	1.91	0.51
1:A:5:ALA:N	1:A:279:ILE:O	2.42	0.51
1:A:389:VAL:HG12	1:A:390:ASP:H	1.76	0.51
1:E:1315:GLY:O	1:E:1357:PHE:N	2.42	0.51
4:H:3542:PRO:HB2	4:H:3669:LYS:HB2	1.93	0.51
1:I:2260:CYS:H	2:J:2782:ARG:HH22	1.58	0.51
2:J:2569:HIS:O	2:J:2599:GLY:N	2.44	0.51
3:O:5035:LEU:HD23	3:O:5036:TRP:N	2.25	0.51
1:A:315:GLY:O	1:A:357:PHE:N	2.42	0.51
2:J:2508:ASN:OD1	2:J:2610:THR:OG1	2.11	0.51
4:D:549:LEU:HD12	4:D:560:VAL:HG21	1.93	0.51
1:E:1117:ASP:OD1	1:E:1181:TYR:OH	2.20	0.51
2:F:1676:VAL:HB	4:H:3595:ASN:ND2	2.20	0.51
4:H:3643:TYR:HA	4:H:3644:PRO:C	2.36	0.51
4:D:542:PRO:HB2	4:D:669:LYS:HB2	1.93	0.51
4:D:630:THR:HG22	4:D:632:LYS:HB2	1.92	0.51
2:F:1569:HIS:O	2:F:1599:GLY:N	2.44	0.51
4:H:3549:LEU:HD12	4:H:3560:VAL:HG21	1.93	0.51
4:L:4514:PRO:HG2	4:L:4609:LEU:O	2.03	0.51
3:O:5107:TRP:HB2	4:P:5546:PHE:CB	2.40	0.51
2:F:1675:THR:HB	4:H:3526:ILE:HG22	1.86	0.51
4:H:3630:THR:HG22	4:H:3632:LYS:HB2	1.91	0.51
4:P:5514:PRO:HG2	4:P:5609:LEU:O	2.03	0.51
4:P:5643:TYR:HA	4:P:5644:PRO:C	2.36	0.51
3:C:2:ILE:CD1	3:C:98:ARG:HH11	2.15	0.51
3:C:13:ASN:OD1	3:C:116:SER:O	2.29	0.51
1:E:1389:VAL:HG12	1:E:1390:ASP:H	1.76	0.51
2:F:1733:ASP:OD1	2:F:1734:THR:N	2.44	0.51
4:H:3589:PHE:CE1	4:H:3603:GLY:HA3	2.46	0.51
4:L:4589:PHE:CE1	4:L:4603:GLY:HA3	2.46	0.51
3:O:5032:TYR:CD1	3:O:5100:TYR:HB2	2.46	0.51
3:O:5057:GLU:C	3:O:5058:PRO:CD	2.74	0.51
4:D:653:VAL:CG2	4:D:658:VAL:HG21	2.35	0.50
3:G:3035:LEU:HD23	3:G:3036:TRP:N	2.25	0.50

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:K:4013:ASN:OD1	3:K:4116:SER:O	2.29	0.50
4:P:5549:LEU:HD12	4:P:5560:VAL:HG21	1.93	0.50
1:A:260:CYS:H	2:B:782:ARG:HH22	1.58	0.50
3:C:32:TYR:CD1	3:C:100:TYR:HB2	2.46	0.50
4:D:589:PHE:CE1	4:D:603:GLY:HA3	2.46	0.50
3:G:3011:VAL:HB	3:G:3151:PRO:HB2	1.87	0.50
3:G:3013:ASN:OD1	3:G:3116:SER:O	2.29	0.50
1:I:2203:ASP:OD1	1:I:2204:LEU:N	2.43	0.50
1:M:3389:VAL:HG12	1:M:3390:ASP:H	1.76	0.50
2:N:3569:HIS:O	2:N:3599:GLY:N	2.44	0.50
3:O:5032:TYR:CE1	3:O:5100:TYR:HD1	1.97	0.50
2:B:508:ASN:OD1	2:B:610:THR:OG1	2.11	0.50
2:B:733:ASP:OD1	2:B:734:THR:N	2.44	0.50
1:E:1203:ASP:OD1	1:E:1204:LEU:N	2.43	0.50
1:I:2389:VAL:HG12	1:I:2390:ASP:H	1.76	0.50
1:M:3203:ASP:OD1	1:M:3204:LEU:N	2.43	0.50
3:O:5013:ASN:OD1	3:O:5116:SER:O	2.29	0.50
4:P:5589:PHE:CE1	4:P:5603:GLY:HA3	2.46	0.50
3:G:3107:TRP:HB2	4:H:3546:PHE:CB	2.40	0.50
1:I:2315:GLY:O	1:I:2357:PHE:N	2.42	0.50
3:K:4032:TYR:CD1	3:K:4100:TYR:HB2	2.46	0.50
1:A:15:TYR:O	1:A:17:ALA:N	2.44	0.50
1:A:388:ILE:HD12	1:A:388:ILE:O	2.12	0.50
3:G:3032:TYR:CD1	3:G:3100:TYR:HB2	2.46	0.50
2:J:2559:THR:HB	4:L:4532:SER:HB3	1.62	0.50
4:H:3549:LEU:HD12	4:H:3560:VAL:CG2	2.42	0.50
1:M:3015:TYR:O	1:M:3017:ALA:N	2.44	0.50
2:B:569:HIS:O	2:B:599:GLY:N	2.44	0.50
3:C:11:VAL:HB	3:C:151:PRO:HB2	1.87	0.50
4:L:4643:TYR:HA	4:L:4644:PRO:C	2.36	0.50
2:B:559:THR:CB	4:D:532:SER:HB3	2.42	0.50
2:F:1559:THR:HG21	4:H:3532:SER:N	2.22	0.50
1:M:3221:LYS:O	1:M:3235:THR:OG1	2.19	0.50
4:P:5549:LEU:HD12	4:P:5560:VAL:CG2	2.42	0.50
1:I:2388:ILE:HD12	1:I:2388:ILE:O	2.12	0.50
2:J:2678:SER:CB	4:L:4595:ASN:C	2.85	0.50
4:L:4549:LEU:HD12	4:L:4560:VAL:HG21	1.93	0.50
3:O:5037:VAL:HG21	3:O:5107:TRP:HH2	1.70	0.50
1:I:2007:MET:SD	1:I:2279:ILE:HD12	2.52	0.49
4:L:4542:PRO:HB3	4:L:4669:LYS:CD	2.42	0.49
3:C:24:ALA:HB1	3:C:27:TYR:HE1	1.75	0.49

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:45:PHE:HZ	4:D:546:PHE:HZ	0.62	0.49
1:E:1388:ILE:HD12	1:E:1388:ILE:O	2.12	0.49
1:I:2015:TYR:O	1:I:2017:ALA:N	2.44	0.49
4:L:4542:PRO:HB2	4:L:4669:LYS:HB2	1.93	0.49
1:A:22:PRO:CB	1:I:2382:LYS:CB	2.76	0.49
2:B:677:PRO:C	4:D:594:TYR:O	2.50	0.49
2:J:2678:SER:HB2	4:L:4594:TYR:O	2.11	0.49
4:H:3542:PRO:HB3	4:H:3669:LYS:CD	2.42	0.49
3:K:4045:PHE:HZ	4:L:4546:PHE:HZ	0.62	0.49
4:L:4549:LEU:HD12	4:L:4560:VAL:CG2	2.42	0.49
2:N:3780:THR:OG1	2:N:3791:THR:O	2.30	0.49
4:D:520:LEU:N	4:D:520:LEU:CD2	2.70	0.49
4:D:643:TYR:HA	4:D:644:PRO:C	2.36	0.49
3:K:4102:ILE:HB	4:L:4552:ASP:CA	2.40	0.49
1:M:3301:GLU:O	1:M:3320:ALA:N	2.43	0.49
2:N:3679:GLY:H	4:P:5596:ASN:ND2	2.10	0.49
1:A:203:ASP:OD1	1:A:204:LEU:N	2.43	0.49
2:F:1796:GLU:N	2:F:1796:GLU:OE1	2.45	0.49
3:G:3035:LEU:HB3	3:G:3097:VAL:HB	1.95	0.49
4:P:5542:PRO:HB2	4:P:5669:LYS:HB2	1.92	0.49
1:A:89:TRP:N	2:B:515:ASP:OD2	2.46	0.49
3:G:3078:THR:CG2	3:G:3080:TYR:OH	2.48	0.49
3:K:4104:LEU:N	4:L:4536:ASN:OD1	2.43	0.49
4:P:5506:GLN:OE1	4:P:5601:GLY:HA3	2.13	0.49
3:C:35:LEU:HB3	3:C:97:VAL:HB	1.95	0.49
4:D:549:LEU:HD12	4:D:560:VAL:CG2	2.42	0.49
2:F:1678:SER:CB	4:H:3593:TRP:HE1	2.23	0.49
3:K:4024:ALA:HB1	3:K:4027:TYR:HE1	1.75	0.49
1:M:3388:ILE:HD12	1:M:3388:ILE:O	2.12	0.49
3:O:5078:THR:CG2	3:O:5080:TYR:CE2	2.84	0.49
1:A:265:GLU:OE1	1:A:268:ARG:NH2	2.46	0.49
1:A:301:GLU:O	1:A:320:ALA:N	2.43	0.49
4:D:506:GLN:OE1	4:D:601:GLY:HA3	2.13	0.49
1:E:1197:LYS:O	1:E:1200:SER:OG	2.18	0.49
4:L:4506:GLN:OE1	4:L:4601:GLY:HA3	2.13	0.49
4:P:5512:THR:HG22	4:P:5608:VAL:HG22	1.95	0.49
4:H:3597:LEU:HD12	4:H:3597:LEU:C	2.38	0.49
3:K:4011:VAL:CG2	3:K:4152:GLU:N	2.70	0.49
4:D:512:THR:HG22	4:D:608:VAL:HG22	1.95	0.48
1:E:1015:TYR:O	1:E:1017:ALA:N	2.44	0.48
3:G:3048:MET:HG2	3:G:3064:PHE:CE1	2.48	0.48

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:2265:GLU:OE1	1:I:2268:ARG:NH2	2.46	0.48
3:K:4035:LEU:HB3	3:K:4097:VAL:HB	1.95	0.48
3:C:2:ILE:HA	3:C:25:SER:O	2.13	0.48
3:C:48:MET:HG2	3:C:64:PHE:CE1	2.48	0.48
3:C:102:ILE:HB	4:D:552:ASP:CA	2.40	0.48
1:E:1007:MET:SD	1:E:1279:ILE:HD12	2.52	0.48
3:G:3024:ALA:HB1	3:G:3027:TYR:HE1	1.75	0.48
1:I:2117:ASP:OD1	1:I:2181:TYR:OH	2.20	0.48
1:M:3007:MET:SD	1:M:3279:ILE:HD12	2.52	0.48
1:A:7:MET:SD	1:A:279:ILE:HD12	2.52	0.48
1:E:1265:GLU:OE1	1:E:1268:ARG:NH2	2.46	0.48
1:I:2301:GLU:OE1	1:I:2303:LYS:NZ	2.40	0.48
4:L:4597:LEU:C	4:L:4597:LEU:HD12	2.38	0.48
1:M:3037:ARG:HH12	1:M:3132:MET:HG3	1.79	0.48
3:O:5018:VAL:O	3:O:5082:GLN:HA	2.14	0.48
4:P:5597:LEU:C	4:P:5597:LEU:HD12	2.38	0.48
4:D:597:LEU:C	4:D:597:LEU:HD12	2.38	0.48
2:J:2796:GLU:OE1	2:J:2796:GLU:N	2.46	0.48
1:M:3268:ARG:NE	1:M:3270:GLU:OE2	2.47	0.48
1:A:371:CYS:O	1:A:372:THR:OG1	2.25	0.48
3:C:217:ARG:HH21	4:D:622:PRO:CD	2.08	0.48
1:E:1096:CYS:O	1:E:1100:ASN:ND2	2.46	0.48
1:I:2089:TRP:N	2:J:2515:ASP:OD2	2.46	0.48
4:L:4512:THR:HG22	4:L:4608:VAL:HG22	1.95	0.48
1:M:3265:GLU:OE1	1:M:3268:ARG:NH2	2.46	0.48
3:O:5039:GLN:CD	3:O:5045:PHE:CE1	2.87	0.48
3:K:4002:ILE:HA	3:K:4025:SER:O	2.13	0.48
2:N:3796:GLU:OE1	2:N:3796:GLU:N	2.45	0.48
3:O:5011:VAL:CB	3:O:5151:PRO:CB	2.86	0.48
4:P:5507:GLU:OE2	4:P:5521:THR:OG1	2.23	0.48
2:B:796:GLU:OE1	2:B:796:GLU:N	2.46	0.48
1:I:2037:ARG:HH12	1:I:2132:MET:HG3	1.79	0.48
1:I:2268:ARG:NE	1:I:2270:GLU:OE2	2.47	0.48
1:M:3260:CYS:H	2:N:3782:ARG:NH2	2.11	0.48
1:E:1268:ARG:NE	1:E:1270:GLU:OE2	2.47	0.48
1:M:3129:VAL:HG22	1:M:3149:VAL:HG11	1.96	0.48
3:G:3018:VAL:O	3:G:3082:GLN:HA	2.14	0.48
4:H:3512:THR:HG22	4:H:3608:VAL:HG22	1.95	0.48
3:O:5048:MET:HG2	3:O:5064:PHE:CE1	2.48	0.48
1:A:37:ARG:HH12	1:A:132:MET:HG3	1.79	0.48
3:C:18:VAL:O	3:C:82:GLN:HA	2.14	0.48

