



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 12, 2026 – 02:31 PM UTC

PDB ID : 2Q08 / pdb_00002q08
Title : Crystal structure of the protein BH0493 from Bacillus halodurans C-125 complexed with ZN
Authors : Fedorov, A.A.; Fedorov, E.V.; Patskovsky, Y.; Sauder, J.M.; Burley, S.K.; Raushel, F.; Almo, S.C.; New York SGX Research Center for Structural Genomics (NYSGXRC)
Deposited on : 2007-05-21
Resolution : 2.00 Å(reported)

This is a Full wwPDB X-ray Structure 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/XrayValidationReportHelp>

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:

MolProbity	:	4-5-2 with Phenix2.0
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

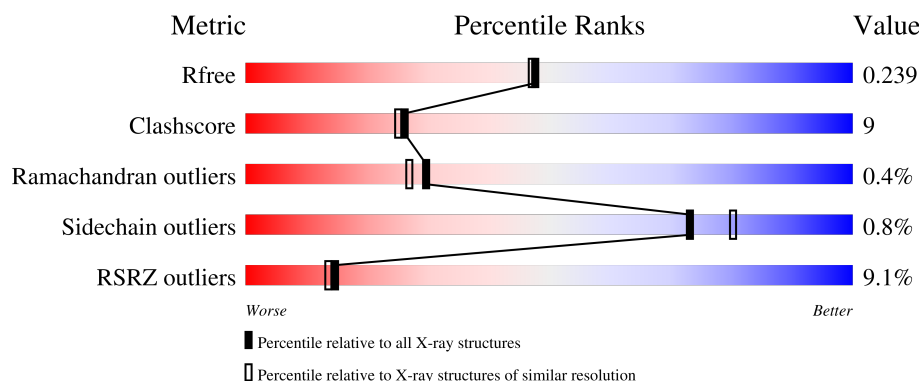
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.00 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)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	10052 (2.00-2.00)
Clashscore	190562	11152 (2.00-2.00)
Ramachandran outliers	187476	11031 (2.00-2.00)
Sidechain outliers	187428	11029 (2.00-2.00)
RSRZ outliers	180081	10067 (2.00-2.00)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower 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 electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	427	8% 74% 21% ..
1	B	427	10% 74% 21% ..
1	C	427	11% 74% 20% ..
1	D	427	8% 74% 21% ..
1	E	427	10% 73% 22% ..

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
1	F	427	10% 75% 20%
1	G	427	9% 74% 20%
1	H	427	9% 74% 22%
1	I	427	6% 75% 20%
1	J	427	8% 75% 21%
1	K	427	10% 75% 20%
1	L	427	7% 74% 21%

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 41791 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, 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 BH0493 protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	413	Total	C	N	O	S	0	0	0
			3401	2169	585	626	21			
1	B	413	Total	C	N	O	S	0	0	0
			3401	2169	585	626	21			
1	C	413	Total	C	N	O	S	0	0	0
			3401	2169	585	626	21			
1	D	413	Total	C	N	O	S	0	0	0
			3401	2169	585	626	21			
1	E	413	Total	C	N	O	S	0	0	0
			3401	2169	585	626	21			
1	F	413	Total	C	N	O	S	0	0	0
			3401	2169	585	626	21			
1	G	413	Total	C	N	O	S	0	0	0
			3401	2169	585	626	21			
1	H	413	Total	C	N	O	S	0	0	0
			3401	2169	585	626	21			
1	I	413	Total	C	N	O	S	0	0	0
			3401	2169	585	626	21			
1	J	413	Total	C	N	O	S	0	0	0
			3401	2169	585	626	21			
1	K	413	Total	C	N	O	S	0	0	0
			3401	2169	585	626	21			
1	L	413	Total	C	N	O	S	0	0	0
			3401	2169	585	626	21			

- Molecule 2 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	2	Total	Zn	0	0
			2	2		
2	B	1	Total	Zn	0	0
			1	1		

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	C	1	Total 1	Zn 1	0	0
2	D	2	Total 2	Zn 2	0	0
2	E	1	Total 1	Zn 1	0	0
2	F	1	Total 1	Zn 1	0	0
2	G	1	Total 1	Zn 1	0	0
2	H	2	Total 2	Zn 2	0	0
2	I	1	Total 1	Zn 1	0	0
2	J	2	Total 2	Zn 2	0	0
2	K	1	Total 1	Zn 1	0	0
2	L	1	Total 1	Zn 1	0	0

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	91	Total 91	O 91	0	0
3	B	121	Total 121	O 121	0	0
3	C	84	Total 84	O 84	0	0
3	D	77	Total 77	O 77	0	0
3	E	73	Total 73	O 73	0	0
3	F	82	Total 82	O 82	0	0
3	G	79	Total 79	O 79	0	0
3	H	73	Total 73	O 73	0	0
3	I	83	Total 83	O 83	0	0

Continued on next page...

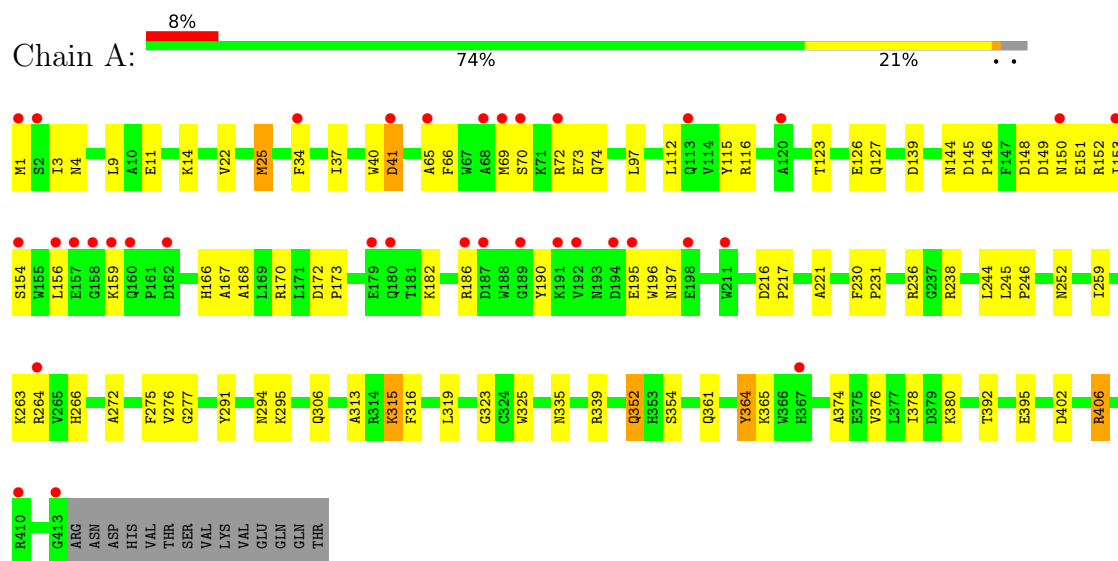
Continued from previous page...

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	J	61	Total 61	O 61	0	0
3	K	70	Total 70	O 70	0	0
3	L	69	Total 69	O 69	0	0

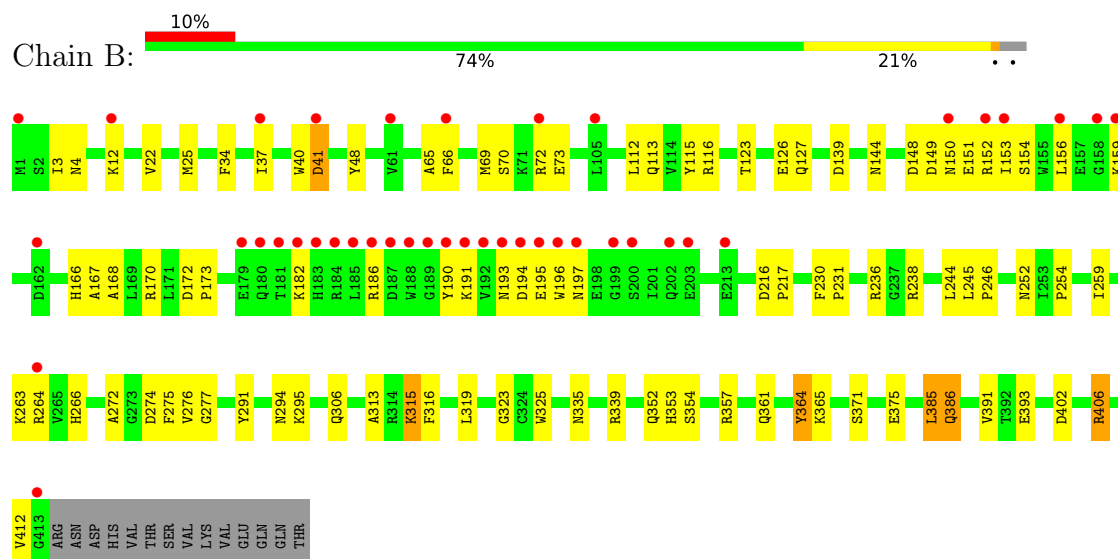
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron 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 dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). 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.

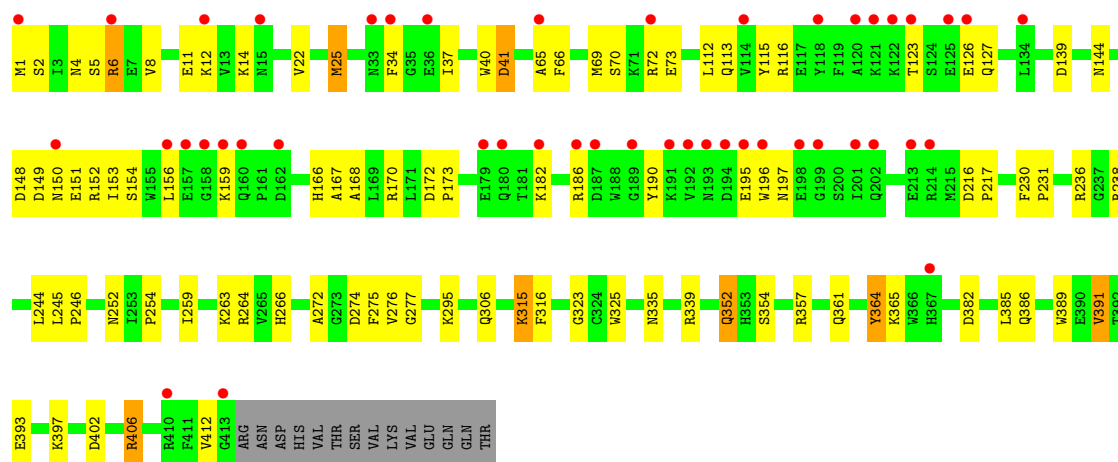
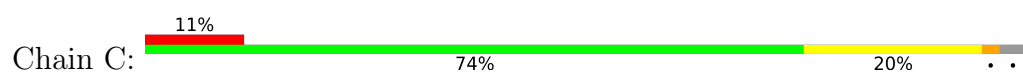
• Molecule 1: BH0493 protein



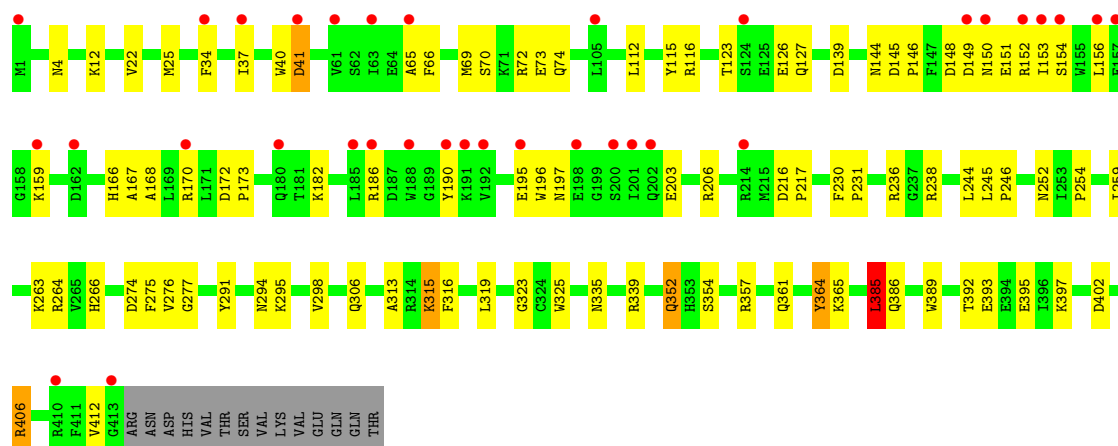
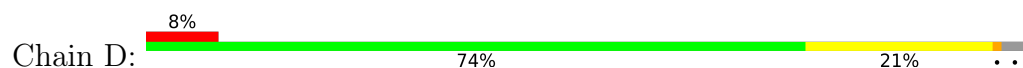
• Molecule 1: BH0493 protein



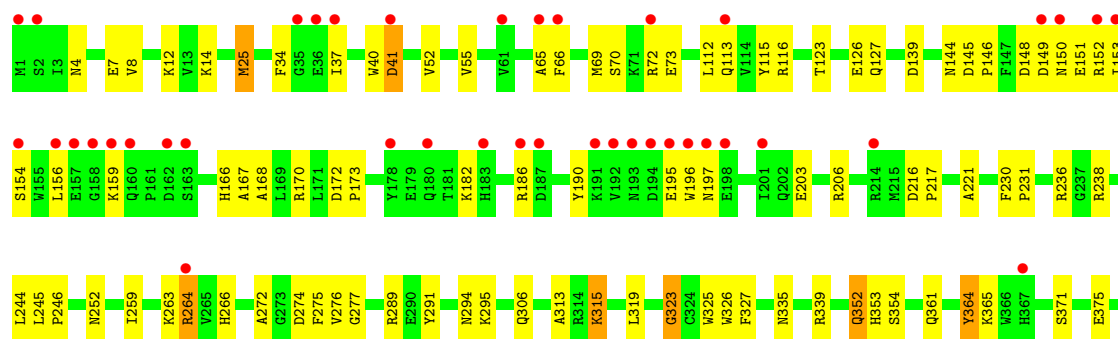
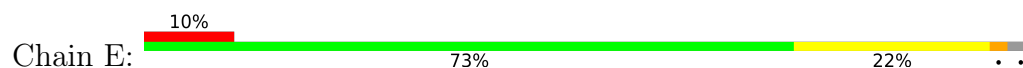
• Molecule 1: BH0493 protein

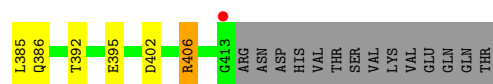


• Molecule 1: BH0493 protein

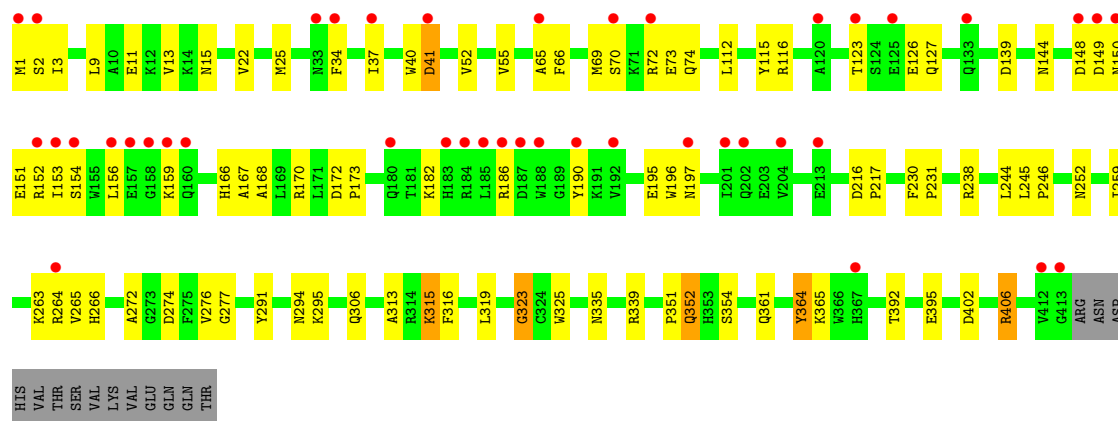
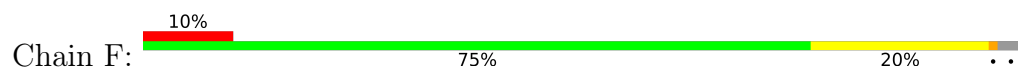


