



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 7, 2026 – 01:38 AM UTC

PDB ID : 4UV3 / pdb_00004uv3
Title : Structure of the curli transport lipoprotein CsgG in its membrane- bound conformation
Authors : Goyal, P.; Krasteva, P.V.; Gerven, N.V.; Gubellini, F.; Broeck, I.V.D.; Troupiotis-Tsailaki, A.; Jonckheere, W.; Pehau-Arnaudet, G.; Pinkner, J.S.; Chapman, M.R.; Hultgren, S.J.; Howorka, S.; Fronzes, R.; Remaut, H.
Deposited on : 2014-08-04
Resolution : 3.59 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

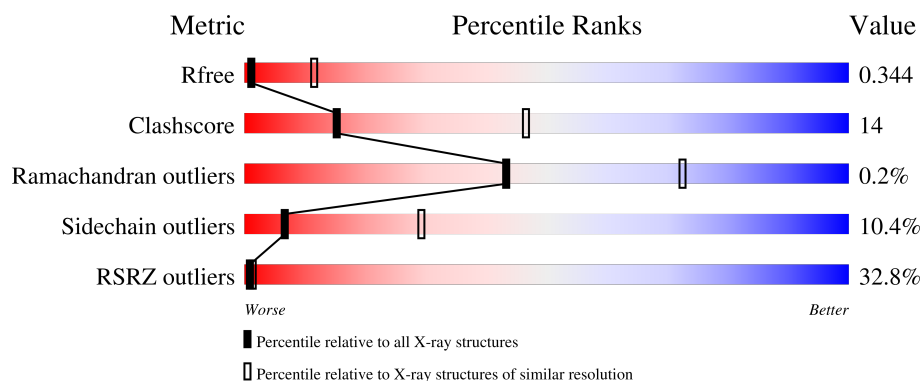
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.59 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	1747 (3.70-3.50)
Clashscore	190562	1827 (3.70-3.50)
Ramachandran outliers	187476	1773 (3.70-3.50)
Sidechain outliers	187428	1772 (3.70-3.50)
RSRZ outliers	180081	1745 (3.70-3.50)

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	262	24% 65% 27% • 5%
1	B	262	24% 63% 27% 5% 5%
1	C	262	26% 65% 26% • 6%
1	D	262	24% 64% 27% • 5%
1	E	262	35% 59% 31% • 6%

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
1	F	262	
1	G	262	
1	H	262	
1	I	262	
1	J	262	
1	K	262	
1	L	262	
1	M	262	
1	N	262	
1	O	262	
1	P	262	
1	Q	262	
1	R	262	

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 34255 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 CURLI PRODUCTION ASSEMBLY/TRANSPORT COMPONENT CSGG.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	248	Total	C	N	O	S	0	0	0
			1911	1204	333	367	7			
1	B	248	Total	C	N	O	S	0	0	0
			1911	1204	333	367	7			
1	C	247	Total	C	N	O	S	0	0	0
			1900	1198	329	366	7			
1	D	248	Total	C	N	O	S	0	0	0
			1911	1204	333	367	7			
1	E	247	Total	C	N	O	S	0	0	0
			1900	1198	329	366	7			
1	F	247	Total	C	N	O	S	0	0	0
			1900	1198	329	366	7			
1	G	247	Total	C	N	O	S	0	0	0
			1900	1198	329	366	7			
1	H	248	Total	C	N	O	S	0	0	0
			1911	1204	333	367	7			
1	I	247	Total	C	N	O	S	0	0	0
			1900	1198	329	366	7			
1	J	248	Total	C	N	O	S	0	0	0
			1911	1204	333	367	7			
1	K	247	Total	C	N	O	S	0	0	0
			1900	1198	329	366	7			
1	L	247	Total	C	N	O	S	0	0	0
			1900	1198	329	366	7			
1	M	247	Total	C	N	O	S	0	0	0
			1900	1198	329	366	7			
1	N	247	Total	C	N	O	S	0	0	0
			1900	1198	329	366	7			
1	O	247	Total	C	N	O	S	0	0	0
			1900	1198	329	366	7			
1	P	247	Total	C	N	O	S	0	0	0
			1900	1198	329	366	7			

Continued on next page...