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:1260:CYS:H	2:F:1782:ARG:NH2	2.11	0.48
3:G:3002:ILE:HA	3:G:3025:SER:O	2.13	0.48
3:O:5002:ILE:HA	3:O:5025:SER:O	2.13	0.48
1:A:268:ARG:NE	1:A:270:GLU:OE2	2.47	0.47
4:H:3703:HIS:ND1	4:H:3703:HIS:N	2.62	0.47
3:O:5097:VAL:HG21	3:O:5107:TRP:CD2	2.49	0.47
1:A:391:TYR:CE2	2:B:784:LEU:HD11	2.49	0.47
3:K:4018:VAL:O	3:K:4082:GLN:HA	2.14	0.47
1:M:3391:TYR:CE2	2:N:3784:LEU:HD11	2.49	0.47
3:O:5035:LEU:HG	3:O:5047:TRP:NE1	2.29	0.47
4:P:5689:GLU:HA	4:P:5711:ARG:CZ	2.44	0.47
4:P:5703:HIS:N	4:P:5703:HIS:ND1	2.62	0.47
1:E:1089:TRP:N	2:F:1515:ASP:OD2	2.46	0.47
3:G:3097:VAL:HG22	3:G:3107:TRP:CE3	2.49	0.47
1:I:2312:ASP:OD1	1:I:2313:PHE:N	2.48	0.47
1:M:3312:ASP:OD1	1:M:3313:PHE:N	2.48	0.47
3:O:5035:LEU:HB3	3:O:5097:VAL:HB	1.95	0.47
1:A:129:VAL:HG22	1:A:149:VAL:HG11	1.96	0.47
1:A:390:ASP:O	2:B:823:TRP:HB3	2.14	0.47
3:C:48:MET:HE1	3:C:81:LEU:HD21	1.97	0.47
4:D:703:HIS:ND1	4:D:703:HIS:N	2.62	0.47
4:H:3506:GLN:OE1	4:H:3601:GLY:HA3	2.13	0.47
1:I:2260:CYS:H	2:J:2782:ARG:NH2	2.12	0.47
3:O:5032:TYR:CZ	3:O:5100:TYR:CZ	2.84	0.47
3:C:97:VAL:HG21	3:C:107:TRP:CD2	2.50	0.47
4:D:689:GLU:HA	4:D:711:ARG:CZ	2.45	0.47
4:H:3507:GLU:O	4:H:3604:THR:OG1	2.27	0.47
1:I:2323:SER:N	1:I:2350:SER:OG	2.47	0.47
3:K:4048:MET:HG2	3:K:4064:PHE:CE1	2.47	0.47
1:M:3096:CYS:O	1:M:3100:ASN:ND2	2.46	0.47
2:B:780:THR:OG1	2:B:791:THR:O	2.30	0.47
1:E:1323:SER:N	1:E:1350:SER:OG	2.47	0.47
3:G:3048:MET:HE1	3:G:3081:LEU:HD21	1.97	0.47
3:K:4035:LEU:HG	3:K:4047:TRP:NE1	2.29	0.47
3:K:4107:TRP:CB	4:L:4546:PHE:HB2	2.45	0.47
1:M:3323:SER:N	1:M:3350:SER:OG	2.47	0.47
1:A:260:CYS:H	2:B:782:ARG:NH2	2.11	0.47
1:A:312:ASP:OD1	1:A:313:PHE:N	2.48	0.47
3:C:107:TRP:CB	4:D:546:PHE:HB2	2.45	0.47
1:E:1229:ILE:HG21	2:F:1513:ARG:HE	1.80	0.47
1:E:1371:CYS:O	1:E:1372:THR:OG1	2.25	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:2391:TYR:CE2	2:J:2784:LEU:HD11	2.49	0.47
3:O:5021:SER:CB	3:O:5080:TYR:HE2	2.13	0.47
3:O:5103:SER:HA	4:P:5598:TRP:CH2	2.50	0.47
1:A:246:ARG:NH1	1:A:247:ASP:OD2	2.48	0.47
3:C:35:LEU:HG	3:C:47:TRP:NE1	2.29	0.47
3:G:3032:TYR:OH	3:G:3100:TYR:CE2	2.37	0.47
3:C:103:SER:HA	4:D:598:TRP:CH2	2.50	0.47
1:E:1246:ARG:NH1	1:E:1247:ASP:OD2	2.48	0.47
4:L:4549:LEU:HA	4:L:4560:VAL:HG21	1.97	0.47
4:L:4669:LYS:HB3	4:L:4669:LYS:HE2	1.73	0.47
1:M:3229:ILE:HG21	2:N:3513:ARG:HE	1.80	0.47
3:O:5035:LEU:HD23	3:O:5035:LEU:C	2.40	0.47
4:P:5656:THR:HA	4:P:5657:PRO:HD2	1.62	0.47
1:A:323:SER:N	1:A:350:SER:OG	2.47	0.47
1:E:1037:ARG:HH12	1:E:1132:MET:HG3	1.79	0.47
1:E:1312:ASP:OD1	1:E:1313:PHE:N	2.48	0.47
3:G:3035:LEU:HD23	3:G:3035:LEU:C	2.40	0.47
3:G:3103:SER:HA	4:H:3598:TRP:CH2	2.50	0.47
4:H:3549:LEU:HA	4:H:3560:VAL:HG21	1.97	0.47
1:I:2016:LYS:O	1:I:2332:HIS:ND1	2.48	0.47
1:I:2229:ILE:HG21	2:J:2513:ARG:HE	1.80	0.47
1:I:2390:ASP:O	2:J:2823:TRP:HB3	2.14	0.47
3:K:4103:SER:HA	4:L:4598:TRP:CH2	2.50	0.47
1:M:3016:LYS:O	1:M:3332:HIS:ND1	2.48	0.47
3:O:5107:TRP:CB	4:P:5546:PHE:HB2	2.45	0.47
3:G:3035:LEU:HG	3:G:3047:TRP:NE1	2.29	0.46
3:G:3045:PHE:HE1	4:H:3589:PHE:CZ	2.33	0.46
4:H:3689:GLU:HA	4:H:3711:ARG:CZ	2.45	0.46
3:K:4045:PHE:HE1	4:L:4589:PHE:CZ	2.33	0.46
4:L:4557:ARG:CD	4:L:4558:SER:O	2.63	0.46
4:L:4703:HIS:ND1	4:L:4703:HIS:N	2.62	0.46
1:M:3246:ARG:NH1	1:M:3247:ASP:OD2	2.48	0.46
1:M:3390:ASP:O	2:N:3823:TRP:HB3	2.14	0.46
1:A:16:LYS:O	1:A:332:HIS:ND1	2.48	0.46
1:A:229:ILE:HG21	2:B:513:ARG:HE	1.80	0.46
1:E:1391:TYR:CE2	2:F:1784:LEU:HD11	2.49	0.46
2:F:1558:LYS:HG3	4:H:3532:SER:HB3	1.96	0.46
3:G:3097:VAL:HG21	3:G:3107:TRP:CD2	2.50	0.46
2:J:2780:THR:OG1	2:J:2791:THR:O	2.30	0.46
4:L:4689:GLU:HA	4:L:4711:ARG:CZ	2.45	0.46
3:C:72:LEU:HD13	3:C:74:ILE:CG1	2.46	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:O:5012:LYS:HD2	3:O:5016:GLU:OE1	2.16	0.46
3:C:12:LYS:HD2	3:C:16:GLU:OE1	2.16	0.46
4:D:542:PRO:HB3	4:D:669:LYS:CD	2.42	0.46
1:I:2129:VAL:HG22	1:I:2149:VAL:HG11	1.96	0.46
2:J:2678:SER:CB	4:L:4594:TYR:O	2.62	0.46
4:L:4662:MET:HB2	4:L:4662:MET:HE3	1.59	0.46
3:O:5024:ALA:HB1	3:O:5027:TYR:HE1	1.75	0.46
3:O:5048:MET:HE1	3:O:5081:LEU:HD21	1.97	0.46
4:P:5549:LEU:HA	4:P:5560:VAL:HG21	1.97	0.46
3:C:45:PHE:HE1	4:D:589:PHE:CZ	2.33	0.46
3:C:47:TRP:NE1	3:C:49:GLY:O	2.49	0.46
3:C:97:VAL:CG1	3:C:104:LEU:HB3	2.46	0.46
1:E:1016:LYS:O	1:E:1332:HIS:ND1	2.48	0.46
1:E:1390:ASP:O	2:F:1823:TRP:HB3	2.14	0.46
1:I:2246:ARG:NH1	1:I:2247:ASP:OD2	2.48	0.46
2:N:3661:ASP:OD1	2:N:3663:SER:OG	2.28	0.46
1:E:1129:VAL:HG22	1:E:1149:VAL:HG11	1.96	0.46
3:G:3047:TRP:NE1	3:G:3049:GLY:O	2.49	0.46
3:K:4035:LEU:HD23	3:K:4035:LEU:C	2.40	0.46
3:K:4048:MET:HE1	3:K:4081:LEU:HD21	1.97	0.46
3:O:5097:VAL:HG22	3:O:5107:TRP:CD2	2.51	0.46
4:P:5557:ARG:CD	4:P:5558:SER:O	2.63	0.46
3:C:97:VAL:HG22	3:C:107:TRP:CE3	2.49	0.46
3:G:3067:ARG:HH22	3:G:3090:ASP:CG	2.24	0.46
3:G:3107:TRP:CB	4:H:3546:PHE:HB2	2.45	0.46
3:K:4097:VAL:CG1	3:K:4104:LEU:HB3	2.46	0.46
4:P:5653:VAL:H	4:P:5658:VAL:HG23	1.81	0.46
3:C:97:VAL:HG22	3:C:107:TRP:CD2	2.51	0.46
1:E:1301:GLU:O	1:E:1320:ALA:N	2.43	0.46
3:G:3012:LYS:HD2	3:G:3016:GLU:OE1	2.16	0.46
3:G:3033:PRO:CB	3:G:3051:ILE:O	2.64	0.46
2:J:2678:SER:HG	4:L:4596:ASN:N	2.12	0.46
3:K:4047:TRP:NE1	3:K:4049:GLY:O	2.49	0.46
3:K:4067:ARG:HH22	3:K:4090:ASP:CG	2.24	0.46
3:O:5047:TRP:NE1	3:O:5049:GLY:O	2.49	0.46
3:O:5072:LEU:HD13	3:O:5074:ILE:CG1	2.46	0.46
3:C:35:LEU:HD23	3:C:35:LEU:C	2.40	0.46
4:D:549:LEU:HA	4:D:560:VAL:HG21	1.97	0.46
4:D:557:ARG:CD	4:D:558:SER:O	2.63	0.46
3:G:3097:VAL:CG1	3:G:3104:LEU:HB3	2.46	0.46
1:I:2371:CYS:O	1:I:2372:THR:OG1	2.25	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M:3263:ALA:HB3	1:M:3268:ARG:HE	1.81	0.46
3:O:5045:PHE:HE1	4:P:5589:PHE:CZ	2.33	0.46
3:G:3011:VAL:CG2	3:G:3152:GLU:N	2.70	0.45
3:K:4033:PRO:CB	3:K:4051:ILE:O	2.64	0.45
3:O:5097:VAL:HG22	3:O:5107:TRP:CE3	2.49	0.45
3:C:33:PRO:CB	3:C:51:ILE:O	2.64	0.45
3:C:67:ARG:HH22	3:C:90:ASP:CG	2.24	0.45
4:D:653:VAL:H	4:D:658:VAL:HG23	1.81	0.45
3:G:3045:PHE:HZ	4:H:3546:PHE:HZ	0.62	0.45
3:K:4097:VAL:HG22	3:K:4107:TRP:CE3	2.49	0.45
4:P:5669:LYS:HB3	4:P:5669:LYS:HE2	1.73	0.45
1:A:261:SER:O	1:A:270:GLU:N	2.50	0.45
3:C:30:THR:CG2	3:C:54:ASN:ND2	2.78	0.45
1:E:1391:TYR:CZ	2:F:1784:LEU:CD1	2.99	0.45
1:I:2261:SER:O	1:I:2270:GLU:N	2.50	0.45
3:K:4097:VAL:HG22	3:K:4107:TRP:CD2	2.51	0.45
4:D:563:ARG:CZ	4:D:564:PHE:HE2	2.30	0.45
3:G:3097:VAL:HG22	3:G:3107:TRP:CD2	2.51	0.45
4:L:4653:VAL:H	4:L:4658:VAL:HG23	1.81	0.45
4:P:5563:ARG:CZ	4:P:5564:PHE:HE2	2.30	0.45
2:B:566:ASP:OD1	2:B:567:ASN:N	2.50	0.45
4:H:3563:ARG:CZ	4:H:3564:PHE:HE2	2.30	0.45
1:I:2096:CYS:O	1:I:2100:ASN:ND2	2.46	0.45
1:I:2391:TYR:CZ	2:J:2784:LEU:CD1	2.99	0.45
3:K:4012:LYS:HD2	3:K:4016:GLU:OE1	2.16	0.45
1:M:3261:SER:O	1:M:3270:GLU:N	2.50	0.45
1:M:3391:TYR:CZ	2:N:3784:LEU:CD1	2.99	0.45
3:O:5097:VAL:CG1	3:O:5104:LEU:HB3	2.46	0.45
3:O:5102:ILE:HB	4:P:5552:ASP:CA	2.40	0.45
3:K:4097:VAL:HG21	3:K:4107:TRP:CD2	2.49	0.45
3:O:5217:ARG:HH21	4:P:5622:PRO:CD	2.08	0.45
3:C:103:SER:OG	4:D:551:GLY:HA3	2.17	0.45
1:I:2263:ALA:HB3	1:I:2268:ARG:HE	1.81	0.45
3:K:4047:TRP:CZ2	3:K:4049:GLY:HA2	2.52	0.45
2:N:3547:VAL:HG12	3:O:5031:GLU:CD	2.41	0.45
1:A:96:CYS:O	1:A:100:ASN:ND2	2.46	0.45
3:C:102:ILE:O	4:D:534:CYS:HB3	2.17	0.45
1:E:1263:ALA:HB3	1:E:1268:ARG:HE	1.81	0.45
2:F:1566:ASP:OD1	2:F:1567:ASN:N	2.50	0.45
3:G:3030:THR:CG2	3:G:3054:ASN:ND2	2.78	0.45
4:H:3653:VAL:H	4:H:3658:VAL:HG23	1.81	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:2301:GLU:O	1:I:2320:ALA:N	2.43	0.45
3:K:4103:SER:OG	4:L:4551:GLY:HA3	2.17	0.45
1:M:3089:TRP:N	2:N:3515:ASP:OD2	2.46	0.45
3:O:5102:ILE:O	4:P:5534:CYS:HB3	2.17	0.45
3:O:5103:SER:OG	4:P:5551:GLY:HA3	2.17	0.45
3:C:47:TRP:CZ2	3:C:49:GLY:HA2	2.52	0.45
1:E:1380:ASP:OD1	1:E:1381:CYS:N	2.50	0.45
2:F:1676:VAL:CB	4:H:3595:ASN:ND2	2.73	0.45
2:F:1780:THR:OG1	2:F:1791:THR:O	2.30	0.45
3:G:3047:TRP:CZ2	3:G:3049:GLY:HA2	2.52	0.45
3:G:3057:GLU:C	3:G:3058:PRO:CD	2.74	0.45
3:K:4072:LEU:HD13	3:K:4074:ILE:CG1	2.46	0.45
3:K:4102:ILE:O	4:L:4534:CYS:HB3	2.17	0.45
3:O:5033:PRO:CB	3:O:5051:ILE:O	2.64	0.45
1:A:327:GLY:O	1:A:347:LEU:N	2.50	0.45
1:A:391:TYR:CZ	2:B:784:LEU:CD1	2.99	0.45
4:D:557:ARG:HD2	4:D:558:SER:N	2.32	0.45
4:D:662:MET:HE3	4:D:662:MET:HB2	1.60	0.45
4:H:3557:ARG:HD2	4:H:3558:SER:N	2.32	0.45
3:K:4011:VAL:CB	3:K:4151:PRO:CB	2.86	0.45
3:O:5047:TRP:CZ2	3:O:5049:GLY:HA2	2.52	0.45
3:C:11:VAL:CB	3:C:151:PRO:CB	2.86	0.44
4:D:539:GLN:NE2	4:D:541:LYS:HE3	2.32	0.44
1:E:1261:SER:O	1:E:1270:GLU:N	2.50	0.44
2:F:1661:ASP:OD1	2:F:1663:SER:OG	2.28	0.44
3:G:3021:SER:CB	3:G:3080:TYR:HE2	2.13	0.44
3:G:3104:LEU:N	4:H:3536:ASN:OD1	2.43	0.44
4:L:4539:GLN:NE2	4:L:4541:LYS:HE3	2.32	0.44
3:O:5012:LYS:O	3:O:5115:VAL:HA	2.17	0.44
1:I:2380:ASP:OD1	1:I:2381:CYS:N	2.50	0.44
2:J:2566:ASP:OD1	2:J:2567:ASN:N	2.50	0.44
2:B:571:ARG:HG3	2:B:597:THR:OG1	2.18	0.44
3:C:12:LYS:O	3:C:115:VAL:HA	2.17	0.44
3:C:123:PRO:HB3	3:C:149:TYR:HB3	2.00	0.44
1:E:1327:GLY:O	1:E:1347:LEU:N	2.50	0.44
3:G:3011:VAL:CB	3:G:3151:PRO:CB	2.86	0.44
3:G:3072:LEU:HD13	3:G:3074:ILE:CG1	2.46	0.44
3:K:4100:TYR:CD2	3:K:4101:PHE:CE2	3.06	0.44
3:K:4107:TRP:CB	4:L:4546:PHE:CB	2.95	0.44
2:N:3543:LYS:HZ1	3:O:5100:TYR:HE1	1.57	0.44
3:G:3103:SER:OG	4:H:3551:GLY:HA3	2.17	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:H:3539:GLN:NE2	4:H:3541:LYS:HE3	2.32	0.44
4:H:3638:THR:C	4:H:3639:ILE:HG13	2.43	0.44
4:H:3689:GLU:O	4:H:3689:GLU:HG3	2.18	0.44
3:K:4175:GLN:CG	4:L:4663:GLU:OE2	2.60	0.44
3:K:4217:ARG:HH21	4:L:4622:PRO:CD	2.08	0.44
4:L:4557:ARG:HD2	4:L:4558:SER:N	2.32	0.44
2:N:3566:ASP:OD1	2:N:3567:ASN:N	2.50	0.44
1:A:263:ALA:HB3	1:A:268:ARG:HE	1.81	0.44
3:C:107:TRP:CB	4:D:546:PHE:CB	2.95	0.44
4:D:638:THR:C	4:D:639:ILE:HG13	2.42	0.44
3:G:3107:TRP:CB	4:H:3546:PHE:CB	2.95	0.44
4:H:3523:ARG:HG3	4:H:3523:ARG:NH1	2.32	0.44
4:L:4656:THR:HA	4:L:4657:PRO:HD2	1.62	0.44
3:C:100:TYR:CD2	3:C:101:PHE:CE2	3.06	0.44
1:E:1312:ASP:O	1:E:1314:GLY:N	2.50	0.44
3:K:4012:LYS:O	3:K:4115:VAL:HA	2.17	0.44
3:O:5067:ARG:HH22	3:O:5090:ASP:CG	2.24	0.44
3:O:5107:TRP:CB	4:P:5546:PHE:CB	2.95	0.44
4:H:3556:ARG:HD3	4:H:3560:VAL:HG12	2.00	0.44
2:J:2571:ARG:HG3	2:J:2597:THR:OG1	2.17	0.44
3:K:4078:THR:CG2	3:K:4080:TYR:OH	2.48	0.44