• Molecule 1: BH0493 protein

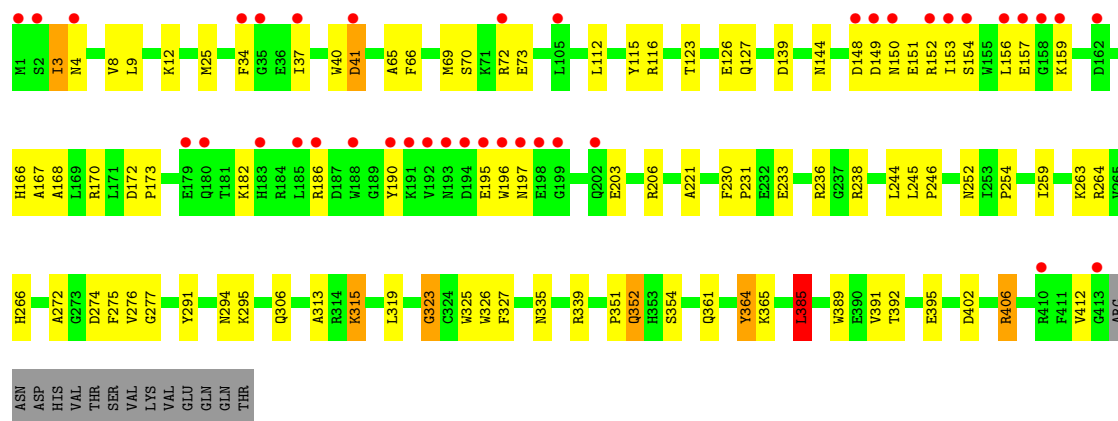
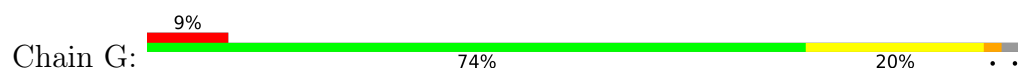




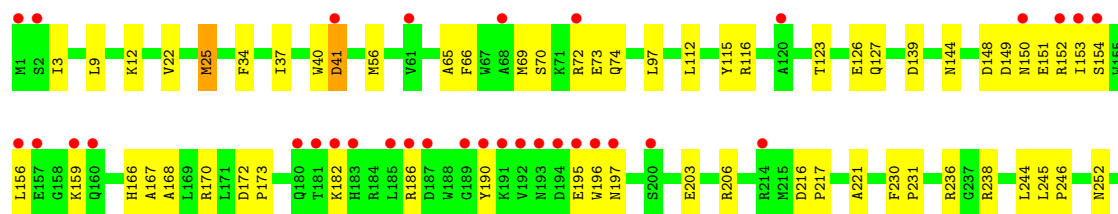
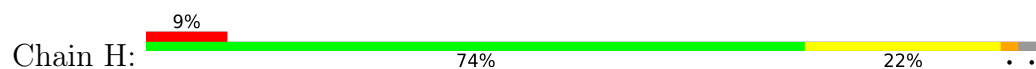
• Molecule 1: BH0493 protein

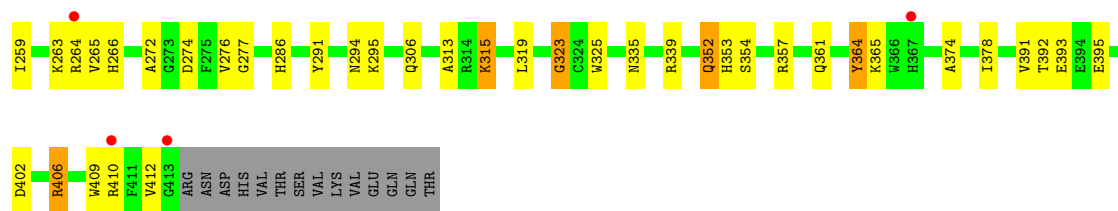


• Molecule 1: BH0493 protein

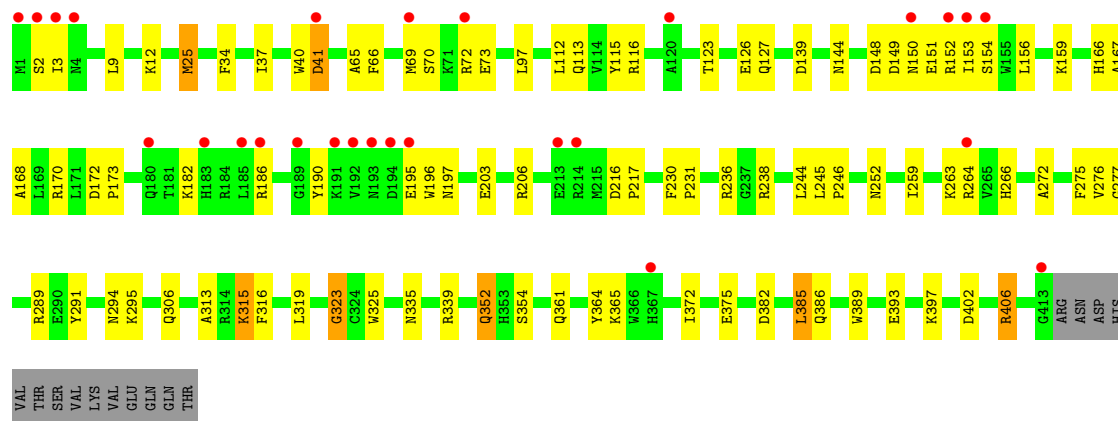
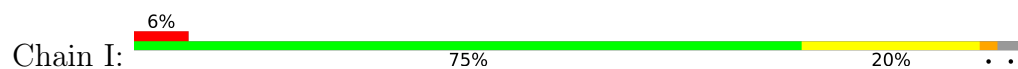


• Molecule 1: BH0493 protein

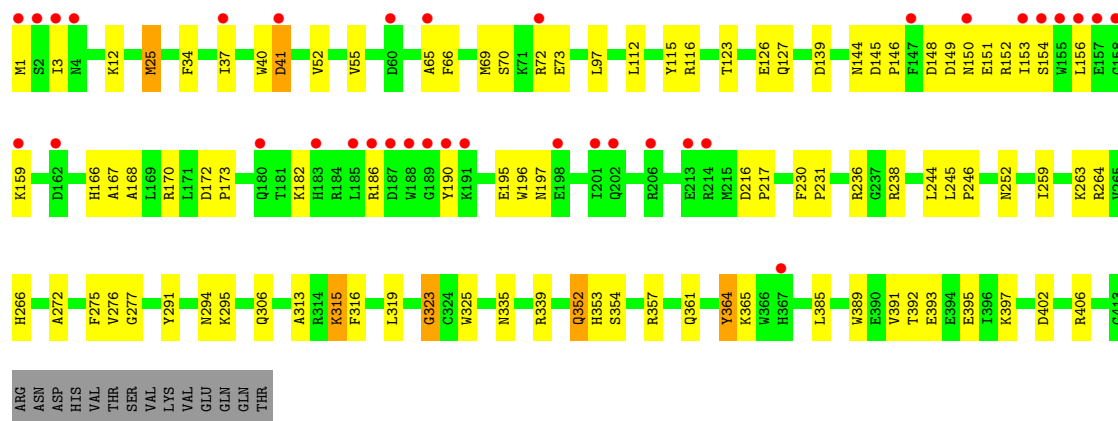
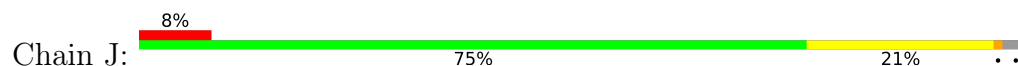




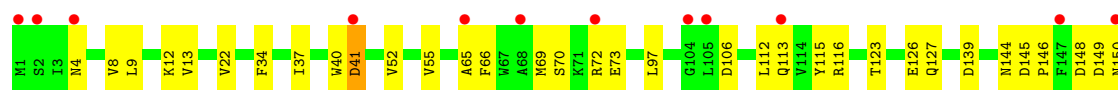
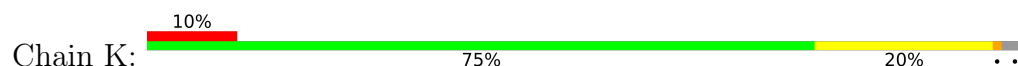
• Molecule 1: BH0493 protein

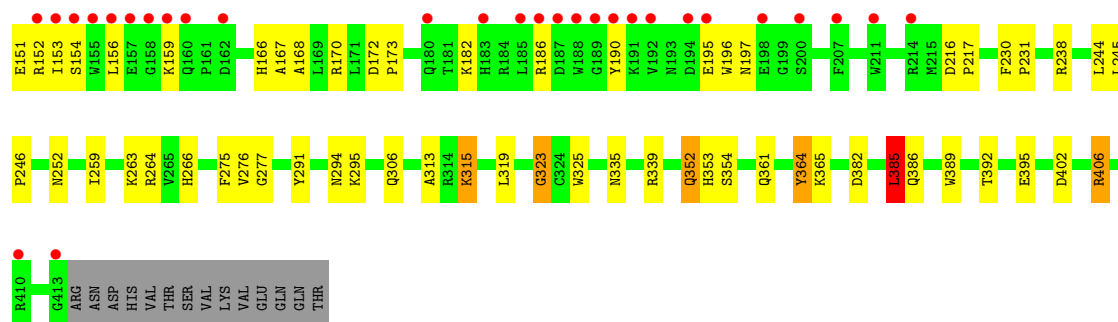


• Molecule 1: BH0493 protein

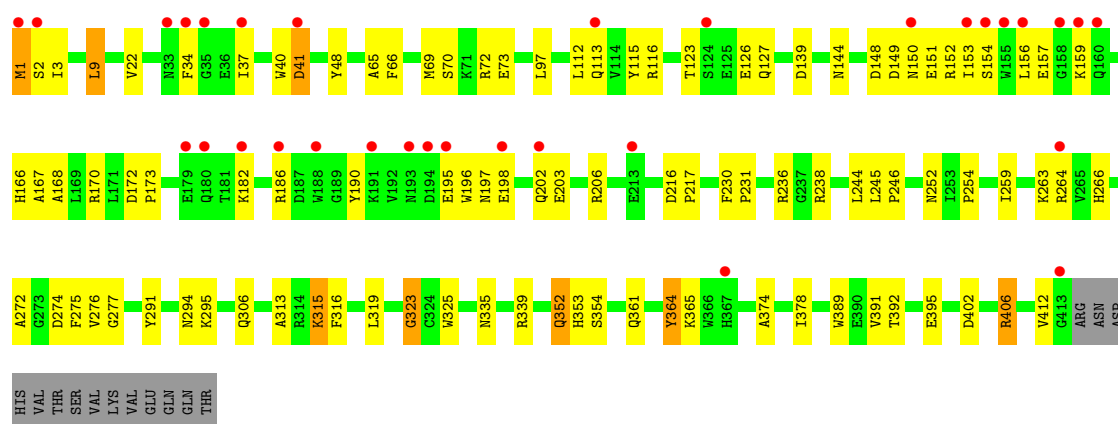
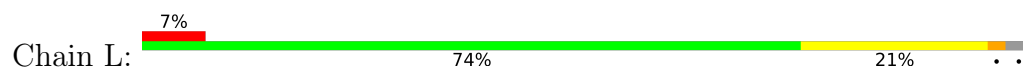


• Molecule 1: BH0493 protein





• Molecule 1: BH0493 protein



4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	121.27Å 120.97Å 126.24Å 78.82° 78.67° 80.42°	Depositor
Resolution (Å)	24.93 – 2.00 24.93 – 2.00	Depositor EDS
% Data completeness (in resolution range)	90.1 (24.93-2.00) 90.0 (24.93-2.00)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.52 (at 1.98Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.226 , 0.239 0.226 , 0.239	Depositor DCC
R_{free} test set	22357 reflections (4.95%)	wwPDB-VP
Wilson B-factor (Å ²)	25.3	Xtriage
Anisotropy	0.242	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 46.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.006 for l,h,k 0.006 for k,l,h 0.084 for -k,-h,-l 0.009 for -h,-l,-k 0.012 for -l,-k,-h	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	41791	wwPDB-VP
Average B, all atoms (Å ²)	34.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 30.62 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 1.2677e-03. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

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

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	0.41	0/3485	0.93	11/4722 (0.2%)
1	B	0.43	0/3485	0.93	12/4722 (0.3%)
1	C	0.41	0/3485	0.92	12/4722 (0.3%)
1	D	0.40	0/3485	0.92	13/4722 (0.3%)
1	E	0.39	0/3485	0.92	9/4722 (0.2%)
1	F	0.40	0/3485	0.93	9/4722 (0.2%)
1	G	0.40	0/3485	0.92	10/4722 (0.2%)
1	H	0.38	0/3485	0.92	11/4722 (0.2%)
1	I	0.39	0/3485	0.92	9/4722 (0.2%)
1	J	0.38	0/3485	0.92	9/4722 (0.2%)
1	K	0.39	0/3485	0.93	10/4722 (0.2%)
1	L	0.39	0/3485	0.92	10/4722 (0.2%)
All	All	0.40	0/41820	0.92	125/56664 (0.2%)

There are no bond length outliers.

All (125) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	K	4	ASN	N-CA-C	7.87	120.95	111.82
1	E	306	GLN	N-CA-C	7.72	119.33	111.07
1	F	306	GLN	N-CA-C	7.58	119.18	111.07
1	L	306	GLN	N-CA-C	7.58	119.18	111.07
1	C	306	GLN	N-CA-C	7.58	119.17	111.07
1	I	306	GLN	N-CA-C	7.57	119.17	111.07
1	A	306	GLN	N-CA-C	7.52	119.11	111.07
1	G	306	GLN	N-CA-C	7.50	119.10	111.07
1	K	306	GLN	N-CA-C	7.50	119.10	111.07
1	D	306	GLN	N-CA-C	7.48	119.07	111.07
1	H	306	GLN	N-CA-C	7.42	119.01	111.07
1	A	259	ILE	N-CA-C	7.41	119.75	108.71

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	J	306	GLN	N-CA-C	7.38	118.97	111.07
1	J	259	ILE	N-CA-C	7.38	119.70	108.71
1	B	306	GLN	N-CA-C	7.30	118.88	111.07
1	G	259	ILE	N-CA-C	7.16	119.38	108.71
1	B	259	ILE	N-CA-C	7.10	119.29	108.71
1	L	259	ILE	N-CA-C	7.08	119.25	108.71
1	K	259	ILE	N-CA-C	7.07	119.24	108.71
1	F	259	ILE	N-CA-C	7.03	119.19	108.71
1	H	259	ILE	N-CA-C	7.03	119.18	108.71
1	C	259	ILE	N-CA-C	6.97	119.09	108.71
1	D	259	ILE	N-CA-C	6.96	119.08	108.71
1	L	406	ARG	N-CA-C	6.90	118.80	111.28
1	I	259	ILE	N-CA-C	6.89	118.97	108.71
1	E	259	ILE	N-CA-C	6.85	118.91	108.71
1	K	325	TRP	N-CA-C	6.68	119.97	109.96
1	J	325	TRP	N-CA-C	6.58	119.83	109.96
1	B	4	ASN	N-CA-C	6.57	119.44	111.82
1	B	406	ARG	N-CA-C	6.51	118.38	111.28
1	I	325	TRP	N-CA-C	6.45	119.64	109.96
1	I	406	ARG	N-CA-C	6.38	118.24	111.28
1	A	406	ARG	N-CA-C	6.35	118.20	111.28
1	F	325	TRP	N-CA-C	6.31	119.79	109.76
1	C	406	ARG	N-CA-C	6.26	117.77	111.07
1	F	406	ARG	N-CA-C	6.25	118.09	111.28
1	E	406	ARG	N-CA-C	6.23	118.87	111.33
1	G	325	TRP	N-CA-C	6.21	119.64	109.76
1	D	325	TRP	N-CA-C	6.20	119.61	109.76
1	E	325	TRP	N-CA-C	6.17	119.57	109.76
1	A	325	TRP	N-CA-C	6.15	119.54	109.76
1	C	385	LEU	N-CA-C	-6.15	104.66	111.36
1	L	325	TRP	N-CA-C	6.14	119.53	109.76
1	B	264	ARG	N-CA-C	6.13	119.85	111.39
1	E	264	ARG	N-CA-C	6.09	119.80	111.39
1	H	325	TRP	N-CA-C	6.07	119.41	109.76
1	C	325	TRP	N-CA-C	6.07	119.41	109.76
1	L	264	ARG	N-CA-C	6.04	119.72	111.39
1	H	406	ARG	N-CA-C	6.03	117.85	111.28
1	A	264	ARG	N-CA-C	6.03	119.71	111.39
1	J	264	ARG	N-CA-C	6.02	119.69	111.39
1	K	385	LEU	N-CA-C	-6.01	104.81	111.36
1	D	385	LEU	N-CA-C	-6.00	104.83	111.36
1	K	264	ARG	N-CA-C	5.97	119.63	111.39