2:F:1571:ARG:HG3	2:F:1597:THR:OG1	2.18	0.44
3:G:3002:ILE:HD13	3:G:3098:ARG:HH11	1.80	0.44
3:G:3123:PRO:HB3	3:G:3149:TYR:HB3	2.00	0.44
4:H:3542:PRO:CB	4:H:3669:LYS:CD	2.95	0.44
1:A:380:ASP:OD1	1:A:381:CYS:N	2.50	0.44
4:D:683:LEU:HD22	4:D:687:ALA:CB	2.48	0.44
3:G:3100:TYR:CD2	3:G:3101:PHE:CE2	3.06	0.44
4:H:3669:LYS:HE2	4:H:3669:LYS:HB3	1.73	0.44
1:M:3380:ASP:OD1	1:M:3381:CYS:N	2.50	0.44
4:P:5542:PRO:CB	4:P:5669:LYS:CD	2.95	0.44
4:P:5556:ARG:HD3	4:P:5560:VAL:HG12	2.00	0.44
4:D:656:THR:HA	4:D:657:PRO:HD2	1.62	0.43
2:F:1556:ASN:O	2:F:1559:THR:OG1	2.30	0.43
3:G:3012:LYS:O	3:G:3115:VAL:HA	2.17	0.43
4:L:4520:LEU:N	4:L:4520:LEU:CD2	2.70	0.43
4:L:4523:ARG:HG3	4:L:4523:ARG:NH1	2.32	0.43
1:I:2152:GLU:OE1	1:I:2152:GLU:N	2.52	0.43
3:O:5104:LEU:N	4:P:5536:ASN:OD1	2.43	0.43
4:P:5539:GLN:NE2	4:P:5541:LYS:HE3	2.33	0.43
3:C:11:VAL:CG2	3:C:152:GLU:N	2.70	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:523:ARG:NH1	4:D:523:ARG:HG3	2.32	0.43
3:G:3102:ILE:O	4:H:3534:CYS:HB3	2.17	0.43
1:I:2312:ASP:O	1:I:2314:GLY:N	2.51	0.43
1:M:3327:GLY:O	1:M:3347:LEU:N	2.50	0.43
4:P:5683:LEU:HD22	4:P:5687:ALA:CB	2.48	0.43
1:A:312:ASP:O	1:A:314:GLY:N	2.51	0.43
4:H:3557:ARG:CD	4:H:3558:SER:O	2.63	0.43
3:K:4078:THR:HB	3:K:4080:TYR:CE1	2.53	0.43
4:L:4563:ARG:CZ	4:L:4564:PHE:HE2	2.30	0.43
4:L:4683:LEU:HD22	4:L:4687:ALA:CB	2.48	0.43
1:M:3007:MET:O	1:M:3277:ILE:N	2.48	0.43
2:N:3571:ARG:HG3	2:N:3597:THR:OG1	2.18	0.43
3:O:5100:TYR:CD2	3:O:5101:PHE:CE2	3.06	0.43
3:O:5123:PRO:HB3	3:O:5149:TYR:HB3	2.00	0.43
2:F:1558:LYS:HG3	4:H:3532:SER:CB	2.46	0.43
3:G:3078:THR:HB	3:G:3080:TYR:CE1	2.54	0.43
4:H:3623:PRO:CG	4:H:3633:ALA:HB1	2.49	0.43
4:H:3683:LEU:HD22	4:H:3687:ALA:CB	2.48	0.43
1:M:3152:GLU:N	1:M:3152:GLU:OE1	2.52	0.43
4:P:5523:ARG:HG3	4:P:5523:ARG:NH1	2.32	0.43
4:P:5557:ARG:HD2	4:P:5558:SER:N	2.32	0.43
4:D:623:PRO:CG	4:D:633:ALA:HB1	2.49	0.43
3:K:4123:PRO:HB3	3:K:4149:TYR:HB3	2.00	0.43
4:L:4556:ARG:HD3	4:L:4560:VAL:HG12	2.00	0.43
1:M:3150:ASN:CG	1:M:3153:THR:HG1	2.20	0.43
3:O:5032:TYR:CZ	3:O:5100:TYR:CG	2.96	0.43
1:A:152:GLU:OE1	1:A:152:GLU:N	2.52	0.43
3:C:32:TYR:CZ	3:C:100:TYR:CZ	2.84	0.43
1:M:3312:ASP:O	1:M:3314:GLY:N	2.51	0.43
4:P:5623:PRO:CG	4:P:5633:ALA:HB1	2.49	0.43
1:A:7:MET:O	1:A:277:ILE:N	2.48	0.43
4:D:514:PRO:HG2	4:D:609:LEU:O	2.03	0.43
3:K:4039:GLN:OE1	3:K:4045:PHE:CZ	2.72	0.43
3:O:5078:THR:HB	3:O:5080:TYR:CE1	2.54	0.43
4:P:5542:PRO:HB3	4:P:5669:LYS:CD	2.42	0.43
2:B:666:SER:N	2:B:673:LYS:O	2.52	0.43
3:C:68:PHE:CD1	3:C:83:ILE:HG12	2.54	0.43
3:G:3102:ILE:HB	4:H:3552:ASP:CA	2.40	0.43
4:L:4540:GLU:HB2	4:L:4546:PHE:CE1	2.54	0.43
1:M:3102:GLN:NE2	1:M:3104:SER:OG	2.47	0.43
3:O:5107:TRP:HB2	4:P:5546:PHE:HB2	2.01	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:L:4689:GLU:O	4:L:4689:GLU:HG3	2.18	0.42
4:P:5638:THR:C	4:P:5639:ILE:HG13	2.42	0.42
3:C:78:THR:HB	3:C:80:TYR:CE1	2.54	0.42
3:G:3088:ASN:O	3:G:3091:THR:HG23	2.20	0.42
4:H:3540:GLU:HB2	4:H:3546:PHE:CE1	2.54	0.42
4:L:4623:PRO:CG	4:L:4633:ALA:HB1	2.49	0.42
4:L:4638:THR:C	4:L:4639:ILE:HG13	2.42	0.42
4:P:5549:LEU:HD12	4:P:5549:LEU:HA	1.85	0.42
3:C:39:GLN:OE1	3:C:45:PHE:CZ	2.72	0.42
3:O:5088:ASN:O	3:O:5091:THR:HG23	2.19	0.42
4:P:5507:GLU:O	4:P:5604:THR:OG1	2.27	0.42
1:A:150:ASN:CG	1:A:153:THR:HG1	2.24	0.42
4:D:540:GLU:HB2	4:D:546:PHE:CE1	2.54	0.42
3:G:3045:PHE:HE2	4:H:3546:PHE:CE1	2.16	0.42
3:K:4021:SER:HG	3:K:4080:TYR:HE2	0.51	0.42
2:N:3666:SER:N	2:N:3673:LYS:O	2.52	0.42
4:P:5639:ILE:HG22	4:P:5642:PHE:CD2	2.54	0.42
4:D:669:LYS:HB3	4:D:669:LYS:HE2	1.73	0.42
4:H:3561:PRO:CG	4:H:3563:ARG:NH1	2.82	0.42
3:K:4107:TRP:HB2	4:L:4546:PHE:HB2	2.01	0.42
4:L:4639:ILE:HG22	4:L:4642:PHE:CD2	2.54	0.42
2:N:3547:VAL:HG12	3:O:5031:GLU:OE2	2.19	0.42
4:D:561:PRO:HG2	4:D:563:ARG:HH12	1.85	0.42
4:D:583:GLU:HG2	4:D:583:GLU:H	1.59	0.42
3:G:3013:ASN:CG	3:G:3117:SER:HA	2.45	0.42
3:G:3068:PHE:CD1	3:G:3083:ILE:HG12	2.54	0.42
3:K:4032:TYR:CZ	3:K:4100:TYR:CG	2.96	0.42
3:K:4088:ASN:O	3:K:4091:THR:HG23	2.19	0.42
2:N:3505:ASP:OD2	2:N:3513:ARG:NH2	2.53	0.42
3:O:5002:ILE:CD1	3:O:5098:ARG:HH11	2.15	0.42
4:P:5540:GLU:HB2	4:P:5546:PHE:CE1	2.54	0.42
1:E:1152:GLU:OE1	1:E:1152:GLU:N	2.51	0.42
2:F:1630:GLU:HB2	2:N:3507:PRO:CB	2.49	0.42
2:F:1666:SER:N	2:F:1673:LYS:O	2.52	0.42
3:G:3018:VAL:HG11	3:G:3113:LEU:HD13	2.02	0.42
3:G:3037:VAL:HB	3:G:3107:TRP:HZ3	1.84	0.42
3:G:3039:GLN:OE1	3:G:3045:PHE:CZ	2.72	0.42
4:H:3526:ILE:HG22	4:H:3526:ILE:O	2.19	0.42
3:O:5013:ASN:CG	3:O:5117:SER:HA	2.45	0.42
4:D:621:PHE:HA	4:D:622:PRO:HD3	1.88	0.42
4:D:689:GLU:O	4:D:689:GLU:HG3	2.18	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M:3075:ASP:HB2	1:M:3216:ALA:HB3	2.02	0.42
3:O:5004:LEU:HD23	3:O:5024:ALA:HA	2.01	0.42
3:O:5011:VAL:CG2	3:O:5152:GLU:N	2.70	0.42
4:P:5587:ILE:HG12	4:P:5605:LYS:HG3	2.02	0.42
4:P:5686:ARG:H	4:P:5686:ARG:HG2	1.64	0.42
4:P:5689:GLU:O	4:P:5689:GLU:HG3	2.18	0.42
3:C:104:LEU:N	4:D:536:ASN:OD1	2.43	0.42
3:G:3004:LEU:HD23	3:G:3024:ALA:HA	2.01	0.42
1:I:2075:ASP:HB2	1:I:2216:ALA:HB3	2.02	0.42
2:J:2666:SER:N	2:J:2673:LYS:O	2.52	0.42
3:K:4068:PHE:CD1	3:K:4083:ILE:HG12	2.54	0.42
4:L:4504:VAL:HG13	4:L:4522:CYS:SG	2.60	0.42
4:L:4556:ARG:HD3	4:L:4560:VAL:O	2.20	0.42
1:M:3038:ILE:HG23	1:M:3129:VAL:HG12	2.02	0.42
2:N:3676:VAL:C	4:P:5595:ASN:HD22	2.28	0.42
2:N:3678:SER:HB2	4:P:5596:ASN:HA	1.24	0.42
3:O:5002:ILE:HD13	3:O:5098:ARG:HH11	1.81	0.42
4:P:5662:MET:HB2	4:P:5662:MET:HE3	1.59	0.42
1:A:75:ASP:HB2	1:A:216:ALA:HB3	2.02	0.42
4:D:556:ARG:HD3	4:D:560:VAL:HG12	2.00	0.42
4:D:561:PRO:CG	4:D:563:ARG:NH1	2.82	0.42
4:D:689:GLU:CA	4:D:711:ARG:HH21	2.33	0.42
4:H:3689:GLU:CA	4:H:3711:ARG:NH2	2.83	0.42
3:K:4004:LEU:HD23	3:K:4024:ALA:HA	2.01	0.42
3:K:4013:ASN:CG	3:K:4117:SER:HA	2.45	0.42
3:C:13:ASN:CG	3:C:117:SER:HA	2.45	0.41
4:D:639:ILE:HG22	4:D:642:PHE:CD2	2.54	0.41
4:H:3504:VAL:HG13	4:H:3522:CYS:SG	2.60	0.41
4:H:3593:TRP:CZ3	4:H:3597:LEU:CA	3.03	0.41
4:H:3689:GLU:CA	4:H:3711:ARG:HH21	2.33	0.41
3:K:4173:LEU:HD12	4:L:4665:THR:CG2	2.39	0.41
3:O:5068:PHE:CD1	3:O:5083:ILE:HG12	2.54	0.41
4:P:5556:ARG:HD3	4:P:5560:VAL:O	2.20	0.41
3:C:4:LEU:HD23	3:C:24:ALA:HA	2.01	0.41
3:C:18:VAL:HG11	3:C:113:LEU:HD13	2.02	0.41
3:C:107:TRP:HB2	4:D:546:PHE:HB2	2.01	0.41
1:E:1075:ASP:HB2	1:E:1216:ALA:HB3	2.02	0.41
2:F:1507:PRO:CB	2:J:2630:GLU:HB2	2.49	0.41
3:O:5039:GLN:OE1	3:O:5045:PHE:CZ	2.72	0.41
4:P:5582:THR:HG1	4:P:5610:GLY:HA3	1.82	0.41
3:C:37:VAL:HB	3:C:107:TRP:HZ3	1.84	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:88:ASN:O	3:C:91:THR:HG23	2.19	0.41
4:D:556:ARG:HD3	4:D:560:VAL:O	2.20	0.41
4:D:620:LEU:HD23	4:D:620:LEU:HA	1.89	0.41
2:F:1505:ASP:OD2	2:F:1513:ARG:NH2	2.53	0.41
3:G:3107:TRP:HB2	4:H:3546:PHE:HB2	2.01	0.41
4:H:3556:ARG:HD3	4:H:3560:VAL:O	2.20	0.41
4:H:3639:ILE:HG22	4:H:3642:PHE:CD2	2.54	0.41
1:I:2038:ILE:HG23	1:I:2129:VAL:HG12	2.02	0.41
2:J:2505:ASP:OD2	2:J:2513:ARG:NH2	2.53	0.41
3:O:5030:THR:CG2	3:O:5054:ASN:ND2	2.78	0.41
3:O:5037:VAL:HB	3:O:5107:TRP:HZ3	1.85	0.41
3:O:5107:TRP:CG	4:P:5546:PHE:HB3	2.55	0.41
4:P:5504:VAL:HG13	4:P:5522:CYS:SG	2.60	0.41
2:B:505:ASP:OD2	2:B:513:ARG:NH2	2.53	0.41
4:D:504:VAL:HG13	4:D:522:CYS:SG	2.60	0.41
4:D:593:TRP:CZ3	4:D:597:LEU:CA	3.03	0.41
1:E:1391:TYR:CE2	2:F:1784:LEU:CD1	3.04	0.41
4:H:3521:THR:HG21	4:H:3572:LYS:HE2	2.03	0.41
2:J:2637:CYS:SG	2:J:2750:CYS:N	2.93	0.41
3:K:4030:THR:CG2	3:K:4054:ASN:ND2	2.78	0.41
3:K:4037:VAL:HB	3:K:4107:TRP:HZ3	1.84	0.41
3:K:4107:TRP:CG	4:L:4546:PHE:HB3	2.55	0.41
4:L:4526:ILE:O	4:L:4526:ILE:HG22	2.19	0.41
4:L:4689:GLU:CA	4:L:4711:ARG:NH2	2.83	0.41
1:M:3391:TYR:CE2	2:N:3784:LEU:CD1	3.04	0.41
3:O:5119:LYS:O	3:O:5150:PHE:HD2	2.04	0.41
4:P:5561:PRO:HG2	4:P:5563:ARG:HH12	1.85	0.41
4:D:579:GLY:O	4:D:580:ALA:C	2.64	0.41
1:E:1134:ASN:OD1	1:E:1135:ILE:N	2.54	0.41
1:I:2293:GLU:OE1	1:I:2293:GLU:N	2.54	0.41
3:K:4119:LYS:O	3:K:4150:PHE:HD2	2.04	0.41
3:K:4170:PHE:HA	3:K:4171:PRO:HD3	1.95	0.41
1:A:134:ASN:OD1	1:A:135:ILE:N	2.54	0.41
4:D:587:ILE:HG12	4:D:605:LYS:HG3	2.02	0.41
1:E:1007:MET:O	1:E:1277:ILE:N	2.48	0.41
1:E:1293:GLU:OE1	1:E:1293:GLU:N	2.54	0.41
2:F:1637:CYS:SG	2:F:1750:CYS:N	2.93	0.41
3:K:4021:SER:CB	3:K:4080:TYR:HE2	2.13	0.41
4:L:4587:ILE:HG12	4:L:4605:LYS:HG3	2.02	0.41
3:O:5018:VAL:HG11	3:O:5113:LEU:HD13	2.02	0.41
1:A:293:GLU:N	1:A:293:GLU:OE1	2.54	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:391:TYR:CE2	2:B:784:LEU:CD1	3.04	0.41
3:C:78:THR:CB	3:C:80:TYR:CE1	3.04	0.41
2:F:1558:LYS:HE2	4:H:3532:SER:HB2	1.02	0.41
3:G:3107:TRP:CG	4:H:3546:PHE:HB3	2.55	0.41
2:J:2558:LYS:HE3	4:L:4595:ASN:HD21	1.85	0.41
4:P:5526:ILE:O	4:P:5526:ILE:HG22	2.19	0.41
4:D:526:ILE:O	4:D:526:ILE:HG22	2.19	0.41
4:H:3656:THR:HA	4:H:3657:PRO:HD2	1.62	0.41
3:K:4018:VAL:HG11	3:K:4113:LEU:HD13	2.02	0.41
3:K:4067:ARG:NH1	3:K:4090:ASP:OD2	2.52	0.41
4:L:4514:PRO:HD2	4:L:4609:LEU:HB3	2.03	0.41
4:L:4521:THR:HG21	4:L:4572:LYS:HE2	2.03	0.41
4:L:4581:GLN:C	4:L:4608:VAL:HG11	2.46	0.41
4:L:4593:TRP:CZ3	4:L:4597:LEU:CA	3.03	0.41
4:P:5561:PRO:CG	4:P:5563:ARG:NH1	2.82	0.41
4:P:5581:GLN:C	4:P:5608:VAL:HG11	2.46	0.41
2:B:502:TYR:HE2	2:B:504:ALA:HB2	1.86	0.41
3:C:107:TRP:CG	4:D:546:PHE:HB3	2.55	0.41
3:G:3011:VAL:HB	3:G:3151:PRO:CB	2.51	0.41
4:H:3587:ILE:HG12	4:H:3605:LYS:HG3	2.02	0.41
1:I:2134:ASN:OD1	1:I:2135:ILE:N	2.54	0.41
1:I:2391:TYR:CE2	2:J:2784:LEU:CD1	3.04	0.41
3:K:4011:VAL:CG2	3:K:4152:GLU:O	2.68	0.41
1:M:3134:ASN:OD1	1:M:3135:ILE:N	2.54	0.41
2:N:3502:TYR:HE2	2:N:3504:ALA:HB2	1.86	0.41
4:P:5683:LEU:CD1	4:P:5694:TYR:CE2	3.01	0.41
4:P:5689:GLU:OE2	4:P:5711:ARG:NH2	2.54	0.41
1:A:102:GLN:NE2	1:A:104:SER:OG	2.47	0.41
3:C:175:GLN:CG	4:D:663:GLU:OE2	2.60	0.41
4:D:514:PRO:CD	4:D:609:LEU:C	2.89	0.41
1:E:1265:GLU:O	1:E:1267:LEU:N	2.54	0.41
3:K:4057:GLU:HA	3:K:4058:PRO:CD	2.51	0.41
3:K:4067:ARG:NH2	3:K:4090:ASP:OD2	2.52	0.41
3:K:4091:THR:O	3:K:4092:ALA:HB2	2.21	0.41
4:L:4609:LEU:HD12	4:L:4609:LEU:HA	1.87	0.41
3:O:5091:THR:O	3:O:5092:ALA:HB2	2.21	0.41
4:P:5695:SER:CB	4:P:5708:SER:OG	2.64	0.41
4:D:521:THR:HG21	4:D:572:LYS:HE2	2.03	0.40
4:D:689:GLU:OE2	4:D:711:ARG:NH2	2.54	0.40
3:G:3002:ILE:CD1	3:G:3098:ARG:HH11	2.15	0.40
4:H:3683:LEU:CD1	4:H:3694:TYR:CE2	3.01	0.40

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:J:2502:TYR:HE2	2:J:2504:ALA:HB2	1.86	0.40
1:M:3265:GLU:O	1:M:3267:LEU:N	2.54	0.40
3:O:5057:GLU:HA	3:O:5058:PRO:CD	2.51	0.40
4:P:5521:THR:HG21	4:P:5572:LYS:HE2	2.03	0.40
4:P:5593:TRP:CZ3	4:P:5597:LEU:CA	3.03	0.40
1:A:38:ILE:HG23	1:A:129:VAL:HG12	2.02	0.40
3:C:119:LYS:O	3:C:150:PHE:HD2	2.04	0.40
3:G:3119:LYS:O	3:G:3150:PHE:HD2	2.04	0.40
3:K:4032:TYR:CE1	3:K:4100:TYR:HB2	2.56	0.40
4:L:4561:PRO:HG2	4:L:4563:ARG:HH12	1.85	0.40
3:O:5078:THR:CB	3:O:5080:TYR:CE1	3.04	0.40
3:C:32:TYR:CZ	3:C:100:TYR:CG	2.96	0.40
1:E:1038:ILE:HG23	1:E:1129:VAL:HG12	2.02	0.40
1:I:2265:GLU:O	1:I:2267:LEU:N	2.54	0.40
1:M:3293:GLU:OE1	1:M:3293:GLU:N	2.54	0.40
1:A:265:GLU:O	1:A:267:LEU:N	2.54	0.40
2:B:579:VAL:O	2:B:580:SER:OG	2.33	0.40
4:D:581:GLN:C	4:D:608:VAL:HG11	2.46	0.40
4:D:628:LEU:HD23	4:D:628:LEU:HA	1.89	0.40
3:G:3078:THR:CB	3:G:3080:TYR:CE1	3.04	0.40
3:G:3097:VAL:HG11	3:G:3104:LEU:HB3	2.04	0.40
3:O:5145:LEU:CD1	4:P:5680:TYR:CE2	3.03	0.40
3:C:32:TYR:CE1	3:C:100:TYR:HB2	2.56	0.40
1:I:2327:GLY:O	1:I:2347:LEU:N	2.50	0.40
3:K:4011:VAL:HB	3:K:4151:PRO:CB	2.51	0.40
3:K:4170:PHE:HE1	4:L:4676:MET:HB2	1.87	0.40
3:O:5175:GLN:NE2	4:P:5663:GLU:HG3	2.37	0.40
4:P:5689:GLU:CA	4:P:5711:ARG:HH21	2.33	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	398/441 (90%)	322 (81%)	72 (18%)	4 (1%)	12	48
1	E	398/441 (90%)	322 (81%)	72 (18%)	4 (1%)	12	48
1	I	398/441 (90%)	322 (81%)	72 (18%)	4 (1%)	12	48
1	M	398/441 (90%)	322 (81%)	72 (18%)	4 (1%)	12	48
2	B	323/420 (77%)	258 (80%)	65 (20%)	0	100	100
2	F	323/420 (77%)	259 (80%)	64 (20%)	0	100	100
2	J	323/420 (77%)	259 (80%)	64 (20%)	0	100	100
2	N	323/420 (77%)	259 (80%)	64 (20%)	0	100	100
3	C	216/218 (99%)	196 (91%)	15 (7%)	5 (2%)	5	28
3	G	216/218 (99%)	196 (91%)	15 (7%)	5 (2%)	5	28
3	K	216/218 (99%)	196 (91%)	15 (7%)	5 (2%)	5	28
3	O	216/218 (99%)	196 (91%)	15 (7%)	5 (2%)	5	28
4	D	209/214 (98%)	188 (90%)	19 (9%)	2 (1%)	12	48
4	H	209/214 (98%)	188 (90%)	19 (9%)	2 (1%)	12	48
4	L	209/214 (98%)	188 (90%)	19 (9%)	2 (1%)	12	48
4	P	209/214 (98%)	188 (90%)	19 (9%)	2 (1%)	12	48
All	All	4584/5172 (89%)	3859 (84%)	681 (15%)	44 (1%)	15	48