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	H	264	ARG	N-CA-C	5.97	119.62	111.39
1	F	264	ARG	N-CA-C	5.96	119.61	111.39
1	D	264	ARG	N-CA-C	5.95	119.60	111.39
1	G	4	ASN	N-CA-C	5.95	120.26	112.89
1	B	325	TRP	N-CA-C	5.91	119.16	109.76
1	G	264	ARG	N-CA-C	5.91	119.54	111.39
1	B	385	LEU	N-CA-C	-5.88	104.95	111.36
1	I	264	ARG	N-CA-C	5.83	119.44	111.39
1	G	263	LYS	N-CA-C	5.83	118.91	110.28
1	C	264	ARG	N-CA-C	5.78	119.37	111.39
1	E	263	LYS	N-CA-C	5.78	118.83	110.28
1	G	406	ARG	N-CA-C	5.75	117.55	111.28
1	C	263	LYS	N-CA-C	5.74	118.77	110.28
1	D	263	LYS	N-CA-C	5.71	118.73	110.28
1	B	263	LYS	N-CA-C	5.66	118.65	110.28
1	J	263	LYS	N-CA-C	5.66	118.65	110.28
1	K	263	LYS	N-CA-C	5.64	118.63	110.28
1	D	4	ASN	N-CA-C	5.64	119.88	112.89
1	H	352	GLN	N-CA-C	5.61	117.59	109.07
1	F	263	LYS	N-CA-C	5.60	118.57	110.28
1	H	263	LYS	N-CA-C	5.60	118.56	110.28
1	I	263	LYS	N-CA-C	5.60	118.56	110.28
1	D	406	ARG	N-CA-C	5.57	117.36	111.28
1	L	263	LYS	N-CA-C	5.57	118.53	110.28
1	F	352	GLN	N-CA-C	5.53	117.48	109.07
1	L	352	GLN	N-CA-C	5.42	117.31	109.07
1	D	352	GLN	N-CA-C	5.41	117.29	109.07
1	A	263	LYS	N-CA-C	5.38	118.23	110.28
1	J	352	GLN	N-CA-C	5.35	117.20	109.07
1	C	352	GLN	N-CA-C	5.33	117.18	109.07
1	A	22	VAL	N-CA-C	5.31	116.62	108.71
1	L	22	VAL	N-CA-C	5.30	116.61	108.71
1	D	316	PHE	N-CA-C	5.29	117.01	108.34
1	K	22	VAL	N-CA-C	5.25	116.84	108.87
1	E	352	GLN	N-CA-C	5.24	117.04	109.07
1	K	406	ARG	N-CA-C	5.23	116.98	111.28
1	B	357	ARG	N-CA-C	-5.22	107.29	113.97
1	L	316	PHE	N-CA-C	5.20	116.86	108.34
1	A	352	GLN	N-CA-C	5.19	116.97	109.07
1	K	352	GLN	N-CA-C	5.18	116.94	109.07
1	H	22	VAL	N-CA-C	5.17	116.41	108.71
1	L	48	TYR	N-CA-C	-5.17	102.96	110.24

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	I	352	GLN	N-CA-C	5.16	116.92	109.07
1	D	357	ARG	N-CA-C	-5.14	107.39	113.97
1	F	316	PHE	N-CA-C	5.14	116.77	108.34
1	B	22	VAL	N-CA-C	5.13	116.36	108.71
1	J	357	ARG	N-CA-C	-5.13	107.40	113.97
1	G	352	GLN	N-CA-C	5.13	116.86	109.07
1	C	25	MET	N-CA-C	5.11	120.42	113.37
1	C	357	ARG	N-CA-C	-5.11	107.44	113.97
1	D	22	VAL	N-CA-C	5.11	116.32	108.71
1	A	25	MET	N-CA-C	5.10	120.41	113.37
1	A	221	ALA	N-CA-C	5.10	117.42	109.52
1	C	316	PHE	N-CA-C	5.08	116.67	108.34
1	I	316	PHE	N-CA-C	5.07	116.66	108.34
1	H	357	ARG	N-CA-C	-5.07	107.49	113.97
1	J	316	PHE	N-CA-C	5.07	116.65	108.34
1	E	25	MET	N-CA-C	5.06	120.35	113.37
1	B	48	TYR	N-CA-C	-5.05	103.11	110.24
1	B	316	PHE	N-CA-C	5.05	116.63	108.34
1	C	22	VAL	N-CA-C	5.05	116.24	108.71
1	A	316	PHE	N-CA-C	5.05	116.62	108.34
1	G	221	ALA	N-CA-C	5.04	117.34	109.52
1	D	298	VAL	N-CA-C	5.04	115.97	108.46
1	F	22	VAL	N-CA-C	5.04	116.22	108.71
1	H	25	MET	N-CA-C	5.04	120.32	113.37
1	E	221	ALA	N-CA-C	5.04	117.32	109.52
1	G	385	LEU	N-CA-C	-5.04	105.87	111.36
1	I	25	MET	N-CA-C	5.02	120.30	113.37
1	H	221	ALA	N-CA-C	5.01	117.28	109.52
1	J	25	MET	N-CA-C	5.00	120.27	113.37

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3401	0	3327	66	0
1	B	3401	0	3327	69	2
1	C	3401	0	3327	79	0
1	D	3401	0	3327	63	0
1	E	3401	0	3327	70	0
1	F	3401	0	3327	67	0
1	G	3401	0	3327	65	2
1	H	3401	0	3327	68	0
1	I	3401	0	3327	65	0
1	J	3401	0	3327	66	0
1	K	3401	0	3327	63	0
1	L	3401	0	3327	80	0
2	A	2	0	0	0	0
2	B	1	0	0	0	0
2	C	1	0	0	0	0
2	D	2	0	0	0	0
2	E	1	0	0	0	0
2	F	1	0	0	0	0
2	G	1	0	0	0	0
2	H	2	0	0	0	0
2	I	1	0	0	0	0
2	J	2	0	0	0	0
2	K	1	0	0	0	0
2	L	1	0	0	0	0
3	A	91	0	0	3	0
3	B	121	0	0	4	0
3	C	84	0	0	3	0
3	D	77	0	0	2	0
3	E	73	0	0	2	0
3	F	82	0	0	2	0
3	G	79	0	0	3	0
3	H	73	0	0	5	0
3	I	83	0	0	3	0
3	J	61	0	0	2	0
3	K	70	0	0	1	0
3	L	69	0	0	2	0
All	All	41791	0	39924	757	2

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 9.

All (757) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:123:THR:OG1	1:L:198:GLU:HG2	1.41	1.18
1:G:152:ARG:HH12	1:L:157:GLU:HG2	1.05	1.14
1:G:152:ARG:NH1	1:L:157:GLU:HG2	1.65	1.11
1:C:8:VAL:O	1:C:12:LYS:HG2	1.57	1.04
1:E:40:TRP:O	1:E:41:ASP:HB2	1.58	1.04
1:C:40:TRP:O	1:C:41:ASP:HB2	1.58	1.03
1:A:40:TRP:O	1:A:41:ASP:HB2	1.58	1.02
1:L:40:TRP:O	1:L:41:ASP:HB2	1.58	1.02
1:F:40:TRP:O	1:F:41:ASP:HB2	1.58	1.02
1:I:40:TRP:O	1:I:41:ASP:HB2	1.60	1.02
1:K:40:TRP:O	1:K:41:ASP:HB2	1.59	1.01
1:B:40:TRP:O	1:B:41:ASP:HB2	1.59	1.01
1:G:40:TRP:O	1:G:41:ASP:HB2	1.59	0.99
1:H:40:TRP:O	1:H:41:ASP:HB2	1.60	0.98
1:J:40:TRP:O	1:J:41:ASP:HB2	1.60	0.97
1:D:40:TRP:O	1:D:41:ASP:HB2	1.59	0.96
1:E:8:VAL:O	1:E:12:LYS:HG2	1.68	0.93
1:A:14:LYS:HD3	1:E:7:GLU:HG2	1.52	0.91
1:C:123:THR:HG1	1:L:198:GLU:HG2	1.34	0.91
1:B:236:ARG:HD2	3:B:1002:HOH:O	1.70	0.90
1:L:335:ASN:HD21	1:L:339:ARG:HE	1.18	0.89
1:K:335:ASN:HD21	1:K:339:ARG:HE	1.19	0.88
1:B:335:ASN:HD21	1:B:339:ARG:HE	1.20	0.88
1:A:335:ASN:HD21	1:A:339:ARG:HE	1.20	0.87
1:B:386:GLN:HG3	1:F:1:MET:HG2	1.56	0.87
1:I:335:ASN:HD21	1:I:339:ARG:HE	1.21	0.87
1:E:335:ASN:HD21	1:E:339:ARG:HE	1.18	0.86
1:J:335:ASN:HD21	1:J:339:ARG:HE	1.21	0.86
1:H:236:ARG:HD2	3:H:1005:HOH:O	1.73	0.86
1:D:335:ASN:HD21	1:D:339:ARG:HE	1.22	0.86
1:F:335:ASN:HD21	1:F:339:ARG:HE	1.21	0.86
1:D:236:ARG:HD2	3:D:1023:HOH:O	1.76	0.84
1:G:335:ASN:HD21	1:G:339:ARG:HE	1.22	0.84
1:H:335:ASN:HD21	1:H:339:ARG:HE	1.20	0.83
1:L:236:ARG:HD2	3:L:1004:HOH:O	1.77	0.83
1:C:335:ASN:HD21	1:C:339:ARG:HE	1.22	0.83
1:C:126:GLU:OE2	1:L:202:GLN:NE2	2.12	0.83
1:C:123:THR:OG1	1:L:198:GLU:CG	2.26	0.81
1:E:236:ARG:HD2	3:E:1039:HOH:O	1.79	0.80
1:C:123:THR:HG21	1:L:198:GLU:OE1	1.84	0.78
1:A:354:SER:HB2	1:A:365:LYS:HG2	1.66	0.77
1:C:1:MET:HE2	1:C:4:ASN:ND2	2.00	0.77

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:191:LYS:O	3:B:1084:HOH:O	2.02	0.77
1:G:236:ARG:HD2	3:G:1008:HOH:O	1.85	0.77
1:H:354:SER:HB2	1:H:365:LYS:HG2	1.67	0.76
1:C:354:SER:HB2	1:C:365:LYS:HG2	1.67	0.76
1:F:354:SER:HB2	1:F:365:LYS:HG2	1.68	0.76
1:K:354:SER:HB2	1:K:365:LYS:HG2	1.67	0.75
1:B:354:SER:HB2	1:B:365:LYS:HG2	1.68	0.75
1:L:354:SER:HB2	1:L:365:LYS:HG2	1.68	0.75
1:A:315:LYS:O	1:B:266:HIS:HD2	1.68	0.75
1:J:236:ARG:HD2	3:J:1048:HOH:O	1.86	0.75
1:J:385:LEU:HD21	1:J:391:VAL:HG22	1.67	0.75
1:A:236:ARG:HD2	3:A:1060:HOH:O	1.87	0.74
1:J:354:SER:HB2	1:J:365:LYS:HG2	1.68	0.74
1:G:354:SER:HB2	1:G:365:LYS:HG2	1.67	0.73
1:D:354:SER:HB2	1:D:365:LYS:HG2	1.69	0.73
1:E:354:SER:HB2	1:E:365:LYS:HG2	1.68	0.73
1:I:354:SER:HB2	1:I:365:LYS:HG2	1.70	0.72
1:H:266:HIS:HD2	1:I:315:LYS:O	1.73	0.72
1:C:236:ARG:HD2	3:C:1016:HOH:O	1.88	0.71
1:D:315:LYS:O	1:E:266:HIS:HD2	1.72	0.71
1:L:3:ILE:CG2	1:L:9:LEU:HD13	2.20	0.71
1:B:12:LYS:HD2	1:B:393:GLU:CD	2.16	0.70
1:A:40:TRP:O	1:A:41:ASP:CB	2.39	0.70
1:D:40:TRP:O	1:D:41:ASP:CB	2.40	0.70
1:G:152:ARG:NH1	1:G:156:LEU:HD11	2.06	0.70
1:L:152:ARG:NH1	1:L:156:LEU:HD11	2.07	0.69
1:E:371:SER:O	1:E:375:GLU:HG3	1.91	0.69
1:E:66:PHE:HA	1:E:69:MET:HE2	1.74	0.69
1:I:66:PHE:HA	1:I:69:MET:HE2	1.74	0.69
1:F:152:ARG:NH1	1:F:156:LEU:HD11	2.07	0.69
1:C:152:ARG:NH1	1:C:156:LEU:HD11	2.07	0.69
1:D:152:ARG:NH1	1:D:156:LEU:HD11	2.07	0.69
1:E:152:ARG:NH1	1:E:156:LEU:HD11	2.08	0.69
1:L:66:PHE:HA	1:L:69:MET:HE2	1.75	0.69
1:H:66:PHE:HA	1:H:69:MET:HE2	1.74	0.69
1:F:66:PHE:HA	1:F:69:MET:HE2	1.74	0.69
1:I:236:ARG:HD2	3:I:1038:HOH:O	1.92	0.68
1:C:11:GLU:HB2	1:F:15:ASN:HD21	1.57	0.68
1:I:40:TRP:O	1:I:41:ASP:CB	2.41	0.68
1:A:152:ARG:NH1	1:A:156:LEU:HD11	2.08	0.68
1:C:66:PHE:HA	1:C:69:MET:HE2	1.75	0.68

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:152:ARG:NH1	1:K:156:LEU:HD11	2.08	0.68
1:I:152:ARG:NH1	1:I:156:LEU:HD11	2.08	0.68
1:A:66:PHE:HA	1:A:69:MET:HE2	1.76	0.68
1:C:123:THR:CG2	1:L:198:GLU:OE1	2.42	0.68
1:A:266:HIS:HD2	1:C:315:LYS:O	1.76	0.68
1:K:40:TRP:O	1:K:41:ASP:CB	2.40	0.68
1:J:152:ARG:NH1	1:J:156:LEU:HD11	2.09	0.67
1:J:66:PHE:HA	1:J:69:MET:HE2	1.75	0.67
1:H:152:ARG:NH1	1:H:156:LEU:HD11	2.09	0.67
1:B:152:ARG:NH1	1:B:156:LEU:HD11	2.09	0.67
1:J:315:LYS:O	1:L:266:HIS:HD2	1.76	0.67
1:K:66:PHE:HA	1:K:69:MET:HE2	1.75	0.67
1:E:40:TRP:O	1:E:41:ASP:CB	2.39	0.67
1:D:66:PHE:HA	1:D:69:MET:HE2	1.75	0.67
1:B:66:PHE:HA	1:B:69:MET:HE2	1.76	0.66
1:B:315:LYS:O	1:C:266:HIS:HD2	1.76	0.66
1:G:66:PHE:HA	1:G:69:MET:HE2	1.76	0.66
1:C:8:VAL:HG13	1:C:12:LYS:HE2	1.76	0.66
1:G:266:HIS:HD2	1:H:315:LYS:O	1.78	0.65
1:J:40:TRP:O	1:J:41:ASP:CB	2.41	0.65
1:B:12:LYS:HD2	1:B:393:GLU:OE2	1.96	0.65
1:D:266:HIS:HD2	1:F:315:LYS:O	1.80	0.64
1:E:315:LYS:O	1:F:266:HIS:HD2	1.81	0.64
1:H:40:TRP:O	1:H:41:ASP:CB	2.40	0.63
1:I:323:GLY:HA2	1:I:352:GLN:HA	1.81	0.63
1:C:14:LYS:NZ	1:F:11:GLU:OE1	2.27	0.62
1:J:323:GLY:HA2	1:J:352:GLN:HA	1.82	0.62
1:C:323:GLY:HA2	1:C:352:GLN:HA	1.82	0.62
1:K:323:GLY:HA2	1:K:352:GLN:HA	1.81	0.62
1:D:34:PHE:HB3	1:D:37:ILE:HD11	1.82	0.62
1:F:323:GLY:HA2	1:F:352:GLN:HA	1.81	0.62
1:C:25:MET:HG3	3:C:1014:HOH:O	2.00	0.61
1:D:323:GLY:HA2	1:D:352:GLN:HA	1.82	0.61
1:G:40:TRP:O	1:G:41:ASP:CB	2.39	0.61
1:E:323:GLY:HA2	1:E:352:GLN:HA	1.82	0.61
1:C:40:TRP:O	1:C:41:ASP:CB	2.39	0.61
1:G:315:LYS:O	1:I:266:HIS:HD2	1.82	0.61
1:K:335:ASN:ND2	1:K:339:ARG:HE	1.96	0.61
1:L:323:GLY:HA2	1:L:352:GLN:HA	1.81	0.61
1:B:323:GLY:HA2	1:B:352:GLN:HA	1.82	0.61
1:I:335:ASN:ND2	1:I:339:ARG:HE	1.97	0.61