All (44) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	390	ASP
3	C	43	LYS
4	D	543	ASP
1	E	1390	ASP
3	G	3043	LYS
4	H	3543	ASP
1	I	2390	ASP
3	K	4043	LYS
4	L	4543	ASP
1	M	3390	ASP
3	O	5043	LYS
4	P	5543	ASP
3	C	103	SER
3	G	3103	SER
3	K	4103	SER
3	O	5103	SER

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
3	C	41	PRO
4	D	701	GLU
3	G	3041	PRO
4	H	3701	GLU
3	K	4041	PRO
4	L	4701	GLU
3	O	5041	PRO
4	P	5701	GLU
1	A	265	GLU
1	A	266	PRO
3	C	118	ALA
1	E	1265	GLU
1	E	1266	PRO
3	G	3118	ALA
1	I	2265	GLU
1	I	2266	PRO
3	K	4118	ALA
1	M	3265	GLU
1	M	3266	PRO
3	O	5118	ALA
3	C	119	LYS
3	G	3119	LYS
3	K	4119	LYS
3	O	5119	LYS
1	A	191	PRO
1	E	1191	PRO
1	I	2191	PRO
1	M	3191	PRO

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	339/370 (92%)	339 (100%)	0	100	100
1	E	339/370 (92%)	339 (100%)	0	100	100
1	I	339/370 (92%)	339 (100%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	M	339/370 (92%)	339 (100%)	0	100	100
2	B	282/367 (77%)	282 (100%)	0	100	100
2	F	282/367 (77%)	282 (100%)	0	100	100
2	J	282/367 (77%)	282 (100%)	0	100	100
2	N	282/367 (77%)	282 (100%)	0	100	100
3	C	188/188 (100%)	176 (94%)	12 (6%)	16	37
3	G	188/188 (100%)	176 (94%)	12 (6%)	16	37
3	K	188/188 (100%)	176 (94%)	12 (6%)	16	37
3	O	188/188 (100%)	176 (94%)	12 (6%)	16	37
4	D	178/183 (97%)	145 (82%)	33 (18%)	1	8
4	H	178/183 (97%)	145 (82%)	33 (18%)	1	8
4	L	178/183 (97%)	145 (82%)	33 (18%)	1	8
4	P	178/183 (97%)	145 (82%)	33 (18%)	1	8
All	All	3948/4432 (89%)	3768 (95%)	180 (5%)	25	45

All (180) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	C	1	GLN
3	C	5	VAL
3	C	7	SER
3	C	28	THR
3	C	41	PRO
3	C	43	LYS
3	C	51	ILE
3	C	62	GLU
3	C	63	GLU
3	C	72	LEU
3	C	73	GLU
3	C	142	LEU
4	D	520	LEU
4	D	523	ARG
4	D	536	ASN
4	D	549	LEU
4	D	550	ILE
4	D	554	ASN
4	D	560	VAL

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
4	D	571	ASP
4	D	575	LEU
4	D	581	GLN
4	D	582	THR
4	D	583	GLU
4	D	605	LYS
4	D	609	LEU
4	D	618	VAL
4	D	620	LEU
4	D	626	GLU
4	D	629	GLU
4	D	630	THR
4	D	632	LYS
4	D	635	LEU
4	D	660	GLN
4	D	662	MET
4	D	666	GLN
4	D	670	GLN
4	D	671	SER
4	D	681	LEU
4	D	684	THR
4	D	686	ARG
4	D	689	GLU
4	D	691	HIS
4	D	705	VAL
4	D	709	LEU
3	G	3001	GLN
3	G	3005	VAL
3	G	3007	SER
3	G	3028	THR
3	G	3041	PRO
3	G	3043	LYS
3	G	3051	ILE
3	G	3062	GLU
3	G	3063	GLU
3	G	3072	LEU
3	G	3073	GLU
3	G	3142	LEU
4	H	3520	LEU
4	H	3523	ARG
4	H	3536	ASN
4	H	3549	LEU

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
4	H	3550	ILE
4	H	3554	ASN
4	H	3560	VAL
4	H	3571	ASP
4	H	3575	LEU
4	H	3581	GLN
4	H	3582	THR
4	H	3583	GLU
4	H	3605	LYS
4	H	3609	LEU
4	H	3618	VAL
4	H	3620	LEU
4	H	3626	GLU
4	H	3629	GLU
4	H	3630	THR
4	H	3632	LYS
4	H	3635	LEU
4	H	3660	GLN
4	H	3662	MET
4	H	3666	GLN
4	H	3670	GLN
4	H	3671	SER
4	H	3681	LEU
4	H	3684	THR
4	H	3686	ARG
4	H	3689	GLU
4	H	3691	HIS
4	H	3705	VAL
4	H	3709	LEU
3	K	4001	GLN
3	K	4005	VAL
3	K	4007	SER
3	K	4028	THR
3	K	4041	PRO
3	K	4043	LYS
3	K	4051	ILE
3	K	4062	GLU
3	K	4063	GLU
3	K	4072	LEU
3	K	4073	GLU
3	K	4142	LEU
4	L	4520	LEU

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
4	L	4523	ARG
4	L	4536	ASN
4	L	4549	LEU
4	L	4550	ILE
4	L	4554	ASN
4	L	4560	VAL
4	L	4571	ASP
4	L	4575	LEU
4	L	4581	GLN
4	L	4582	THR
4	L	4583	GLU
4	L	4605	LYS
4	L	4609	LEU
4	L	4618	VAL
4	L	4620	LEU
4	L	4626	GLU
4	L	4629	GLU
4	L	4630	THR
4	L	4632	LYS
4	L	4635	LEU
4	L	4660	GLN
4	L	4662	MET
4	L	4666	GLN
4	L	4670	GLN
4	L	4671	SER
4	L	4681	LEU
4	L	4684	THR
4	L	4686	ARG
4	L	4689	GLU
4	L	4691	HIS
4	L	4705	VAL
4	L	4709	LEU
3	O	5001	GLN
3	O	5005	VAL
3	O	5007	SER
3	O	5028	THR
3	O	5041	PRO
3	O	5043	LYS
3	O	5051	ILE
3	O	5062	GLU
3	O	5063	GLU
3	O	5072	LEU

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
3	O	5073	GLU
3	O	5142	LEU
4	P	5520	LEU
4	P	5523	ARG
4	P	5536	ASN
4	P	5549	LEU
4	P	5550	ILE
4	P	5554	ASN
4	P	5560	VAL
4	P	5571	ASP
4	P	5575	LEU
4	P	5581	GLN
4	P	5582	THR
4	P	5583	GLU
4	P	5605	LYS
4	P	5609	LEU
4	P	5618	VAL
4	P	5620	LEU
4	P	5626	GLU
4	P	5629	GLU
4	P	5630	THR
4	P	5632	LYS
4	P	5635	LEU
4	P	5660	GLN
4	P	5662	MET
4	P	5666	GLN
4	P	5670	GLN
4	P	5671	SER
4	P	5681	LEU
4	P	5684	THR
4	P	5686	ARG
4	P	5689	GLU
4	P	5691	HIS
4	P	5705	VAL
4	P	5709	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (82) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	77	GLN
1	A	102	GLN
1	A	183	HIS

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	328	ASN
1	A	387	HIS
1	A	394	GLN
2	B	528	HIS
2	B	638	ASN
2	B	662	HIS
2	B	825	GLN
3	C	6	GLN
3	C	54	ASN
3	C	82	GLN
3	C	84	ASN
3	C	85	ASN
3	C	109	GLN
3	C	168	HIS
4	D	554	ASN
4	D	555	ASN
4	D	673	ASN
1	E	1102	GLN
1	E	1183	HIS
1	E	1387	HIS
1	E	1394	GLN
2	F	1528	HIS
2	F	1638	ASN
2	F	1642	HIS
2	F	1825	GLN
3	G	3003	GLN
3	G	3006	GLN
3	G	3054	ASN
3	G	3082	GLN
3	G	3084	ASN
3	G	3109	GLN
3	G	3168	HIS
4	H	3554	ASN
4	H	3555	ASN
4	H	3596	ASN
4	H	3673	ASN
1	I	2102	GLN
1	I	2183	HIS
1	I	2328	ASN
1	I	2356	HIS
1	I	2387	HIS
1	I	2394	GLN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
2	J	2528	HIS
2	J	2638	ASN
2	J	2642	HIS
2	J	2662	HIS
2	J	2825	GLN
3	K	4003	GLN
3	K	4006	GLN
3	K	4054	ASN
3	K	4082	GLN
3	K	4084	ASN
3	K	4109	GLN
3	K	4168	HIS
3	K	4175	GLN
4	L	4554	ASN
4	L	4555	ASN
4	L	4595	ASN
4	L	4673	ASN
1	M	3102	GLN
1	M	3183	HIS
1	M	3328	ASN
1	M	3387	HIS
1	M	3394	GLN
2	N	3528	HIS
2	N	3638	ASN
2	N	3662	HIS
2	N	3825	GLN
3	O	5003	GLN
3	O	5006	GLN
3	O	5054	ASN
3	O	5082	GLN
3	O	5084	ASN
3	O	5109	GLN
3	O	5168	HIS
4	P	5554	ASN
4	P	5555	ASN
4	P	5596	ASN
4	P	5673	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

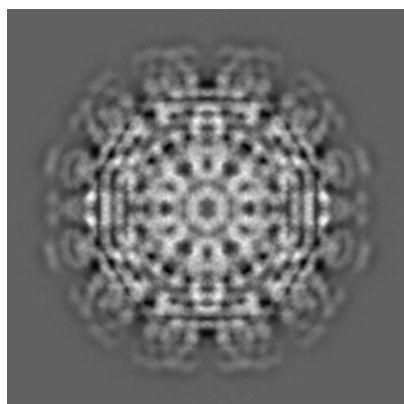
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-9275. These allow visual inspection of the internal detail of the map and identification of artifacts.

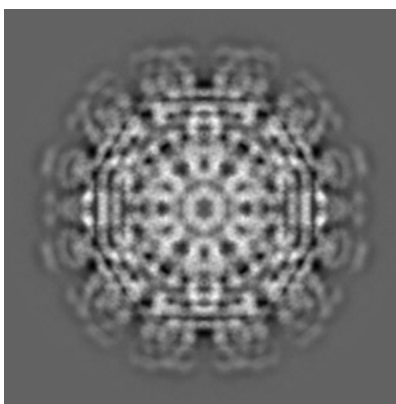
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

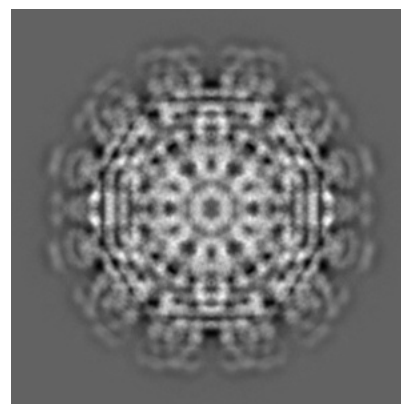
6.1.1 Primary map



X

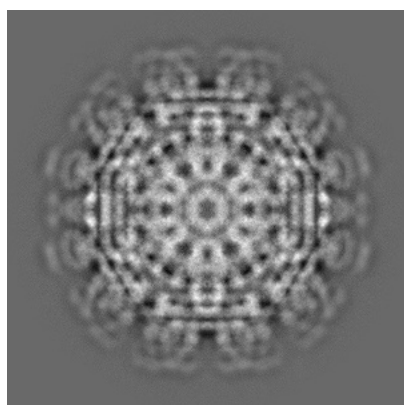


Y

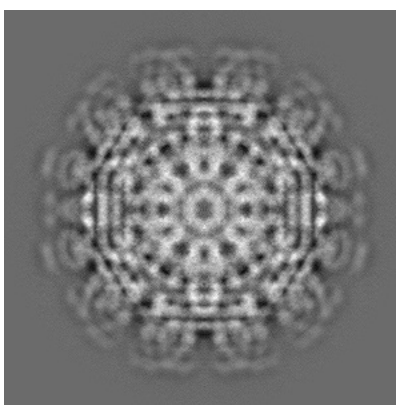


Z

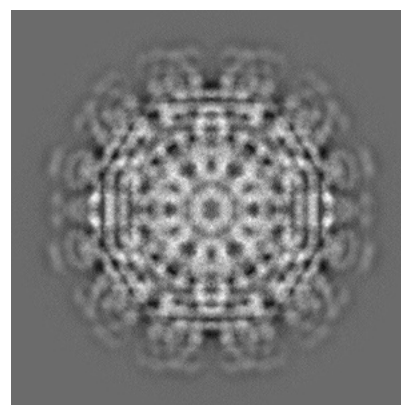
6.1.2 Raw map



X



Y

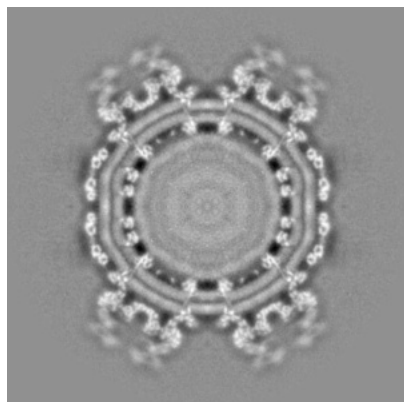


Z

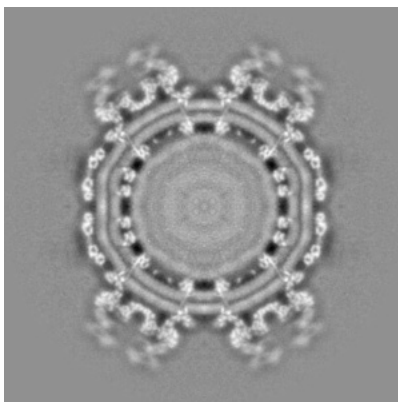
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

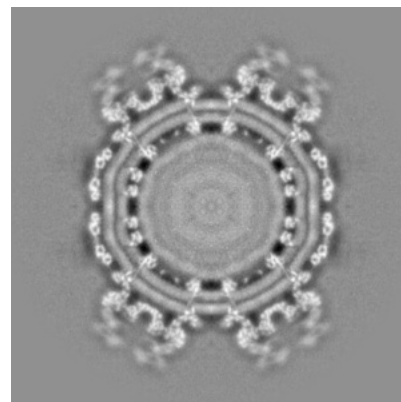
6.2.1 Primary map



X Index: 280

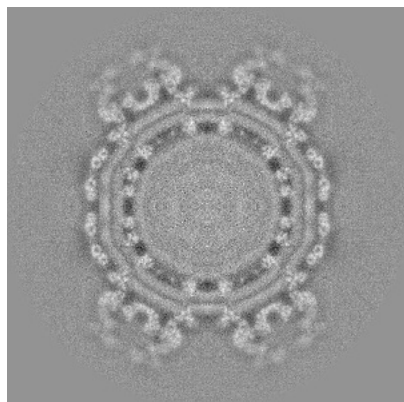


Y Index: 280

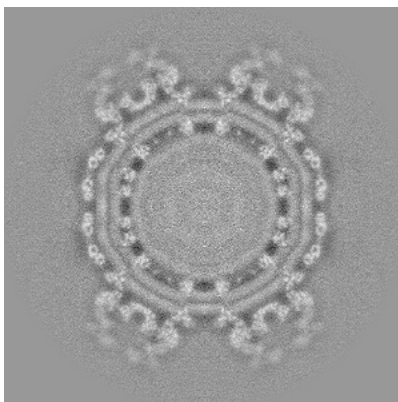


Z Index: 280

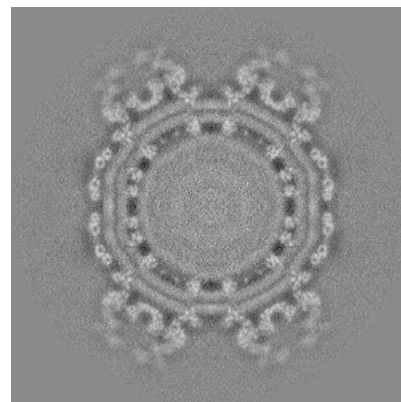
6.2.2 Raw map



X Index: 280



Y Index: 280

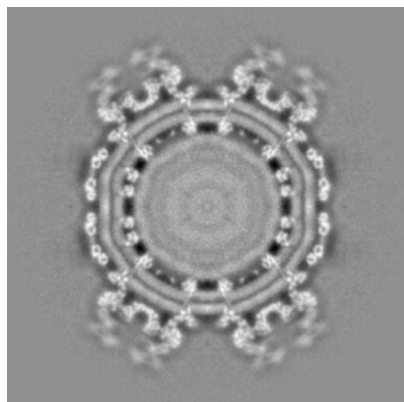


Z Index: 280

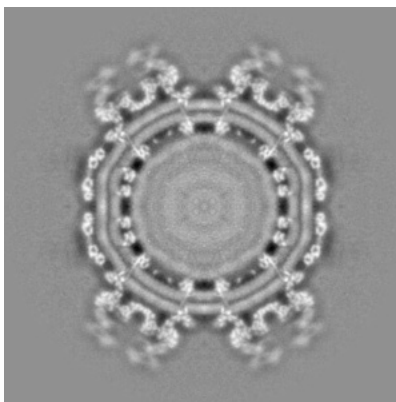
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

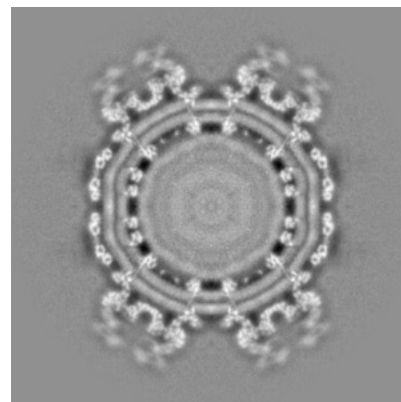
6.3.1 Primary map



X Index: 280

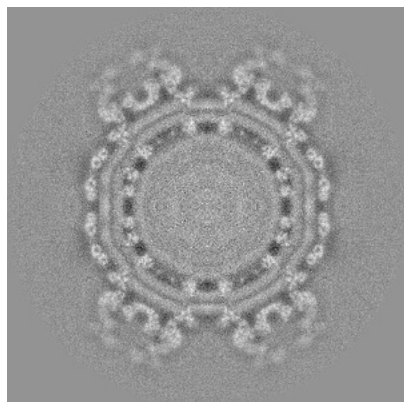


Y Index: 280

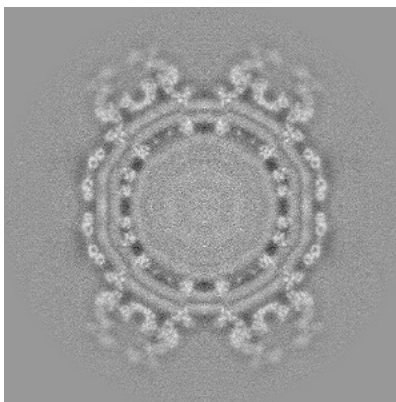


Z Index: 280

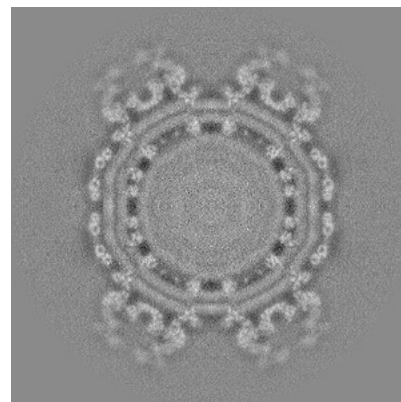
6.3.2 Raw map



X Index: 280



Y Index: 280

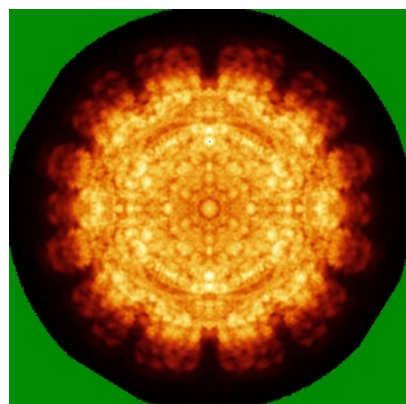


Z Index: 280

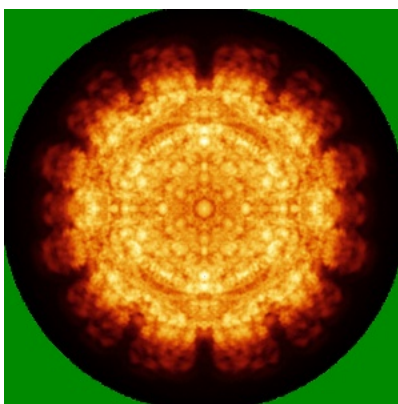
The images above show the largest variance slices of the map in three orthogonal directions.

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

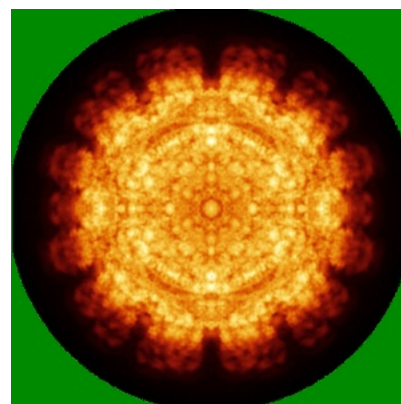
6.4.1 Primary map



X

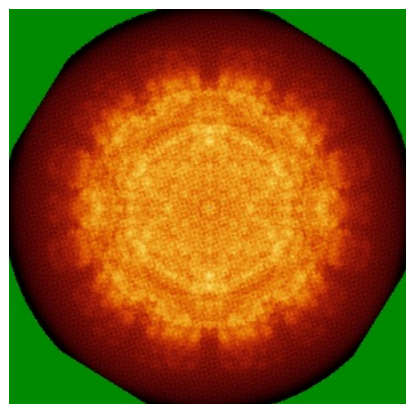


Y

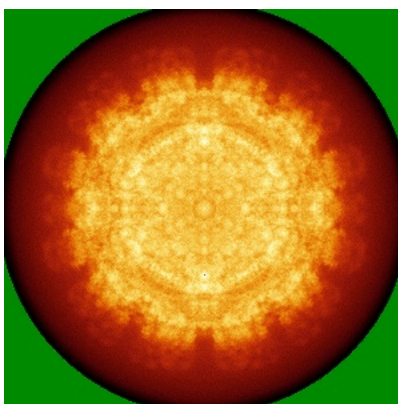


Z

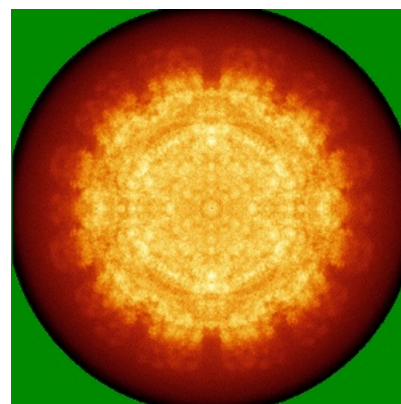
6.4.2 Raw map



X



Y

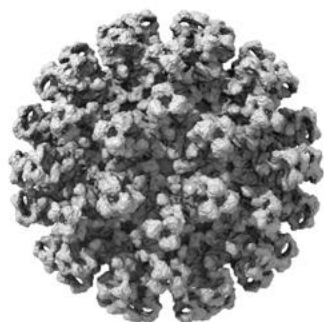


Z

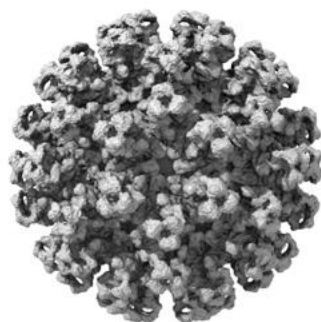
The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

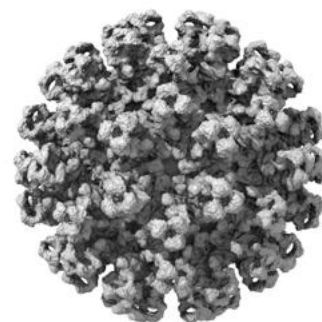
6.5.1 Primary map



X



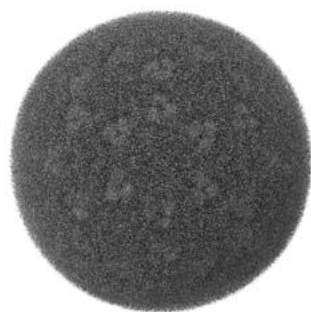
Y



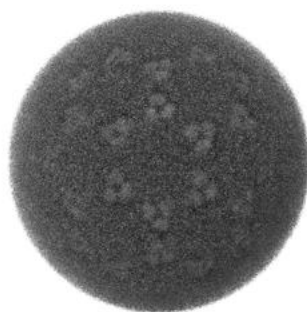
Z

The images above show the 3D surface view of the map at the recommended contour level 0.7. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