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:34:PHE:HB3	1:C:37:ILE:HD11	1.83	0.61
1:F:34:PHE:HB3	1:F:37:ILE:HD11	1.83	0.61
1:H:34:PHE:HB3	1:H:37:ILE:HD11	1.83	0.61
1:B:34:PHE:HB3	1:B:37:ILE:HD11	1.83	0.60
1:H:335:ASN:ND2	1:H:339:ARG:HE	1.96	0.60
1:I:34:PHE:HB3	1:I:37:ILE:HD11	1.82	0.60
1:L:40:TRP:O	1:L:41:ASP:CB	2.39	0.60
1:B:335:ASN:ND2	1:B:339:ARG:HE	1.96	0.60
1:A:34:PHE:HB3	1:A:37:ILE:HD11	1.84	0.60
1:J:34:PHE:HB3	1:J:37:ILE:HD11	1.83	0.60
1:A:323:GLY:HA2	1:A:352:GLN:HA	1.83	0.60
1:D:12:LYS:HD2	1:D:393:GLU:OE2	2.02	0.60
1:K:34:PHE:HB3	1:K:37:ILE:HD11	1.84	0.60
1:G:34:PHE:HB3	1:G:37:ILE:HD11	1.83	0.60
1:L:1:MET:N	1:L:1:MET:HE2	2.16	0.60
1:C:402:ASP:HA	1:C:406:ARG:HB2	1.84	0.60
1:E:335:ASN:ND2	1:E:339:ARG:HE	1.95	0.60
1:E:34:PHE:HB3	1:E:37:ILE:HD11	1.83	0.60
1:L:335:ASN:ND2	1:L:339:ARG:HE	1.96	0.60
1:C:11:GLU:HB2	1:F:15:ASN:ND2	2.17	0.59
1:G:323:GLY:HA2	1:G:352:GLN:HA	1.83	0.59
1:L:34:PHE:HB3	1:L:37:ILE:HD11	1.83	0.59
1:C:335:ASN:ND2	1:C:339:ARG:HE	1.97	0.59
1:A:11:GLU:OE1	1:E:14:LYS:NZ	2.31	0.59
1:H:323:GLY:HA2	1:H:352:GLN:HA	1.83	0.59
1:I:3:ILE:HG21	1:I:9:LEU:HB2	1.84	0.58
1:A:72:ARG:NH2	1:A:116:ARG:HD3	2.18	0.58
1:F:40:TRP:O	1:F:41:ASP:CB	2.39	0.58
1:G:157:GLU:OE1	1:L:152:ARG:NH1	2.37	0.58
1:F:335:ASN:ND2	1:F:339:ARG:HE	1.96	0.58
1:G:335:ASN:ND2	1:G:339:ARG:HE	1.97	0.58
1:H:392:THR:OG1	1:H:395:GLU:HG3	2.03	0.58
1:K:402:ASP:HA	1:K:406:ARG:HB2	1.85	0.58
1:F:123:THR:OG1	1:F:126:GLU:HG3	2.04	0.58
1:L:123:THR:OG1	1:L:126:GLU:HG3	2.04	0.58
1:D:25:MET:HG3	3:D:1013:HOH:O	2.02	0.58
1:L:72:ARG:NH2	1:L:116:ARG:HD3	2.19	0.58
1:A:123:THR:OG1	1:A:126:GLU:HG3	2.04	0.57
1:K:266:HIS:HD2	1:L:315:LYS:O	1.87	0.57
1:B:40:TRP:O	1:B:41:ASP:CB	2.40	0.57
1:J:123:THR:OG1	1:J:126:GLU:HG3	2.04	0.57

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:123:THR:OG1	1:D:126:GLU:HG3	2.05	0.57
1:H:123:THR:OG1	1:H:126:GLU:HG3	2.05	0.57
1:D:72:ARG:NH2	1:D:116:ARG:HD3	2.20	0.57
1:E:123:THR:OG1	1:E:126:GLU:HG3	2.05	0.57
1:I:154:SER:HB2	1:I:159:LYS:HD3	1.87	0.57
1:J:266:HIS:HD2	1:K:315:LYS:O	1.88	0.57
1:J:361:GLN:O	1:J:365:LYS:HB2	2.05	0.57
1:D:335:ASN:ND2	1:D:339:ARG:HE	1.98	0.57
1:G:72:ARG:NH2	1:G:116:ARG:HD3	2.20	0.57
1:G:3:ILE:HG12	1:G:391:VAL:O	2.05	0.57
1:K:8:VAL:O	1:K:12:LYS:HG2	2.04	0.56
1:D:315:LYS:HE2	1:E:272:ALA:O	2.05	0.56
1:G:152:ARG:HH12	1:L:157:GLU:CG	1.98	0.56
1:B:402:ASP:HA	1:B:406:ARG:HB2	1.86	0.56
1:I:123:THR:OG1	1:I:126:GLU:HG3	2.05	0.56
1:K:123:THR:OG1	1:K:126:GLU:HG3	2.05	0.56
1:B:123:THR:OG1	1:B:126:GLU:HG3	2.06	0.56
1:E:154:SER:HB2	1:E:159:LYS:HD3	1.88	0.56
1:F:72:ARG:NH2	1:F:116:ARG:HD3	2.20	0.56
1:I:72:ARG:NH2	1:I:116:ARG:HD3	2.20	0.56
1:A:154:SER:HB2	1:A:159:LYS:HD3	1.88	0.56
1:C:72:ARG:NH2	1:C:116:ARG:HD3	2.20	0.56
1:C:123:THR:CB	1:L:198:GLU:HG2	2.35	0.56
1:G:392:THR:OG1	1:G:395:GLU:HG3	2.06	0.56
1:B:72:ARG:NH2	1:B:116:ARG:HD3	2.20	0.56
1:H:3:ILE:HG21	1:H:9:LEU:HD13	1.88	0.56
1:H:72:ARG:NH2	1:H:116:ARG:HD3	2.20	0.56
1:B:386:GLN:HG2	1:F:1:MET:HE3	1.87	0.56
1:G:154:SER:HB2	1:G:159:LYS:HD3	1.88	0.56
1:D:385:LEU:HD12	1:D:389:TRP:O	2.06	0.56
1:H:361:GLN:O	1:H:365:LYS:HB2	2.06	0.56
1:F:361:GLN:O	1:F:365:LYS:HB2	2.06	0.55
1:G:123:THR:OG1	1:G:126:GLU:HG3	2.06	0.55
1:K:72:ARG:NH2	1:K:116:ARG:HD3	2.20	0.55
1:F:154:SER:HB2	1:F:159:LYS:HD3	1.88	0.55
1:D:154:SER:HB2	1:D:159:LYS:HD3	1.88	0.55
1:D:402:ASP:HA	1:D:406:ARG:HB2	1.88	0.55
1:A:361:GLN:O	1:A:365:LYS:HB2	2.07	0.55
1:E:361:GLN:O	1:E:365:LYS:HB2	2.06	0.55
1:I:361:GLN:O	1:I:365:LYS:HB2	2.07	0.55
1:D:361:GLN:O	1:D:365:LYS:HB2	2.06	0.55

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:72:ARG:NH2	1:E:116:ARG:HD3	2.22	0.55
1:J:154:SER:HB2	1:J:159:LYS:HD3	1.89	0.55
1:L:361:GLN:O	1:L:365:LYS:HB2	2.06	0.55
1:B:151:GLU:HB3	3:B:1036:HOH:O	2.07	0.55
1:B:361:GLN:O	1:B:365:LYS:HB2	2.06	0.55
1:C:6:ARG:O	1:C:6:ARG:HD3	2.06	0.55
1:J:72:ARG:NH2	1:J:116:ARG:HD3	2.21	0.55
1:A:335:ASN:ND2	1:A:339:ARG:HE	1.97	0.55
1:C:123:THR:OG1	1:C:126:GLU:HG3	2.06	0.55
1:A:315:LYS:HD2	1:B:274:ASP:O	2.07	0.55
1:C:154:SER:HB2	1:C:159:LYS:HD3	1.90	0.54
1:A:14:LYS:CD	1:E:7:GLU:HG2	2.33	0.54
1:H:274:ASP:O	1:I:315:LYS:HD2	2.07	0.54
1:B:371:SER:O	1:B:375:GLU:HG3	2.07	0.54
1:D:172:ASP:HB2	1:D:173:PRO:HD3	1.89	0.54
1:K:106:ASP:OD1	3:K:1047:HOH:O	2.18	0.54
1:K:392:THR:OG1	1:K:395:GLU:HG3	2.08	0.54
1:C:361:GLN:O	1:C:365:LYS:HB2	2.07	0.54
1:G:8:VAL:O	1:G:12:LYS:HG2	2.08	0.54
1:E:315:LYS:HD2	1:F:274:ASP:O	2.08	0.54
1:G:144:ASN:HD22	1:G:168:ALA:H	1.56	0.54
1:K:154:SER:HB2	1:K:159:LYS:HD3	1.89	0.54
1:B:385:LEU:HD21	1:B:391:VAL:HG12	1.89	0.54
1:D:144:ASN:HD22	1:D:168:ALA:H	1.56	0.54
1:K:361:GLN:O	1:K:365:LYS:HB2	2.08	0.54
1:H:148:ASP:OD2	1:H:151:GLU:HG3	2.08	0.54
1:H:410:ARG:HD3	3:H:1011:HOH:O	2.08	0.54
1:G:361:GLN:O	1:G:365:LYS:HB2	2.07	0.53
1:B:154:SER:HB2	1:B:159:LYS:HD3	1.89	0.53
1:D:392:THR:OG1	1:D:395:GLU:HG3	2.08	0.53
1:J:144:ASN:HD22	1:J:168:ALA:H	1.56	0.53
1:K:172:ASP:HB2	1:K:173:PRO:HD3	1.91	0.53
1:G:172:ASP:HB2	1:G:173:PRO:HD3	1.91	0.53
1:H:25:MET:HG3	3:H:1038:HOH:O	2.07	0.53
1:L:3:ILE:HG21	1:L:9:LEU:HD13	1.90	0.53
1:I:402:ASP:HA	1:I:406:ARG:HB2	1.90	0.53
1:J:335:ASN:ND2	1:J:339:ARG:HE	1.97	0.53
1:H:154:SER:HB2	1:H:159:LYS:HD3	1.89	0.53
1:F:144:ASN:HD22	1:F:168:ALA:H	1.55	0.53
1:I:12:LYS:HD2	1:I:393:GLU:CD	2.34	0.53
1:B:172:ASP:HB2	1:B:173:PRO:HD3	1.91	0.53

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:389:TRP:HD1	1:C:391:VAL:HG12	1.74	0.53
1:J:3:ILE:HD12	1:J:391:VAL:HG23	1.91	0.53
1:L:1:MET:HE2	1:L:1:MET:H2	1.73	0.53
1:L:144:ASN:HD22	1:L:168:ALA:H	1.57	0.52
1:A:315:LYS:HE2	1:B:272:ALA:O	2.10	0.52
1:E:144:ASN:HD22	1:E:168:ALA:H	1.56	0.52
1:C:6:ARG:HG3	1:C:6:ARG:HH11	1.74	0.52
1:C:144:ASN:HD22	1:C:168:ALA:H	1.57	0.52
1:H:3:ILE:CG2	1:H:9:LEU:HD13	2.39	0.52
1:H:272:ALA:O	1:I:315:LYS:HE2	2.09	0.52
1:L:154:SER:HB2	1:L:159:LYS:HD3	1.90	0.52
1:A:172:ASP:HB2	1:A:173:PRO:HD3	1.91	0.52
1:B:144:ASN:HD22	1:B:168:ALA:H	1.58	0.52
1:F:148:ASP:OD2	1:F:151:GLU:HG3	2.10	0.52
1:L:374:ALA:O	1:L:378:ILE:HG13	2.10	0.52
1:C:382:ASP:O	1:C:386:GLN:HG2	2.09	0.52
1:E:172:ASP:HB2	1:E:173:PRO:HD3	1.91	0.52
1:I:144:ASN:HD22	1:I:168:ALA:H	1.55	0.52
1:A:148:ASP:OD2	1:A:151:GLU:HG3	2.09	0.52
1:C:148:ASP:OD2	1:C:151:GLU:HG3	2.10	0.52
1:I:172:ASP:HB2	1:I:173:PRO:HD3	1.91	0.52
1:J:172:ASP:HB2	1:J:173:PRO:HD3	1.92	0.52
1:C:236:ARG:NH2	3:C:1020:HOH:O	2.42	0.52
1:L:172:ASP:HB2	1:L:173:PRO:HD3	1.91	0.52
1:D:148:ASP:OD2	1:D:151:GLU:HG3	2.09	0.52
1:F:172:ASP:HB2	1:F:173:PRO:HD3	1.92	0.52
1:J:272:ALA:O	1:K:315:LYS:HE2	2.10	0.52
1:E:148:ASP:OD2	1:E:151:GLU:HG3	2.10	0.51
1:H:172:ASP:HB2	1:H:173:PRO:HD3	1.91	0.51
1:J:385:LEU:HD23	1:J:389:TRP:O	2.10	0.51
1:A:3:ILE:CG2	1:A:9:LEU:HD13	2.40	0.51
1:H:144:ASN:HD22	1:H:168:ALA:H	1.57	0.51
1:B:148:ASP:OD2	1:B:151:GLU:HG3	2.11	0.51
1:J:148:ASP:OD2	1:J:151:GLU:HG3	2.10	0.51
1:K:148:ASP:OD2	1:K:151:GLU:HG3	2.09	0.51
1:C:5:SER:OG	1:C:8:VAL:HG23	2.10	0.51
1:I:148:ASP:OD2	1:I:151:GLU:HG3	2.10	0.51
1:J:186:ARG:HA	1:J:190:TYR:O	2.10	0.51
1:K:144:ASN:HD22	1:K:168:ALA:H	1.57	0.51
1:L:148:ASP:OD2	1:L:151:GLU:HG3	2.10	0.51
1:I:25:MET:HG3	3:I:992:HOH:O	2.09	0.51

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:148:ASP:OD2	1:G:151:GLU:HG3	2.10	0.51
1:I:393:GLU:HG2	1:I:397:LYS:NZ	2.26	0.51
1:A:3:ILE:HG21	1:A:9:LEU:HD13	1.93	0.51
1:A:144:ASN:HD22	1:A:168:ALA:H	1.58	0.51
1:H:12:LYS:HD2	1:H:393:GLU:OE2	2.11	0.51
1:K:245:LEU:HB2	1:K:246:PRO:HD3	1.93	0.51
1:C:172:ASP:HB2	1:C:173:PRO:HD3	1.93	0.50
1:K:382:ASP:O	1:K:386:GLN:HG2	2.09	0.50
1:H:245:LEU:HB2	1:H:246:PRO:HD3	1.93	0.50
1:J:276:VAL:HG22	1:J:277:GLY:N	2.26	0.50
1:E:392:THR:OG1	1:E:395:GLU:HG3	2.12	0.50
1:L:151:GLU:HB3	3:L:1018:HOH:O	2.11	0.50
1:A:245:LEU:HB2	1:A:246:PRO:HD3	1.94	0.50
1:D:245:LEU:HB2	1:D:246:PRO:HD3	1.94	0.50
1:E:8:VAL:HG13	1:E:12:LYS:HE2	1.93	0.50
1:F:186:ARG:HA	1:F:190:TYR:O	2.12	0.50
1:I:245:LEU:HB2	1:I:246:PRO:HD3	1.93	0.50
1:D:244:LEU:C	1:D:244:LEU:HD13	2.37	0.49
1:F:245:LEU:HB2	1:F:246:PRO:HD3	1.94	0.49
1:H:230:PHE:HA	1:H:231:PRO:C	2.37	0.49
1:H:402:ASP:HA	1:H:406:ARG:HB2	1.93	0.49
1:J:230:PHE:HA	1:J:231:PRO:C	2.37	0.49
1:C:393:GLU:HG2	1:C:397:LYS:HE3	1.94	0.49
1:J:392:THR:OG1	1:J:395:GLU:HG3	2.12	0.49
1:L:245:LEU:HB2	1:L:246:PRO:HD3	1.94	0.49
1:C:245:LEU:HB2	1:C:246:PRO:HD3	1.94	0.49
1:I:186:ARG:HA	1:I:190:TYR:O	2.13	0.49
1:B:245:LEU:HB2	1:B:246:PRO:HD3	1.94	0.49
1:G:245:LEU:HB2	1:G:246:PRO:HD3	1.95	0.49
1:G:402:ASP:HA	1:G:406:ARG:HB2	1.94	0.49
1:A:230:PHE:HA	1:A:231:PRO:C	2.38	0.49
1:C:1:MET:HG3	1:C:2:SER:O	2.12	0.49
1:I:230:PHE:HA	1:I:231:PRO:C	2.37	0.49
1:K:276:VAL:HG22	1:K:277:GLY:N	2.28	0.49
1:L:230:PHE:HA	1:L:231:PRO:C	2.37	0.49
1:J:315:LYS:HD2	1:L:274:ASP:O	2.12	0.49
1:D:230:PHE:HA	1:D:231:PRO:C	2.37	0.49
1:J:245:LEU:HB2	1:J:246:PRO:HD3	1.95	0.49
1:A:186:ARG:HA	1:A:190:TYR:O	2.13	0.49
1:B:244:LEU:C	1:B:244:LEU:HD13	2.38	0.49
1:G:186:ARG:HA	1:G:190:TYR:O	2.12	0.49