X



Y



Z

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

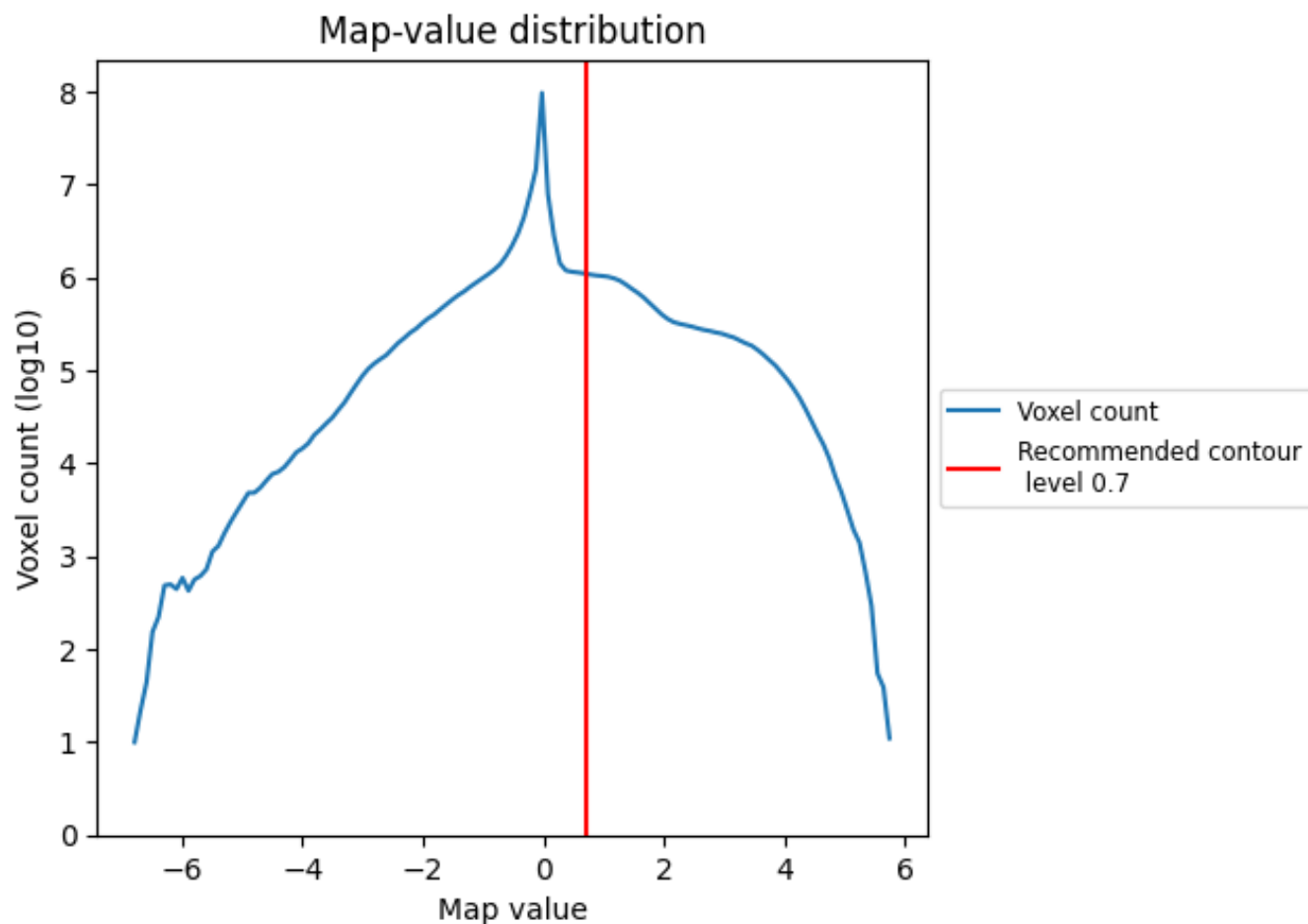
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

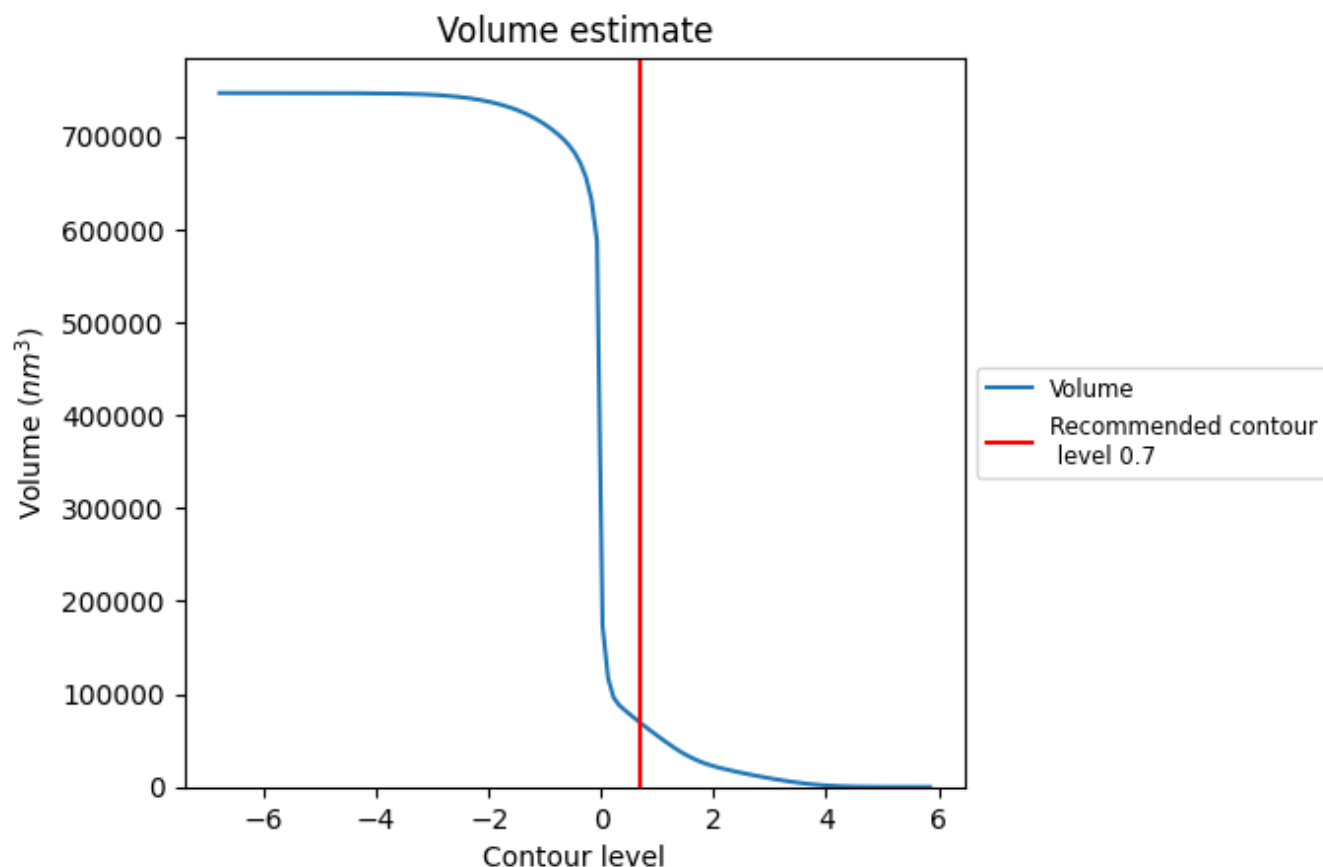
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

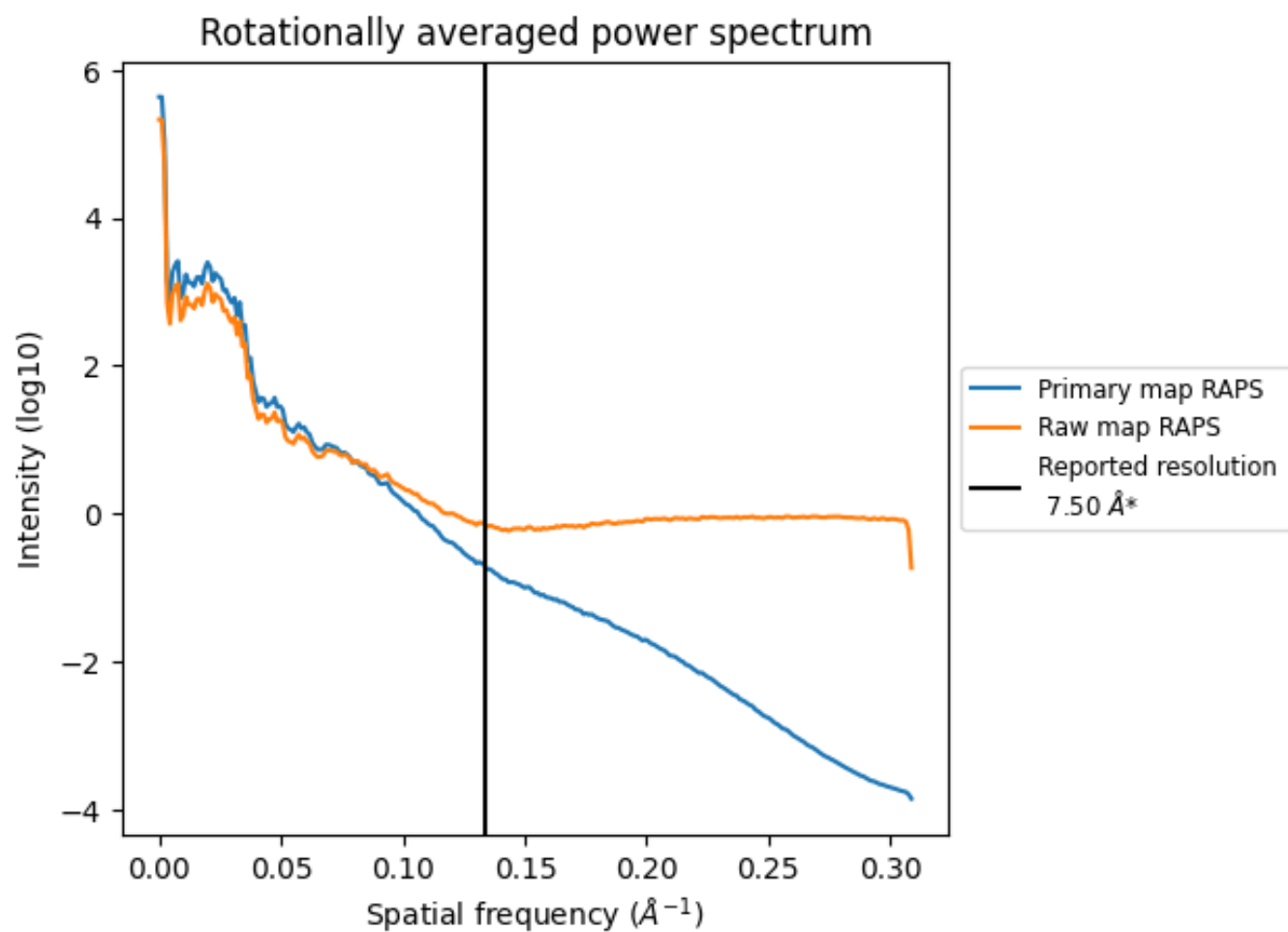
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 68822 nm^3 ; this corresponds to an approximate mass of 62169 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum ⓘ

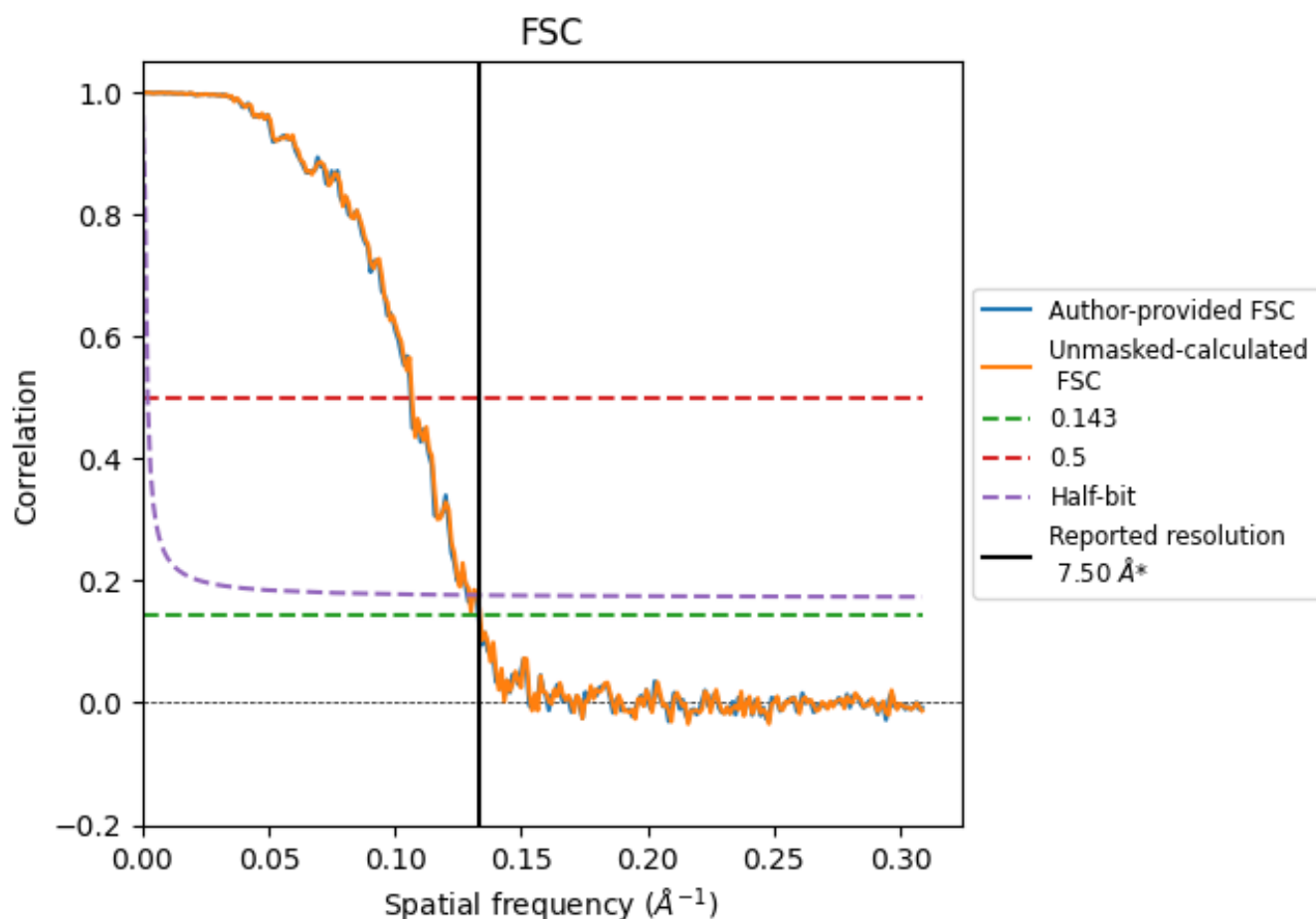


*Reported resolution corresponds to spatial frequency of 0.133 Å⁻¹

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.133 Å⁻¹

8.2 Resolution estimates [i](#)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	7.50	-	-
Author-provided FSC curve	7.51	9.41	7.78
Unmasked-calculated*	7.49	9.36	7.73

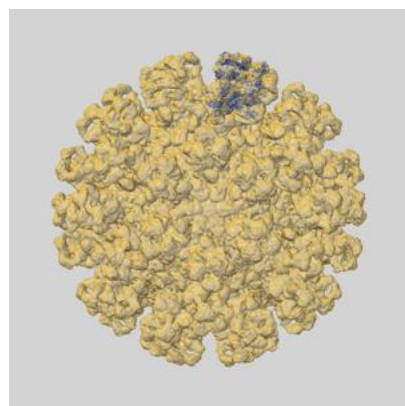
*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

9 Map-model fit [i](#)

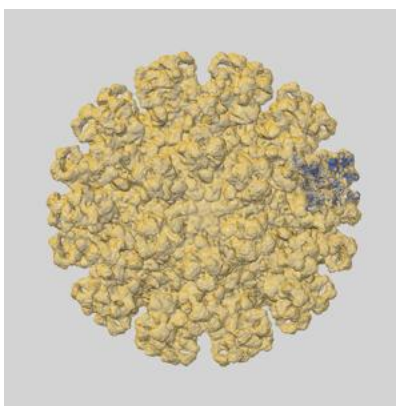
This section contains information regarding the fit between EMDB map EMD-9275 and PDB model 6MWC. Per-residue inclusion information can be found in section 3 on page 6.

9.1 Map-model overlays

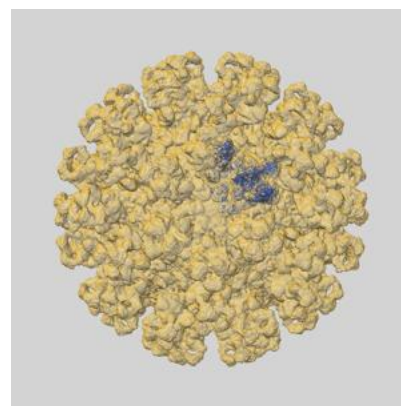
9.1.1 Map-model overlay [i](#)



X

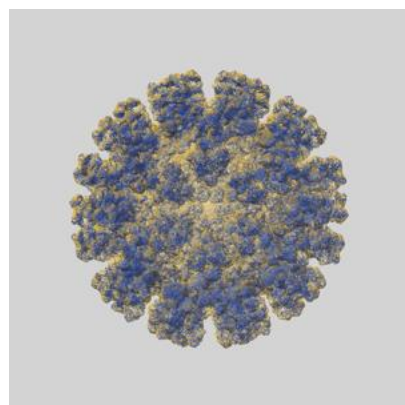


Y

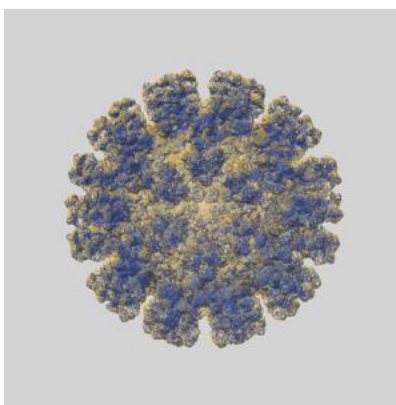


Z

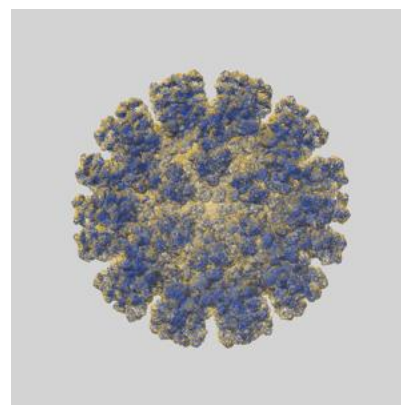
9.1.2 Map-model assembly overlay [i](#)



X



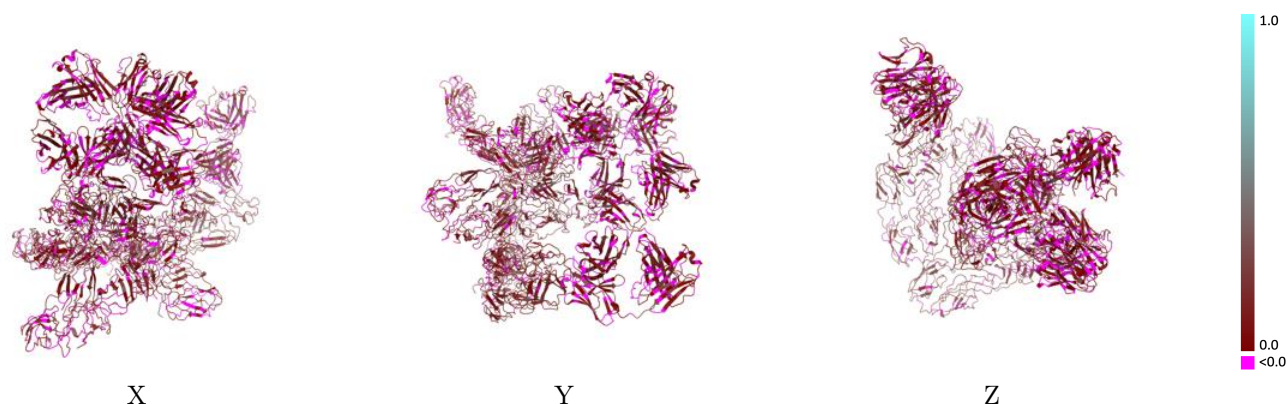
Y



Z

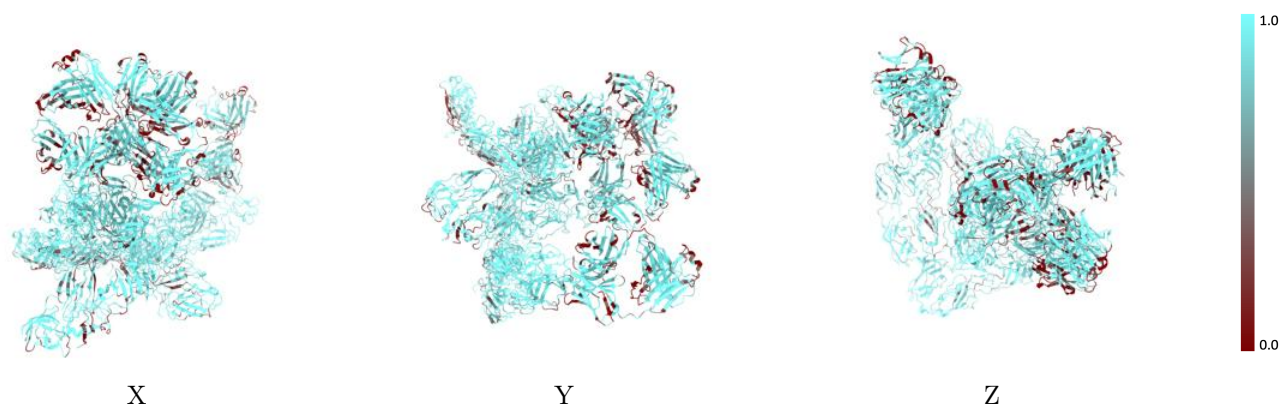
The images above show the 3D surface view of the map at the recommended contour level 0.7 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



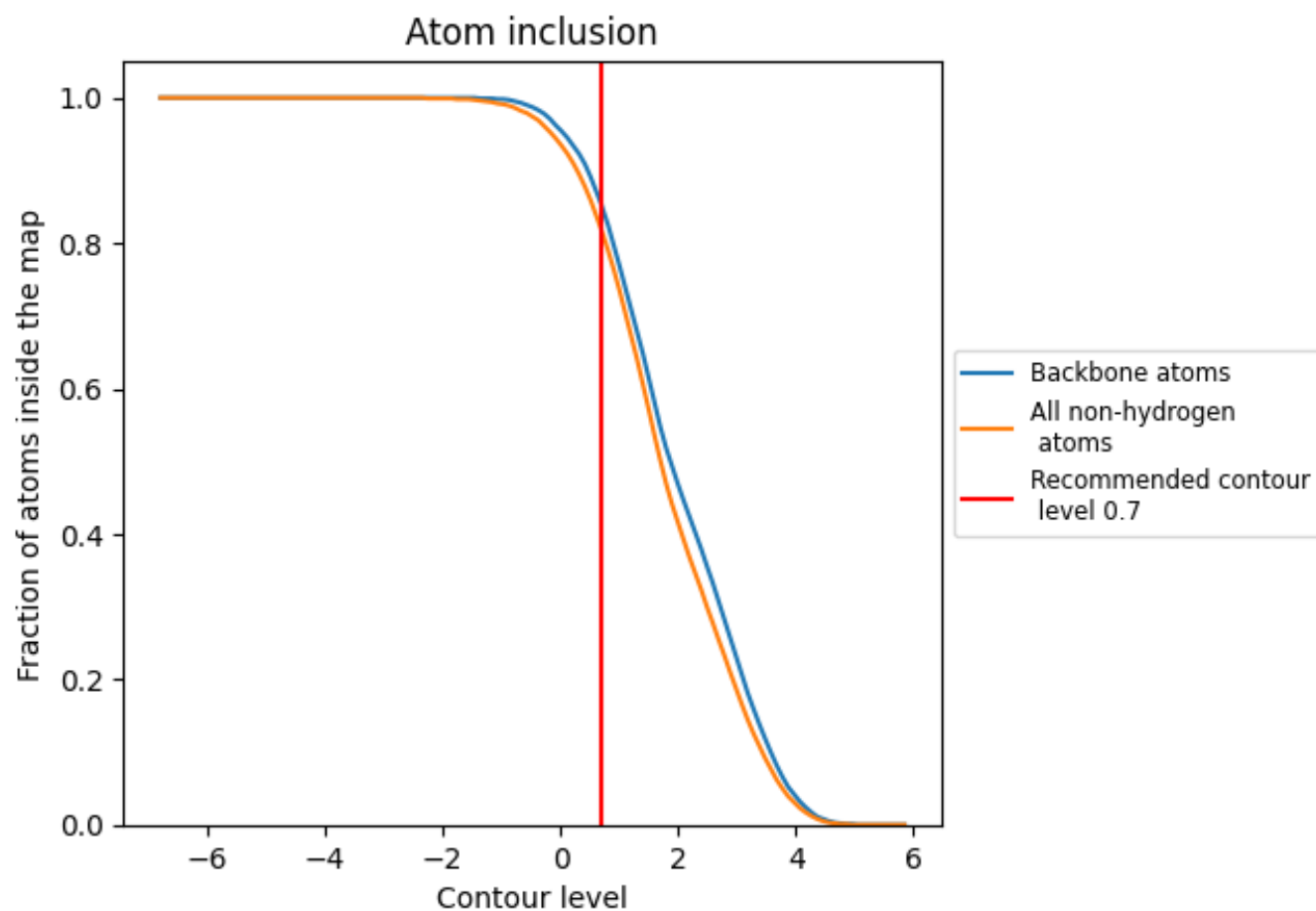
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.7).

9.4 Atom inclusion [i](#)



At the recommended contour level, 85% 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 (0.7) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8190	 0.0870
A	 0.8970	 0.1210
B	 0.9160	 0.1380
C	 0.7290	 0.0550
D	 0.6990	 0.0580
E	 0.8610	 0.1030
F	 0.8970	 0.1120
G	 0.7350	 0.0580
H	 0.7540	 0.0570
I	 0.9080	 0.1160
J	 0.9070	 0.0970
K	 0.6400	 0.0490
L	 0.7000	 0.0400
M	 0.8500	 0.0870
N	 0.8670	 0.0880
O	 0.6960	 0.0520
P	 0.6640	 0.0410