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:186:ARG:HA	1:K:190:TYR:O	2.12	0.49
1:D:254:PRO:HG2	1:D:412:VAL:HG12	1.95	0.49
1:F:276:VAL:HG22	1:F:277:GLY:N	2.26	0.49
1:G:127:GLN:HA	1:G:127:GLN:OE1	2.13	0.48
1:L:244:LEU:C	1:L:244:LEU:HD13	2.38	0.48
1:B:276:VAL:HG22	1:B:277:GLY:N	2.28	0.48
1:F:1:MET:CG	1:F:2:SER:H	2.27	0.48
1:G:230:PHE:HA	1:G:231:PRO:C	2.37	0.48
1:K:230:PHE:HA	1:K:231:PRO:C	2.37	0.48
1:E:315:LYS:HE2	1:F:272:ALA:O	2.13	0.48
1:H:374:ALA:O	1:H:378:ILE:HG13	2.13	0.48
1:D:186:ARG:HA	1:D:190:TYR:O	2.14	0.48
1:A:127:GLN:OE1	1:A:127:GLN:HA	2.14	0.48
1:B:386:GLN:HG3	1:F:1:MET:CG	2.36	0.48
1:C:186:ARG:HA	1:C:190:TYR:O	2.14	0.48
1:D:276:VAL:HG22	1:D:277:GLY:N	2.29	0.48
1:E:230:PHE:HA	1:E:231:PRO:C	2.37	0.48
1:F:230:PHE:HA	1:F:231:PRO:C	2.38	0.48
1:I:276:VAL:HG22	1:I:277:GLY:N	2.29	0.48
1:L:186:ARG:HA	1:L:190:TYR:O	2.13	0.48
1:A:402:ASP:HA	1:A:406:ARG:HB2	1.96	0.48
1:B:170:ARG:NH1	1:B:173:PRO:HD3	2.29	0.48
1:C:1:MET:HE2	1:C:4:ASN:HD22	1.74	0.48
1:C:127:GLN:OE1	1:C:127:GLN:HA	2.14	0.48
1:F:170:ARG:NH1	1:F:173:PRO:HD3	2.29	0.48
1:I:170:ARG:NH1	1:I:173:PRO:HD3	2.29	0.48
1:K:244:LEU:HD13	1:K:244:LEU:C	2.39	0.48
1:L:127:GLN:HA	1:L:127:GLN:OE1	2.14	0.48
1:A:144:ASN:HD21	1:A:167:ALA:HA	1.79	0.47
1:B:230:PHE:HA	1:B:231:PRO:C	2.38	0.47
1:C:276:VAL:HG22	1:C:277:GLY:N	2.29	0.47
1:E:402:ASP:HA	1:E:406:ARG:HB2	1.96	0.47
1:G:351:PRO:HD2	3:G:1030:HOH:O	2.13	0.47
1:A:244:LEU:HD13	1:A:244:LEU:C	2.39	0.47
1:B:182:LYS:O	1:B:186:ARG:HG2	2.13	0.47
1:F:244:LEU:HD13	1:F:244:LEU:C	2.38	0.47
1:H:182:LYS:O	1:H:186:ARG:HG2	2.13	0.47
1:I:144:ASN:ND2	1:I:167:ALA:HA	2.29	0.47
1:J:244:LEU:HD13	1:J:244:LEU:C	2.39	0.47
1:C:148:ASP:OD2	1:C:150:ASN:HB3	2.15	0.47
1:C:244:LEU:HD13	1:C:244:LEU:C	2.40	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:144:ASN:ND2	1:E:167:ALA:HA	2.29	0.47
1:K:144:ASN:ND2	1:K:167:ALA:HA	2.29	0.47
1:D:144:ASN:ND2	1:D:167:ALA:HA	2.29	0.47
1:F:139:ASP:OD1	1:F:166:HIS:HE1	1.98	0.47
1:G:25:MET:HG3	3:G:999:HOH:O	2.15	0.47
1:H:244:LEU:HD13	1:H:244:LEU:C	2.39	0.47
1:K:144:ASN:HD21	1:K:167:ALA:HA	1.79	0.47
1:L:70:SER:OG	1:L:73:GLU:HG3	2.15	0.47
1:L:170:ARG:NH1	1:L:173:PRO:HD3	2.30	0.47
1:J:148:ASP:OD2	1:J:150:ASN:HB3	2.15	0.47
1:A:276:VAL:HG22	1:A:277:GLY:N	2.29	0.47
1:B:127:GLN:HA	1:B:127:GLN:OE1	2.15	0.47
1:E:186:ARG:HA	1:E:190:TYR:O	2.15	0.47
1:G:244:LEU:C	1:G:244:LEU:HD13	2.39	0.47
1:I:244:LEU:C	1:I:244:LEU:HD13	2.39	0.47
1:J:144:ASN:ND2	1:J:167:ALA:HA	2.30	0.47
1:A:182:LYS:O	1:A:186:ARG:HG2	2.15	0.47
1:A:392:THR:OG1	1:A:395:GLU:HG3	2.14	0.47
1:B:139:ASP:OD1	1:B:166:HIS:HE1	1.97	0.47
1:C:230:PHE:HA	1:C:231:PRO:C	2.39	0.47
1:E:244:LEU:C	1:E:244:LEU:HD13	2.39	0.47
1:E:245:LEU:HB2	1:E:246:PRO:HD3	1.96	0.47
1:E:276:VAL:HG22	1:E:277:GLY:N	2.29	0.47
1:F:144:ASN:ND2	1:F:167:ALA:HA	2.29	0.47
1:G:144:ASN:ND2	1:G:167:ALA:HA	2.30	0.47
1:J:127:GLN:HA	1:J:127:GLN:OE1	2.15	0.47
1:J:391:VAL:HG23	1:J:391:VAL:O	2.15	0.47
1:L:276:VAL:HG22	1:L:277:GLY:N	2.28	0.47
1:A:154:SER:CB	1:A:159:LYS:HD3	2.45	0.47
1:A:170:ARG:NH1	1:A:173:PRO:HD3	2.30	0.47
1:C:144:ASN:HD21	1:C:167:ALA:HA	1.79	0.47
1:E:144:ASN:HD21	1:E:167:ALA:HA	1.80	0.47
1:F:144:ASN:HD21	1:F:167:ALA:HA	1.80	0.47
1:I:182:LYS:O	1:I:186:ARG:HG2	2.15	0.47
1:G:274:ASP:O	1:H:315:LYS:HD2	2.15	0.47
1:A:144:ASN:ND2	1:A:167:ALA:HA	2.30	0.47
1:B:315:LYS:HD2	1:C:274:ASP:O	2.14	0.47
1:C:196:TRP:CD1	1:C:238:ARG:HD2	2.50	0.47
1:E:182:LYS:O	1:E:186:ARG:HG2	2.14	0.47
1:G:70:SER:OG	1:G:73:GLU:HG3	2.15	0.47
1:J:25:MET:HG3	3:J:1007:HOH:O	2.14	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:315:LYS:HE2	1:L:272:ALA:O	2.15	0.47
1:K:170:ARG:NH1	1:K:173:PRO:HD3	2.29	0.47
1:A:25:MET:HG3	3:A:1019:HOH:O	2.15	0.46
1:C:144:ASN:ND2	1:C:167:ALA:HA	2.29	0.46
1:G:170:ARG:NH1	1:G:173:PRO:HD3	2.29	0.46
1:G:276:VAL:HG22	1:G:277:GLY:N	2.30	0.46
1:H:144:ASN:ND2	1:H:167:ALA:HA	2.30	0.46
1:I:65:ALA:O	1:I:69:MET:HG3	2.16	0.46
1:I:144:ASN:HD21	1:I:167:ALA:HA	1.80	0.46
1:I:385:LEU:HD12	1:I:389:TRP:O	2.14	0.46
1:J:170:ARG:NH1	1:J:173:PRO:HD3	2.30	0.46
1:K:149:ASP:O	1:K:153:ILE:HG13	2.15	0.46
1:L:144:ASN:ND2	1:L:167:ALA:HA	2.29	0.46
1:G:315:LYS:HE2	1:I:272:ALA:O	2.15	0.46
1:A:315:LYS:O	1:B:266:HIS:CD2	2.58	0.46
1:B:144:ASN:ND2	1:B:167:ALA:HA	2.30	0.46
1:E:127:GLN:HA	1:E:127:GLN:OE1	2.15	0.46
1:F:127:GLN:OE1	1:F:127:GLN:HA	2.15	0.46
1:G:154:SER:CB	1:G:159:LYS:HD3	2.46	0.46
1:I:154:SER:CB	1:I:159:LYS:HD3	2.45	0.46
1:J:195:GLU:HG3	1:J:197:ASN:HD22	1.80	0.46
1:K:154:SER:CB	1:K:159:LYS:HD3	2.45	0.46
1:A:196:TRP:CD1	1:A:238:ARG:HD2	2.50	0.46
1:A:272:ALA:O	1:C:315:LYS:HE2	2.16	0.46
1:K:70:SER:OG	1:K:73:GLU:HG3	2.15	0.46
1:K:127:GLN:OE1	1:K:127:GLN:HA	2.16	0.46
1:B:25:MET:HG3	3:B:1004:HOH:O	2.14	0.46
1:H:276:VAL:HG22	1:H:277:GLY:N	2.30	0.46
1:J:182:LYS:O	1:J:186:ARG:HG2	2.15	0.46
1:K:182:LYS:O	1:K:186:ARG:HG2	2.16	0.46
1:L:139:ASP:OD1	1:L:166:HIS:HE1	1.98	0.46
1:A:65:ALA:O	1:A:69:MET:HG3	2.16	0.46
1:E:154:SER:CB	1:E:159:LYS:HD3	2.45	0.46
1:F:148:ASP:OD2	1:F:150:ASN:HB3	2.16	0.46
1:G:148:ASP:OD2	1:G:150:ASN:HB3	2.16	0.46
1:H:127:GLN:OE1	1:H:127:GLN:HA	2.16	0.46
1:H:144:ASN:HD21	1:H:167:ALA:HA	1.81	0.46
1:J:65:ALA:O	1:J:69:MET:HG3	2.16	0.46
1:K:139:ASP:OD1	1:K:166:HIS:HE1	1.99	0.46
1:L:196:TRP:CD1	1:L:238:ARG:HD2	2.50	0.46
1:D:170:ARG:NH1	1:D:173:PRO:HD3	2.30	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:139:ASP:OD1	1:H:166:HIS:HE1	1.98	0.46
1:H:196:TRP:CD1	1:H:238:ARG:HD2	2.51	0.46
1:I:148:ASP:OD2	1:I:150:ASN:HB3	2.16	0.46
1:B:149:ASP:O	1:B:153:ILE:HG13	2.16	0.46
1:B:195:GLU:HG3	1:B:197:ASN:HD22	1.81	0.46
1:B:196:TRP:CD1	1:B:238:ARG:HD2	2.51	0.46
1:E:170:ARG:NH1	1:E:173:PRO:HD3	2.30	0.46
1:F:3:ILE:HG21	1:F:9:LEU:HD13	1.96	0.46
1:F:154:SER:CB	1:F:159:LYS:HD3	2.46	0.46
1:L:144:ASN:HD21	1:L:167:ALA:HA	1.81	0.46
1:B:315:LYS:HE2	1:C:272:ALA:O	2.15	0.46
1:C:139:ASP:OD1	1:C:166:HIS:HE1	1.98	0.46
1:C:389:TRP:CD1	1:C:391:VAL:HG12	2.50	0.46
1:D:127:GLN:OE1	1:D:127:GLN:HA	2.15	0.46
1:D:139:ASP:OD1	1:D:166:HIS:HE1	1.98	0.46
1:E:70:SER:OG	1:E:73:GLU:HG3	2.16	0.46
1:F:196:TRP:CD1	1:F:238:ARG:HD2	2.51	0.46
1:G:144:ASN:HD21	1:G:167:ALA:HA	1.81	0.46
1:H:170:ARG:NH1	1:H:173:PRO:HD3	2.31	0.46
1:J:196:TRP:CD1	1:J:238:ARG:HD2	2.50	0.46
1:J:313:ALA:HA	1:J:319:LEU:HD23	1.98	0.46
1:D:70:SER:OG	1:D:73:GLU:HG3	2.16	0.46
1:K:291:TYR:HB3	1:K:294:ASN:HD22	1.81	0.46
1:E:148:ASP:OD2	1:E:150:ASN:HB3	2.16	0.45
1:E:195:GLU:HG3	1:E:197:ASN:HD22	1.82	0.45
1:E:289:ARG:HD3	1:F:265:VAL:O	2.16	0.45
1:F:182:LYS:O	1:F:186:ARG:HG2	2.15	0.45
1:G:65:ALA:O	1:G:69:MET:HG3	2.16	0.45
1:G:385:LEU:HD12	1:G:389:TRP:O	2.16	0.45
1:J:154:SER:CB	1:J:159:LYS:HD3	2.46	0.45
1:A:4:ASN:OD1	1:D:386:GLN:NE2	2.49	0.45
1:A:70:SER:OG	1:A:73:GLU:HG3	2.17	0.45
1:C:170:ARG:NH1	1:C:173:PRO:HD3	2.30	0.45
1:D:148:ASP:OD2	1:D:150:ASN:HB3	2.16	0.45
1:L:148:ASP:OD2	1:L:150:ASN:HB3	2.16	0.45
1:B:148:ASP:OD2	1:B:150:ASN:HB3	2.16	0.45
1:B:186:ARG:HA	1:B:190:TYR:O	2.16	0.45
1:D:65:ALA:O	1:D:69:MET:HG3	2.17	0.45
1:D:144:ASN:HD21	1:D:167:ALA:HA	1.81	0.45
1:H:154:SER:CB	1:H:159:LYS:HD3	2.46	0.45
1:L:1:MET:CE	1:L:1:MET:H3	2.29	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:139:ASP:OD1	1:A:166:HIS:HE1	1.99	0.45
1:A:148:ASP:OD2	1:A:150:ASN:HB3	2.16	0.45
1:D:154:SER:CB	1:D:159:LYS:HD3	2.46	0.45
1:E:65:ALA:O	1:E:69:MET:HG3	2.17	0.45
1:G:149:ASP:O	1:G:153:ILE:HG13	2.16	0.45
1:L:65:ALA:O	1:L:69:MET:HG3	2.16	0.45
1:C:154:SER:CB	1:C:159:LYS:HD3	2.46	0.45
1:D:69:MET:HB3	1:D:73:GLU:HB2	1.99	0.45
1:J:149:ASP:O	1:J:153:ILE:HG13	2.16	0.45
1:L:154:SER:CB	1:L:159:LYS:HD3	2.46	0.45
1:B:154:SER:CB	1:B:159:LYS:HD3	2.47	0.45
1:C:69:MET:HB3	1:C:73:GLU:HB2	1.99	0.45
1:F:149:ASP:O	1:F:153:ILE:HG13	2.17	0.45
1:F:291:TYR:HB3	1:F:294:ASN:HD22	1.81	0.45
1:H:70:SER:OG	1:H:73:GLU:HG3	2.16	0.45
1:I:70:SER:OG	1:I:73:GLU:HG3	2.17	0.45
1:J:139:ASP:OD1	1:J:166:HIS:HE1	1.99	0.45
1:D:182:LYS:O	1:D:186:ARG:HG2	2.16	0.45
1:D:196:TRP:CD1	1:D:238:ARG:HD2	2.52	0.45
1:I:195:GLU:HG3	1:I:197:ASN:HD22	1.82	0.45
1:D:149:ASP:O	1:D:153:ILE:HG13	2.17	0.45
1:D:195:GLU:HG3	1:D:197:ASN:HD22	1.82	0.45
1:K:148:ASP:OD2	1:K:150:ASN:HB3	2.16	0.45
1:A:149:ASP:O	1:A:153:ILE:HG13	2.17	0.45
1:B:144:ASN:HD21	1:B:167:ALA:HA	1.81	0.45
1:C:5:SER:HG	1:C:8:VAL:HG23	1.82	0.45
1:I:393:GLU:HG2	1:I:397:LYS:HZ3	1.80	0.45
1:L:182:LYS:O	1:L:186:ARG:HG2	2.16	0.45
1:A:195:GLU:HG3	1:A:197:ASN:HD22	1.82	0.45
1:C:65:ALA:O	1:C:69:MET:HG3	2.17	0.45
1:C:182:LYS:O	1:C:186:ARG:HG2	2.16	0.45
1:H:313:ALA:HA	1:H:319:LEU:HD23	1.99	0.45
1:J:252:ASN:HD21	1:J:295:LYS:HE2	1.82	0.45
1:C:70:SER:OG	1:C:73:GLU:HG3	2.17	0.44
1:C:126:GLU:HG2	1:L:202:GLN:NE2	2.32	0.44
1:F:313:ALA:HA	1:F:319:LEU:HD23	1.99	0.44
1:G:69:MET:HB3	1:G:73:GLU:HB2	1.99	0.44
1:K:97:LEU:HD13	1:L:389:TRP:HB2	1.99	0.44
1:L:149:ASP:O	1:L:153:ILE:HG13	2.17	0.44
1:L:392:THR:OG1	1:L:395:GLU:HG3	2.17	0.44
1:L:402:ASP:HA	1:L:406:ARG:HB2	2.00	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:374:ALA:O	1:A:378:ILE:HG13	2.17	0.44
1:E:196:TRP:CD1	1:E:238:ARG:HD2	2.52	0.44
1:F:65:ALA:O	1:F:69:MET:HG3	2.17	0.44
1:H:410:ARG:HG2	1:H:410:ARG:HH11	1.82	0.44
1:K:195:GLU:HG3	1:K:197:ASN:HD22	1.82	0.44
1:K:252:ASN:HD21	1:K:295:LYS:HE2	1.82	0.44
1:B:3:ILE:HD12	1:B:391:VAL:HG13	2.00	0.44
1:D:313:ALA:HA	1:D:319:LEU:HD23	1.99	0.44
1:E:25:MET:HG3	3:E:1000:HOH:O	2.17	0.44
1:E:149:ASP:O	1:E:153:ILE:HG13	2.17	0.44
1:F:69:MET:HB3	1:F:73:GLU:HB2	1.99	0.44
1:H:252:ASN:HD21	1:H:295:LYS:HE2	1.82	0.44
1:J:69:MET:HB3	1:J:73:GLU:HB2	1.99	0.44
1:D:291:TYR:HB3	1:D:294:ASN:HD22	1.82	0.44
1:G:182:LYS:O	1:G:186:ARG:HG2	2.17	0.44
1:K:69:MET:HB3	1:K:73:GLU:HB2	1.99	0.44
1:G:195:GLU:HG3	1:G:197:ASN:HD22	1.83	0.44
1:H:112:LEU:HA	1:H:115:TYR:CD2	2.52	0.44
1:H:149:ASP:O	1:H:153:ILE:HG13	2.17	0.44
1:H:195:GLU:HG3	1:H:197:ASN:HD22	1.82	0.44
1:I:127:GLN:OE1	1:I:127:GLN:HA	2.16	0.44
1:I:151:GLU:HB3	3:I:1055:HOH:O	2.18	0.44
1:K:65:ALA:O	1:K:69:MET:HG3	2.18	0.44
1:G:203:GLU:OE1	1:G:206:ARG:NH1	2.51	0.44
1:H:148:ASP:OD2	1:H:150:ASN:HB3	2.18	0.44
1:I:149:ASP:O	1:I:153:ILE:HG13	2.18	0.44
1:K:196:TRP:CD1	1:K:238:ARG:HD2	2.52	0.44
1:B:386:GLN:CG	1:F:1:MET:HE3	2.47	0.44
1:C:149:ASP:O	1:C:153:ILE:HG13	2.17	0.44
1:E:69:MET:HB3	1:E:73:GLU:HB2	1.99	0.44
1:F:70:SER:OG	1:F:73:GLU:HG3	2.17	0.44
1:I:69:MET:HB3	1:I:73:GLU:HB2	2.00	0.44
1:I:382:ASP:O	1:I:386:GLN:HG2	2.17	0.44
1:J:112:LEU:HA	1:J:115:TYR:CD2	2.53	0.44
1:A:313:ALA:HA	1:A:319:LEU:HD23	2.00	0.44
1:C:195:GLU:HG3	1:C:197:ASN:HD22	1.82	0.44
1:F:392:THR:OG1	1:F:395:GLU:HG3	2.18	0.44
1:I:252:ASN:HD21	1:I:295:LYS:HE2	1.83	0.44
1:J:70:SER:OG	1:J:73:GLU:HG3	2.17	0.44
1:A:376:VAL:O	1:A:380:LYS:HD3	2.18	0.44
1:G:139:ASP:OD1	1:G:166:HIS:HE1	2.01	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:97:LEU:HD13	1:K:389:TRP:HB2	1.99	0.44
1:K:252:ASN:ND2	1:K:295:LYS:HE2	2.33	0.44
1:B:69:MET:HB3	1:B:73:GLU:HB2	1.99	0.43
1:I:196:TRP:CD1	1:I:238:ARG:HD2	2.52	0.43
1:H:56:MET:HE3	3:H:1063:HOH:O	2.18	0.43
1:H:186:ARG:HA	1:H:190:TYR:O	2.18	0.43
1:I:372:ILE:O	1:I:375:GLU:HG2	2.18	0.43
1:J:144:ASN:HD21	1:J:167:ALA:HA	1.82	0.43
1:D:112:LEU:HA	1:D:115:TYR:CD2	2.54	0.43
1:E:139:ASP:OD1	1:E:166:HIS:HE1	2.00	0.43
1:E:291:TYR:HB3	1:E:294:ASN:HD22	1.83	0.43
1:H:69:MET:HB3	1:H:73:GLU:HB2	1.99	0.43
1:L:1:MET:HE2	1:L:2:SER:H	1.82	0.43
1:B:70:SER:OG	1:B:73:GLU:HG3	2.18	0.43
1:B:112:LEU:HA	1:B:115:TYR:CD2	2.53	0.43
1:C:252:ASN:HD21	1:C:295:LYS:HE2	1.83	0.43
1:F:112:LEU:HA	1:F:115:TYR:CD2	2.53	0.43
1:D:274:ASP:O	1:F:315:LYS:HD2	2.18	0.43
1:F:351:PRO:HD2	3:F:993:HOH:O	2.18	0.43
1:I:291:TYR:HB3	1:I:294:ASN:HD22	1.84	0.43
1:J:389:TRP:HB2	1:L:97:LEU:HD13	2.00	0.43
1:B:275:PHE:CG	1:B:276:VAL:N	2.87	0.43
1:B:313:ALA:HA	1:B:319:LEU:HD23	1.99	0.43
1:D:12:LYS:HD2	1:D:393:GLU:CD	2.43	0.43
1:D:252:ASN:HD21	1:D:295:LYS:HE2	1.84	0.43
1:I:139:ASP:OD1	1:I:166:HIS:HE1	2.00	0.43
1:J:12:LYS:HD2	1:J:393:GLU:CD	2.43	0.43
1:J:291:TYR:HB3	1:J:294:ASN:HD22	1.83	0.43
1:A:252:ASN:HD21	1:A:295:LYS:HE2	1.83	0.43
1:C:112:LEU:HA	1:C:115:TYR:CD2	2.53	0.43
1:F:170:ARG:HH12	1:F:173:PRO:HD3	1.83	0.43
1:F:195:GLU:HG3	1:F:197:ASN:HD22	1.82	0.43
1:H:65:ALA:O	1:H:69:MET:HG3	2.18	0.43
1:A:216:ASP:N	1:A:217:PRO:CD	2.82	0.43
1:J:364:TYR:CD1	1:J:364:TYR:C	2.97	0.43
1:K:275:PHE:CG	1:K:276:VAL:N	2.86	0.43
1:D:275:PHE:CG	1:D:276:VAL:N	2.87	0.43
1:D:315:LYS:HD2	1:E:274:ASP:O	2.19	0.43
1:F:9:LEU:O	1:F:13:VAL:HG23	2.19	0.43
1:F:364:TYR:CD1	1:F:364:TYR:C	2.97	0.43
1:G:170:ARG:HH12	1:G:173:PRO:HD3	1.83	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:170:ARG:HH12	1:K:173:PRO:HD3	1.84	0.43
1:L:69:MET:HB3	1:L:73:GLU:HB2	1.99	0.43
1:F:1:MET:HG2	1:F:2:SER:H	1.83	0.43
1:F:402:ASP:HA	1:F:406:ARG:HB2	2.01	0.43
1:G:364:TYR:CD1	1:G:364:TYR:C	2.97	0.43
1:L:203:GLU:OE1	1:L:206:ARG:NH1	2.52	0.43
1:C:6:ARG:HG3	1:C:6:ARG:NH1	2.34	0.42
1:I:170:ARG:HH12	1:I:173:PRO:HD3	1.83	0.42
1:L:112:LEU:HA	1:L:115:TYR:CD2	2.53	0.42
1:L:291:TYR:HB3	1:L:294:ASN:HD22	1.83	0.42
1:A:97:LEU:HD13	1:C:389:TRP:HB2	2.02	0.42
1:B:216:ASP:N	1:B:217:PRO:CD	2.82	0.42
1:B:252:ASN:HD21	1:B:295:LYS:HE2	1.83	0.42
1:C:1:MET:HE2	1:C:4:ASN:HD21	1.78	0.42
1:D:364:TYR:CD1	1:D:364:TYR:C	2.97	0.42
1:E:252:ASN:HD21	1:E:295:LYS:HE2	1.84	0.42
1:H:409:TRP:HA	1:H:412:VAL:HG22	2.01	0.42
1:J:275:PHE:CG	1:J:276:VAL:N	2.87	0.42
1:L:195:GLU:HG3	1:L:197:ASN:HD22	1.84	0.42
1:A:69:MET:HB3	1:A:73:GLU:HB2	2.00	0.42
1:B:65:ALA:O	1:B:69:MET:HG3	2.18	0.42
1:B:170:ARG:HH12	1:B:173:PRO:HD3	1.83	0.42
1:G:272:ALA:O	1:H:315:LYS:HE2	2.18	0.42
1:K:313:ALA:HA	1:K:319:LEU:HD23	2.01	0.42
1:A:275:PHE:CG	1:A:276:VAL:N	2.87	0.42
1:E:112:LEU:HA	1:E:115:TYR:CD2	2.54	0.42
1:G:291:TYR:HB3	1:G:294:ASN:HD22	1.85	0.42
1:H:291:TYR:HB3	1:H:294:ASN:HD22	1.85	0.42
1:I:252:ASN:ND2	1:I:295:LYS:HE2	2.34	0.42
1:J:393:GLU:O	1:J:397:LYS:HG3	2.19	0.42
1:L:254:PRO:HG2	1:L:412:VAL:HG12	2.02	0.42
1:F:252:ASN:HD21	1:F:295:LYS:HE2	1.84	0.42
1:G:196:TRP:CD1	1:G:238:ARG:HD2	2.54	0.42
1:H:364:TYR:CD1	1:H:364:TYR:C	2.97	0.42
1:K:112:LEU:HA	1:K:115:TYR:CD2	2.54	0.42
1:L:313:ALA:HA	1:L:319:LEU:HD23	2.01	0.42
1:D:252:ASN:ND2	1:D:295:LYS:HE2	2.34	0.42
1:D:393:GLU:HG2	1:D:397:LYS:HE2	2.02	0.42
1:E:352:GLN:HG3	1:E:353:HIS:N	2.35	0.42
1:F:252:ASN:ND2	1:F:295:LYS:HE2	2.34	0.42
1:H:266:HIS:CD2	1:I:315:LYS:O	2.64	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:252:ASN:ND2	1:J:295:LYS:HE2	2.34	0.42
1:K:9:LEU:O	1:K:13:VAL:HG23	2.19	0.42
1:L:1:MET:N	1:L:1:MET:CE	2.83	0.42
1:G:275:PHE:CG	1:G:276:VAL:N	2.88	0.42
1:K:364:TYR:CD1	1:K:364:TYR:C	2.97	0.42
1:L:216:ASP:N	1:L:217:PRO:CD	2.83	0.42
1:L:275:PHE:CG	1:L:276:VAL:N	2.88	0.42
1:L:364:TYR:CD1	1:L:364:TYR:C	2.97	0.42
1:A:151:GLU:HB3	3:A:1078:HOH:O	2.18	0.42
1:E:252:ASN:ND2	1:E:295:LYS:HE2	2.35	0.42
1:E:313:ALA:HA	1:E:319:LEU:HD23	2.01	0.42
1:H:265:VAL:O	1:I:289:ARG:HD3	2.20	0.42
1:H:286:HIS:HE1	3:H:1018:HOH:O	2.01	0.42
1:J:52:VAL:O	1:J:55:VAL:HG12	2.20	0.42
1:J:195:GLU:HG3	1:J:197:ASN:ND2	2.35	0.42
1:L:1:MET:N	1:L:1:MET:SD	2.86	0.42
1:L:252:ASN:HD21	1:L:295:LYS:HE2	1.84	0.42
1:B:291:TYR:HB3	1:B:294:ASN:HD22	1.84	0.42
1:B:323:GLY:HA3	1:B:353:HIS:ND1	2.35	0.42
1:C:252:ASN:ND2	1:C:295:LYS:HE2	2.34	0.42
1:D:216:ASP:N	1:D:217:PRO:CD	2.83	0.42
1:E:216:ASP:N	1:E:217:PRO:CD	2.82	0.42
1:E:264:ARG:HB2	1:E:264:ARG:NH1	2.35	0.42
1:E:275:PHE:CG	1:E:276:VAL:N	2.87	0.42
1:C:364:TYR:CD1	1:C:364:TYR:C	2.98	0.42
1:F:216:ASP:N	1:F:217:PRO:CD	2.83	0.42
1:G:313:ALA:HA	1:G:319:LEU:HD23	2.01	0.42
1:H:323:GLY:HA3	1:H:353:HIS:ND1	2.35	0.42
1:A:112:LEU:HA	1:A:115:TYR:CD2	2.54	0.41
1:A:364:TYR:CD1	1:A:364:TYR:C	2.97	0.41
1:D:145:ASP:HA	1:D:146:PRO:HD2	1.97	0.41
1:H:252:ASN:ND2	1:H:295:LYS:HE2	2.33	0.41
1:I:275:PHE:CG	1:I:276:VAL:N	2.88	0.41
1:B:252:ASN:ND2	1:B:295:LYS:HE2	2.34	0.41
1:B:254:PRO:HG2	1:B:412:VAL:HG12	2.02	0.41
1:L:170:ARG:HH12	1:L:173:PRO:HD3	1.84	0.41
1:A:70:SER:O	1:A:74:GLN:HG3	2.20	0.41
1:A:145:ASP:HA	1:A:146:PRO:HD2	1.98	0.41
1:E:52:VAL:O	1:E:55:VAL:HG12	2.20	0.41
1:F:25:MET:HG3	3:F:995:HOH:O	2.20	0.41
1:C:216:ASP:N	1:C:217:PRO:CD	2.83	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:254:PRO:HG2	1:C:412:VAL:HG12	2.02	0.41
1:D:203:GLU:OE1	1:D:206:ARG:NH1	2.53	0.41
1:G:254:PRO:HG2	1:G:412:VAL:HG12	2.02	0.41
1:I:203:GLU:OE1	1:I:206:ARG:NH1	2.54	0.41
1:J:352:GLN:HG3	1:J:353:HIS:N	2.36	0.41
1:K:352:GLN:HG3	1:K:353:HIS:N	2.36	0.41
1:G:252:ASN:HD21	1:G:295:LYS:HE2	1.86	0.41
1:J:145:ASP:HA	1:J:146:PRO:HD2	1.96	0.41
1:J:276:VAL:CG2	1:J:277:GLY:N	2.84	0.41
1:K:145:ASP:HA	1:K:146:PRO:HD2	1.96	0.41
1:B:364:TYR:CD1	1:B:364:TYR:C	2.99	0.41
1:E:386:GLN:OE1	1:E:386:GLN:HA	2.21	0.41
1:G:112:LEU:HA	1:G:115:TYR:CD2	2.55	0.41
1:H:70:SER:O	1:H:74:GLN:HG3	2.20	0.41
1:H:391:VAL:HG13	1:H:391:VAL:O	2.20	0.41
1:K:385:LEU:HD12	1:K:385:LEU:HA	1.96	0.41
1:L:252:ASN:ND2	1:L:295:LYS:HE2	2.35	0.41
1:B:195:GLU:HG3	1:B:197:ASN:ND2	2.35	0.41
1:C:113:GLN:NE2	1:C:116:ARG:HH11	2.18	0.41
1:D:170:ARG:HH12	1:D:173:PRO:HD3	1.85	0.41
1:E:145:ASP:HA	1:E:146:PRO:HD2	1.97	0.41
1:G:3:ILE:HG21	1:G:9:LEU:HB2	2.03	0.41
1:I:112:LEU:HA	1:I:115:TYR:CD2	2.56	0.41
1:I:313:ALA:HA	1:I:319:LEU:HD23	2.02	0.41
1:K:52:VAL:O	1:K:55:VAL:HG12	2.21	0.41
1:A:252:ASN:ND2	1:A:295:LYS:HE2	2.35	0.41
1:B:113:GLN:NE2	1:B:116:ARG:HH11	2.19	0.41
1:D:70:SER:O	1:D:74:GLN:HG3	2.21	0.41
1:E:203:GLU:OE1	1:E:206:ARG:NH1	2.54	0.41
1:E:326:TRP:HB3	1:E:327:PHE:H	1.64	0.41
1:E:364:TYR:CD1	1:E:364:TYR:C	2.98	0.41
1:G:252:ASN:ND2	1:G:295:LYS:HE2	2.36	0.41
1:H:216:ASP:N	1:H:217:PRO:CD	2.84	0.41
1:I:113:GLN:NE2	1:I:116:ARG:HH11	2.19	0.41
1:I:216:ASP:N	1:I:217:PRO:CD	2.83	0.41
1:K:113:GLN:NE2	1:K:116:ARG:HH11	2.19	0.41
1:A:170:ARG:HH12	1:A:173:PRO:HD3	1.85	0.41
1:A:291:TYR:HB3	1:A:294:ASN:HD22	1.85	0.41
1:F:276:VAL:CG2	1:F:277:GLY:N	2.83	0.41
1:H:97:LEU:HD13	1:I:389:TRP:HB2	2.03	0.41
1:J:216:ASP:N	1:J:217:PRO:CD	2.83	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:402:ASP:HA	1:J:406:ARG:HB2	2.02	0.41
1:D:315:LYS:O	1:E:266:HIS:CD2	2.63	0.40
1:E:170:ARG:HH12	1:E:173:PRO:HD3	1.85	0.40
1:K:323:GLY:HA3	1:K:353:HIS:ND1	2.35	0.40
1:C:275:PHE:CG	1:C:276:VAL:N	2.89	0.40
1:F:52:VAL:O	1:F:55:VAL:HG12	2.21	0.40
1:J:170:ARG:HH12	1:J:173:PRO:HD3	1.85	0.40
1:K:216:ASP:N	1:K:217:PRO:CD	2.84	0.40
1:E:113:GLN:NE2	1:E:116:ARG:HH11	2.19	0.40
1:G:326:TRP:HB3	1:G:327:PHE:H	1.66	0.40
1:H:203:GLU:OE1	1:H:206:ARG:NH1	2.55	0.40
1:L:352:GLN:HG3	1:L:353:HIS:N	2.36	0.40
1:F:70:SER:O	1:F:74:GLN:HG3	2.21	0.40
1:K:276:VAL:CG2	1:K:277:GLY:N	2.85	0.40
1:L:113:GLN:NE2	1:L:116:ARG:HH11	2.19	0.40
1:G:389:TRP:HB2	1:I:97:LEU:HD13	2.03	0.40
1:K:195:GLU:HG3	1:K:197:ASN:ND2	2.37	0.40
1:L:323:GLY:HA3	1:L:353:HIS:ND1	2.36	0.40

All (2) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:194:ASP:OD2	1:G:233:GLU:N[1_455]	2.11	0.09
1:B:193:ASN:ND2	1:G:238:ARG:NH2[1_455]	2.17	0.03

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 X-ray entries followed by that with respect to entries of similar resolution.

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	411/427 (96%)	401 (98%)	9 (2%)	1 (0%)	43 42

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	411/427 (96%)	400 (97%)	10 (2%)	1 (0%)	43	42
1	C	411/427 (96%)	400 (97%)	10 (2%)	1 (0%)	43	42
1	D	411/427 (96%)	402 (98%)	8 (2%)	1 (0%)	43	42
1	E	411/427 (96%)	401 (98%)	8 (2%)	2 (0%)	24	21
1	F	411/427 (96%)	401 (98%)	8 (2%)	2 (0%)	24	21
1	G	411/427 (96%)	398 (97%)	10 (2%)	3 (1%)	18	14
1	H	411/427 (96%)	400 (97%)	9 (2%)	2 (0%)	24	21
1	I	411/427 (96%)	401 (98%)	7 (2%)	3 (1%)	18	14
1	J	411/427 (96%)	400 (97%)	9 (2%)	2 (0%)	24	21
1	K	411/427 (96%)	402 (98%)	7 (2%)	2 (0%)	24	21
1	L	411/427 (96%)	399 (97%)	10 (2%)	2 (0%)	24	21
All	All	4932/5124 (96%)	4805 (97%)	105 (2%)	22 (0%)	30	27

All (22) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	41	ASP
1	B	41	ASP
1	C	41	ASP
1	D	41	ASP
1	E	41	ASP
1	F	41	ASP
1	G	41	ASP
1	H	41	ASP
1	I	2	SER
1	I	41	ASP
1	J	41	ASP
1	K	41	ASP
1	L	41	ASP
1	F	323	GLY
1	K	323	GLY
1	L	323	GLY
1	G	323	GLY
1	J	323	GLY
1	E	323	GLY
1	G	3	ILE
1	H	323	GLY
1	I	323	GLY

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

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	373/387 (96%)	370 (99%)	3 (1%)	73	80
1	B	373/387 (96%)	370 (99%)	3 (1%)	73	80
1	C	373/387 (96%)	369 (99%)	4 (1%)	65	73
1	D	373/387 (96%)	370 (99%)	3 (1%)	73	80
1	E	373/387 (96%)	369 (99%)	4 (1%)	65	73
1	F	373/387 (96%)	371 (100%)	2 (0%)	81	87
1	G	373/387 (96%)	370 (99%)	3 (1%)	73	80
1	H	373/387 (96%)	371 (100%)	2 (0%)	81	87
1	I	373/387 (96%)	370 (99%)	3 (1%)	73	80
1	J	373/387 (96%)	370 (99%)	3 (1%)	73	80
1	K	373/387 (96%)	370 (99%)	3 (1%)	73	80
1	L	373/387 (96%)	368 (99%)	5 (1%)	61	68
All	All	4476/4644 (96%)	4438 (99%)	38 (1%)	73	80

All (38) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1	MET
1	A	315	LYS
1	A	364	TYR
1	B	315	LYS
1	B	364	TYR
1	B	386	GLN
1	C	6	ARG
1	C	315	LYS
1	C	364	TYR
1	C	391	VAL
1	D	315	LYS
1	D	364	TYR
1	D	385	LEU
1	E	4	ASN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	E	315	LYS
1	E	364	TYR
1	E	385	LEU
1	F	315	LYS
1	F	364	TYR
1	G	315	LYS
1	G	364	TYR
1	G	385	LEU
1	H	315	LYS
1	H	364	TYR
1	I	315	LYS
1	I	364	TYR
1	I	385	LEU
1	J	1	MET
1	J	315	LYS
1	J	364	TYR
1	K	315	LYS
1	K	364	TYR
1	K	385	LEU
1	L	1	MET
1	L	9	LEU
1	L	315	LYS
1	L	364	TYR
1	L	391	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (159) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	15	ASN
1	A	49	HIS
1	A	113	GLN
1	A	144	ASN
1	A	166	HIS
1	A	235	ASN
1	A	252	ASN
1	A	266	HIS
1	A	286	HIS
1	A	293	ASN
1	A	294	ASN
1	A	335	ASN
1	B	15	ASN
1	B	20	GLN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	B	49	HIS
1	B	113	GLN
1	B	144	ASN
1	B	166	HIS
1	B	235	ASN
1	B	252	ASN
1	B	266	HIS
1	B	286	HIS
1	B	293	ASN
1	B	294	ASN
1	B	335	ASN
1	C	4	ASN
1	C	15	ASN
1	C	20	GLN
1	C	49	HIS
1	C	113	GLN
1	C	133	GLN
1	C	144	ASN
1	C	166	HIS
1	C	235	ASN
1	C	252	ASN
1	C	266	HIS
1	C	286	HIS
1	C	293	ASN
1	C	294	ASN
1	C	335	ASN
1	D	15	ASN
1	D	20	GLN
1	D	49	HIS
1	D	113	GLN
1	D	133	GLN
1	D	144	ASN
1	D	166	HIS
1	D	235	ASN
1	D	252	ASN
1	D	266	HIS
1	D	286	HIS
1	D	293	ASN
1	D	294	ASN
1	D	335	ASN
1	D	386	GLN
1	E	4	ASN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	E	15	ASN
1	E	49	HIS
1	E	113	GLN
1	E	144	ASN
1	E	166	HIS
1	E	235	ASN
1	E	252	ASN
1	E	266	HIS
1	E	286	HIS
1	E	293	ASN
1	E	294	ASN
1	E	335	ASN
1	F	15	ASN
1	F	20	GLN
1	F	49	HIS
1	F	113	GLN
1	F	144	ASN
1	F	166	HIS
1	F	235	ASN
1	F	252	ASN
1	F	266	HIS
1	F	286	HIS
1	F	293	ASN
1	F	294	ASN
1	F	335	ASN
1	G	15	ASN
1	G	49	HIS
1	G	101	GLN
1	G	113	GLN
1	G	144	ASN
1	G	166	HIS
1	G	235	ASN
1	G	252	ASN
1	G	266	HIS
1	G	286	HIS
1	G	293	ASN
1	G	294	ASN
1	G	335	ASN
1	G	386	GLN
1	H	15	ASN
1	H	20	GLN
1	H	49	HIS

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	H	113	GLN
1	H	144	ASN
1	H	166	HIS
1	H	235	ASN
1	H	252	ASN
1	H	266	HIS
1	H	286	HIS
1	H	293	ASN
1	H	294	ASN
1	H	335	ASN
1	I	15	ASN
1	I	113	GLN
1	I	144	ASN
1	I	166	HIS
1	I	235	ASN
1	I	252	ASN
1	I	266	HIS
1	I	286	HIS
1	I	293	ASN
1	I	294	ASN
1	I	335	ASN
1	J	15	ASN
1	J	20	GLN
1	J	49	HIS
1	J	113	GLN
1	J	144	ASN
1	J	166	HIS
1	J	235	ASN
1	J	252	ASN
1	J	266	HIS
1	J	286	HIS
1	J	293	ASN
1	J	294	ASN
1	J	335	ASN
1	K	15	ASN
1	K	20	GLN
1	K	101	GLN
1	K	113	GLN
1	K	144	ASN
1	K	166	HIS
1	K	235	ASN
1	K	252	ASN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	K	266	HIS
1	K	286	HIS
1	K	293	ASN
1	K	294	ASN
1	K	335	ASN
1	L	15	ASN
1	L	20	GLN
1	L	49	HIS
1	L	113	GLN
1	L	144	ASN
1	L	166	HIS
1	L	202	GLN
1	L	235	ASN
1	L	252	ASN
1	L	266	HIS
1	L	286	HIS
1	L	293	ASN
1	L	294	ASN
1	L	335	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

Of 16 ligands modelled in this entry, 16 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	413/427 (96%)	0.38	35 (8%) 16 15	17, 32, 53, 62	0
1	B	413/427 (96%)	0.37	41 (9%) 13 11	16, 27, 51, 59	0
1	C	413/427 (96%)	0.49	46 (11%) 10 9	17, 32, 54, 61	0
1	D	413/427 (96%)	0.45	34 (8%) 17 16	18, 33, 54, 61	0
1	E	413/427 (96%)	0.54	41 (9%) 13 11	19, 34, 54, 64	0
1	F	413/427 (96%)	0.48	42 (10%) 12 11	18, 33, 54, 62	0
1	G	413/427 (96%)	0.44	39 (9%) 14 13	19, 32, 51, 58	0
1	H	413/427 (96%)	0.41	37 (8%) 15 14	20, 33, 53, 60	0
1	I	413/427 (96%)	0.36	27 (6%) 25 23	19, 33, 54, 63	0
1	J	413/427 (96%)	0.55	35 (8%) 16 15	22, 38, 55, 61	0
1	K	413/427 (96%)	0.54	41 (9%) 13 11	22, 35, 56, 63	0
1	L	413/427 (96%)	0.43	32 (7%) 19 18	19, 34, 54, 60	0
All	All	4956/5124 (96%)	0.45	450 (9%) 15 13	16, 33, 54, 64	0

All (450) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	191	LYS	9.0
1	E	1	MET	7.4
1	B	194	ASP	6.9
1	B	183	HIS	6.4
1	G	1	MET	6.4
1	B	192	VAL	6.1
1	I	1	MET	6.0
1	F	1	MET	5.7
1	B	189	GLY	5.7
1	B	186	ARG	5.6
1	B	195	GLU	5.6

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	B	182	LYS	5.6
1	C	198	GLU	5.4
1	K	159	LYS	5.4
1	A	1	MET	5.4
1	H	194	ASP	5.3
1	J	1	MET	5.3
1	B	196	TRP	5.0
1	F	156	LEU	5.0
1	K	188	TRP	5.0
1	K	413	GLY	5.0
1	G	195	GLU	4.9
1	G	150	ASN	4.9
1	H	150	ASN	4.9
1	G	154	SER	4.9
1	B	193	ASN	4.9
1	H	192	VAL	4.9
1	K	153	ILE	4.8
1	B	150	ASN	4.8
1	C	1	MET	4.8
1	H	1	MET	4.7
1	B	180	GLN	4.7
1	G	152	ARG	4.7
1	F	154	SER	4.5
1	L	194	ASP	4.5
1	E	180	GLN	4.5
1	K	1	MET	4.4
1	B	187	ASP	4.4
1	H	197	ASN	4.4
1	E	150	ASN	4.3
1	E	152	ARG	4.3
1	L	1	MET	4.3
1	E	194	ASP	4.3
1	I	3	ILE	4.3
1	C	195	GLU	4.3
1	G	153	ILE	4.3
1	H	153	ILE	4.3
1	I	191	LYS	4.2
1	L	159	LYS	4.2
1	B	197	ASN	4.2
1	F	152	ARG	4.1
1	F	150	ASN	4.1
1	F	37	ILE	4.1

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	G	192	VAL	4.0
1	D	154	SER	4.0
1	G	193	ASN	4.0
1	H	191	LYS	3.9
1	C	126	GLU	3.9
1	J	150	ASN	3.8
1	K	41	ASP	3.8
1	H	180	GLN	3.8
1	A	159	LYS	3.8
1	D	152	ARG	3.8
1	G	186	ARG	3.8
1	C	15	ASN	3.7
1	F	159	LYS	3.7
1	H	193	ASN	3.7
1	F	187	ASP	3.7
1	L	156	LEU	3.7
1	G	191	LYS	3.7
1	I	180	GLN	3.7
1	K	191	LYS	3.6
1	K	160	GLN	3.6
1	F	413	GLY	3.6
1	L	413	GLY	3.6
1	E	65	ALA	3.6
1	G	198	GLU	3.6
1	F	158	GLY	3.6
1	A	187	ASP	3.5
1	D	1	MET	3.5
1	C	125	GLU	3.5
1	H	186	ARG	3.5
1	C	367	HIS	3.5
1	B	190	TYR	3.5
1	K	68	ALA	3.5
1	K	154	SER	3.5
1	J	191	LYS	3.5
1	B	185	LEU	3.5
1	C	156	LEU	3.5
1	G	413	GLY	3.5
1	H	195	GLU	3.4
1	B	12	LYS	3.4
1	A	160	GLN	3.4
1	B	153	ILE	3.4
1	H	189	GLY	3.4

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	I	183	HIS	3.4
1	B	179	GLU	3.4
1	G	196	TRP	3.4
1	K	185	LEU	3.4
1	C	150	ASN	3.4
1	K	186	ARG	3.4
1	E	198	GLU	3.4
1	C	162	ASP	3.4
1	F	153	ILE	3.4
1	I	4	ASN	3.3
1	H	413	GLY	3.3
1	G	156	LEU	3.3
1	J	2	SER	3.3
1	B	199	GLY	3.3
1	F	160	GLN	3.3
1	L	153	ILE	3.3
1	K	214	ARG	3.3
1	C	199	GLY	3.2
1	F	157	GLU	3.2
1	E	156	LEU	3.2
1	G	185	LEU	3.2
1	L	191	LYS	3.2
1	B	41	ASP	3.2
1	D	162	ASP	3.2
1	A	157	GLU	3.2
1	D	150	ASN	3.2
1	K	147	PHE	3.2
1	E	2	SER	3.2
1	I	195	GLU	3.2
1	K	150	ASN	3.2
1	K	180	GLN	3.2
1	I	413	GLY	3.2
1	D	157	GLU	3.1
1	I	150	ASN	3.1
1	F	264	ARG	3.1
1	I	186	ARG	3.1
1	H	196	TRP	3.1
1	D	192	VAL	3.1
1	E	153	ILE	3.1
1	C	196	TRP	3.1
1	D	413	GLY	3.1
1	I	41	ASP	3.1

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	K	192	VAL	3.1
1	I	2	SER	3.1
1	K	190	TYR	3.0
1	C	194	ASP	3.0
1	L	2	SER	3.0
1	A	34	PHE	3.0
1	D	191	LYS	3.0
1	L	150	ASN	3.0
1	C	191	LYS	3.0
1	E	196	TRP	3.0
1	G	194	ASP	3.0
1	D	149	ASP	3.0
1	J	162	ASP	3.0
1	E	186	ARG	2.9
1	K	189	GLY	2.9
1	E	191	LYS	2.9
1	G	149	ASP	2.9
1	I	367	HIS	2.9
1	E	154	SER	2.9
1	K	65	ALA	2.9
1	C	121	LYS	2.9
1	D	105	LEU	2.9
1	K	187	ASP	2.9
1	C	180	GLN	2.9
1	G	180	GLN	2.9
1	C	157	GLU	2.9
1	A	211	TRP	2.9
1	B	188	TRP	2.9
1	J	188	TRP	2.9
1	G	159	LYS	2.9
1	G	158	GLY	2.9
1	G	162	ASP	2.9
1	F	133	GLN	2.9
1	B	72	ARG	2.9
1	J	198	GLU	2.9
1	L	195	GLU	2.9
1	E	159	LYS	2.9
1	G	197	ASN	2.9
1	A	41	ASP	2.8
1	C	158	GLY	2.9
1	E	113	GLN	2.8
1	F	123	THR	2.8

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	D	153	ILE	2.8
1	K	157	GLU	2.8
1	C	72	ARG	2.8
1	F	186	ARG	2.8
1	L	367	HIS	2.8
1	E	35	GLY	2.8
1	J	158	GLY	2.8
1	H	185	LEU	2.8
1	F	213	GLU	2.8
1	B	200	SER	2.8
1	K	207	PHE	2.8
1	D	61	VAL	2.8
1	B	159	LYS	2.8
1	H	182	LYS	2.8
1	H	200	SER	2.8
1	L	160	GLN	2.8
1	D	34	PHE	2.8
1	L	158	GLY	2.8
1	G	190	TYR	2.8
1	A	156	LEU	2.8
1	D	156	LEU	2.8
1	K	156	LEU	2.8
1	C	12	LYS	2.8
1	H	159	LYS	2.8
1	J	153	ILE	2.8
1	K	4	ASN	2.7
1	J	367	HIS	2.7
1	E	195	GLU	2.7
1	K	105	LEU	2.7
1	C	186	ARG	2.7
1	I	214	ARG	2.7
1	E	157	GLU	2.7
1	G	188	TRP	2.7
1	F	41	ASP	2.7
1	A	189	GLY	2.7
1	I	189	GLY	2.7
1	D	65	ALA	2.7
1	E	193	ASN	2.7
1	B	203	GLU	2.7
1	H	187	ASP	2.7
1	A	191	LYS	2.7
1	C	159	LYS	2.7

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	B	158	GLY	2.7
1	E	413	GLY	2.7
1	A	186	ARG	2.7
1	F	34	PHE	2.7
1	A	69	MET	2.7
1	E	183	HIS	2.7
1	H	154	SER	2.7
1	K	200	SER	2.7
1	G	41	ASP	2.7
1	L	186	ARG	2.7
1	A	195	GLU	2.6
1	G	34	PHE	2.6
1	C	33	ASN	2.6
1	C	193	ASN	2.6
1	E	197	ASN	2.6
1	J	4	ASN	2.6
1	L	264	ARG	2.6
1	C	36	GLU	2.6
1	L	198	GLU	2.6
1	B	1	MET	2.6
1	J	65	ALA	2.6
1	I	154	SER	2.6
1	A	72	ARG	2.6
1	J	3	ILE	2.6
1	H	183	HIS	2.6
1	C	122	LYS	2.6
1	D	159	LYS	2.6
1	A	162	ASP	2.6
1	D	41	ASP	2.6
1	I	72	ARG	2.6
1	B	61	VAL	2.6
1	J	190	TYR	2.6
1	F	183	HIS	2.6
1	A	264	ARG	2.6
1	C	120	ALA	2.6
1	C	123	THR	2.6
1	B	156	LEU	2.6
1	F	185	LEU	2.6
1	K	183	HIS	2.5
1	B	184	ARG	2.5
1	I	213	GLU	2.5
1	E	61	VAL	2.5

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	J	183	HIS	2.5
1	G	72	ARG	2.5
1	H	410	ARG	2.5
1	J	186	ARG	2.5
1	A	2	SER	2.5
1	A	120	ALA	2.5
1	E	163	SER	2.5
1	F	180	GLN	2.5
1	G	179	GLU	2.5
1	K	211	TRP	2.5
1	H	367	HIS	2.5
1	A	150	ASN	2.5
1	G	4	ASN	2.5
1	A	179	GLU	2.5
1	C	213	GLU	2.5
1	J	180	GLN	2.5
1	J	213	GLU	2.5
1	A	65	ALA	2.5
1	A	158	GLY	2.5
1	C	413	GLY	2.5
1	K	158	GLY	2.5
1	B	37	ILE	2.5
1	K	162	ASP	2.4
1	L	113	GLN	2.4
1	C	214	ARG	2.4
1	L	193	ASN	2.4
1	A	153	ILE	2.4
1	C	201	ILE	2.4
1	F	204	VAL	2.4
1	I	153	ILE	2.4
1	L	188	TRP	2.4
1	C	118	TYR	2.4
1	B	152	ARG	2.4
1	B	264	ARG	2.4
1	C	410	ARG	2.4
1	H	264	ARG	2.4
1	K	410	ARG	2.4
1	B	105	LEU	2.4
1	I	185	LEU	2.4
1	C	187	ASP	2.4
1	E	41	ASP	2.4
1	I	194	ASP	2.4

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	L	41	ASP	2.4
1	D	37	ILE	2.4
1	F	72	ARG	2.4
1	K	72	ARG	2.4
1	K	152	ARG	2.4
1	E	367	HIS	2.4
1	K	195	GLU	2.4
1	D	180	GLN	2.4
1	E	158	GLY	2.4
1	E	201	ILE	2.4
1	G	410	ARG	2.4
1	H	214	ARG	2.4
1	B	181	THR	2.4
1	L	155	TRP	2.4
1	C	160	GLN	2.3
1	B	162	ASP	2.3
1	C	182	LYS	2.3
1	J	154	SER	2.3
1	G	183	HIS	2.3
1	K	194	ASP	2.3
1	D	186	ARG	2.3
1	H	152	ARG	2.3
1	J	214	ARG	2.3
1	L	34	PHE	2.3
1	D	200	SER	2.3
1	K	2	SER	2.3
1	J	157	GLU	2.3
1	L	179	GLU	2.3
1	A	113	GLN	2.3
1	H	160	GLN	2.3
1	J	202	GLN	2.3
1	L	180	GLN	2.3
1	I	193	ASN	2.3
1	E	187	ASP	2.3
1	E	37	ILE	2.3
1	G	37	ILE	2.3
1	C	114	VAL	2.3
1	F	412	VAL	2.3
1	H	61	VAL	2.3
1	E	214	ARG	2.3
1	F	148	ASP	2.3
1	J	187	ASP	2.3

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	G	35	GLY	2.3
1	D	185	LEU	2.3
1	J	156	LEU	2.3
1	J	185	LEU	2.3
1	D	188	TRP	2.3
1	B	202	GLN	2.2
1	L	154	SER	2.2
1	E	72	ARG	2.2
1	L	33	ASN	2.2
1	G	199	GLY	2.2
1	I	69	MET	2.2
1	J	189	GLY	2.2
1	C	134	LEU	2.2
1	D	190	TYR	2.2
1	G	157	GLU	2.2
1	F	2	SER	2.2
1	F	70	SER	2.2
1	I	152	ARG	2.2
1	F	33	ASN	2.2
1	I	192	VAL	2.2
1	E	149	ASP	2.2
1	E	162	ASP	2.2
1	A	413	GLY	2.2
1	A	68	ALA	2.2
1	D	198	GLU	2.2
1	F	65	ALA	2.2
1	L	213	GLU	2.2
1	G	105	LEU	2.2
1	L	182	LYS	2.2
1	F	149	ASP	2.2
1	G	148	ASP	2.2
1	B	213	GLU	2.2
1	F	125	GLU	2.2
1	H	157	GLU	2.2
1	K	198	GLU	2.2
1	E	160	GLN	2.2
1	F	202	GLN	2.2
1	L	202	GLN	2.2
1	E	264	ARG	2.2
1	J	72	ARG	2.2
1	F	190	TYR	2.2
1	F	188	TRP	2.2

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	A	194	ASP	2.2
1	E	36	GLU	2.1
1	E	66	PHE	2.1
1	J	37	ILE	2.1
1	L	37	ILE	2.1
1	D	202	GLN	2.1
1	H	68	ALA	2.1
1	F	184	ARG	2.1
1	G	2	SER	2.1
1	D	195	GLU	2.1
1	H	41	ASP	2.1
1	J	155	TRP	2.1
1	D	201	ILE	2.1
1	A	192	VAL	2.1
1	A	367	HIS	2.1
1	E	192	VAL	2.1
1	F	367	HIS	2.1
1	C	6	ARG	2.1
1	D	410	ARG	2.1
1	F	120	ALA	2.1
1	A	198	GLU	2.1
1	F	197	ASN	2.1
1	G	202	GLN	2.1
1	A	410	ARG	2.1
1	B	413	GLY	2.1
1	D	170	ARG	2.1
1	H	72	ARG	2.1
1	I	264	ARG	2.1
1	J	201	ILE	2.1
1	J	147	PHE	2.1
1	A	70	SER	2.1
1	A	154	SER	2.1
1	H	2	SER	2.1
1	J	60	ASP	2.1
1	H	181	THR	2.1
1	H	190	TYR	2.1
1	J	206	ARG	2.1
1	K	104	GLY	2.1
1	L	35	GLY	2.1
1	F	201	ILE	2.1
1	B	66	PHE	2.1
1	I	120	ALA	2.1

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	L	124	SER	2.1
1	H	156	LEU	2.0
1	A	180	GLN	2.0
1	J	41	ASP	2.0
1	D	214	ARG	2.0
1	E	178	TYR	2.0
1	J	159	LYS	2.0
1	D	63	ILE	2.0
1	C	34	PHE	2.0
1	C	179	GLU	2.0
1	C	192	VAL	2.0
1	F	192	VAL	2.0
1	D	124	SER	2.0
1	C	65	ALA	2.0
1	H	120	ALA	2.0
1	K	155	TRP	2.0
1	C	202	GLN	2.0
1	K	113	GLN	2.0
1	C	189	GLY	2.0

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

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

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q < 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	ZN	F	986	1/1	0.93	0.12	64,64,64,64	0
2	ZN	J	990	1/1	0.93	0.11	75,75,75,75	0
2	ZN	K	991	1/1	0.93	0.13	66,66,66,66	0
2	ZN	H	988	1/1	0.94	0.10	60,60,60,60	0

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	ZN	E	985	1/1	0.94	0.10	70,70,70,70	0
2	ZN	D	984	1/1	0.94	0.10	63,63,63,63	0
2	ZN	L	992	1/1	0.94	0.10	62,62,62,62	0
2	ZN	A	981	1/1	0.95	0.10	62,62,62,62	0
2	ZN	G	987	1/1	0.96	0.09	58,58,58,58	0
2	ZN	J	996	1/1	0.96	0.20	60,60,60,60	0
2	ZN	H	995	1/1	0.97	0.19	57,57,57,57	0
2	ZN	I	989	1/1	0.97	0.10	62,62,62,62	0
2	ZN	B	982	1/1	0.97	0.09	51,51,51,51	0
2	ZN	C	983	1/1	0.97	0.09	67,67,67,67	0
2	ZN	A	993	1/1	0.97	0.12	51,51,51,51	0
2	ZN	D	994	1/1	0.97	0.18	55,55,55,55	0

6.5 Other polymers [i](#)

There are no such residues in this entry.