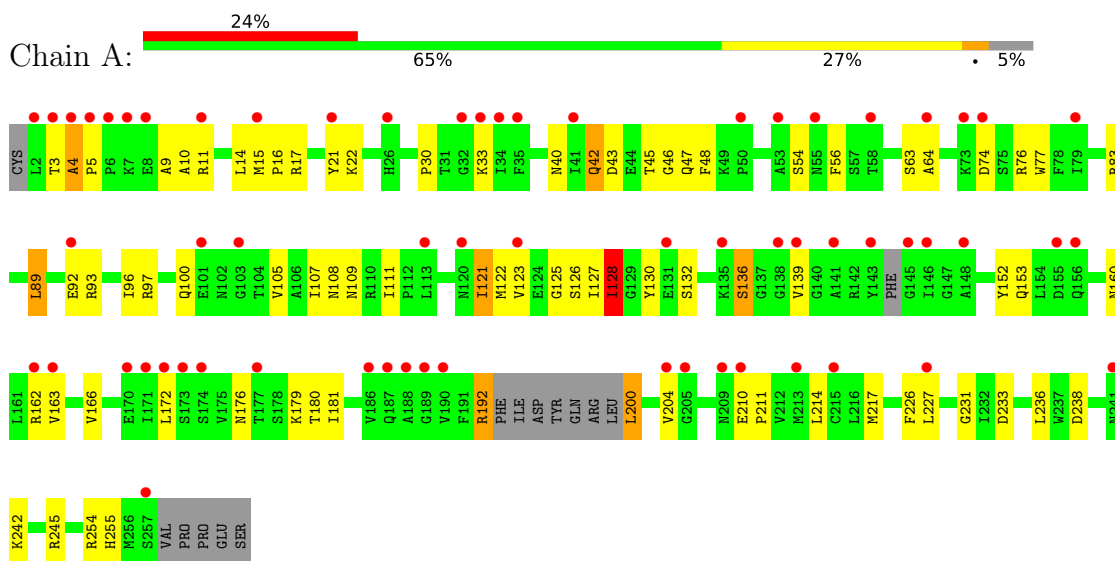
Continued from previous page...

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	Q	247	Total	C	N	O	S	0	0	0
			1900	1198	329	366	7			
1	R	247	Total	C	N	O	S	0	0	0
			1900	1198	329	366	7			

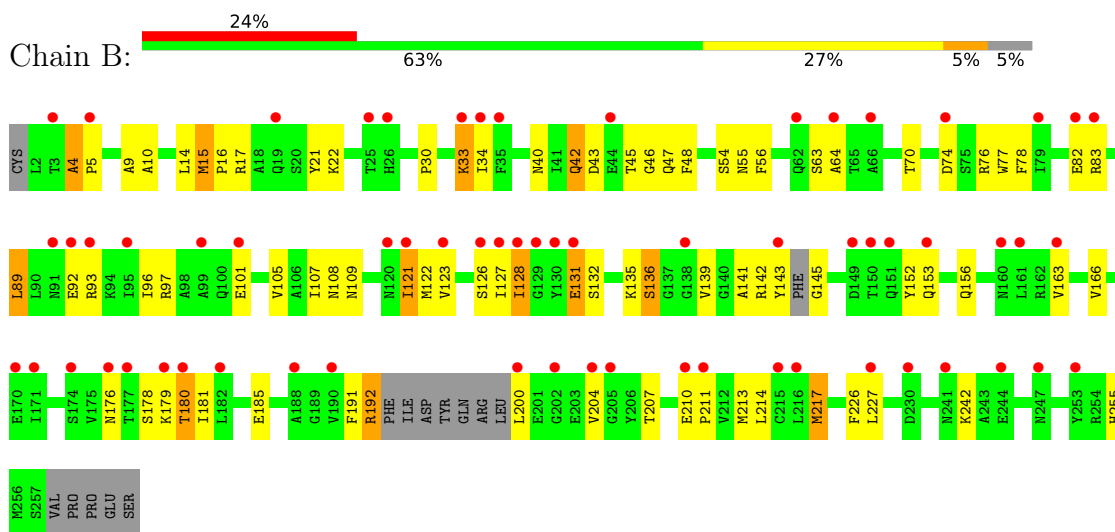
3 Residue-property plots

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 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: CURLI PRODUCTION ASSEMBLY/TRANSPORT COMPONENT CSGG

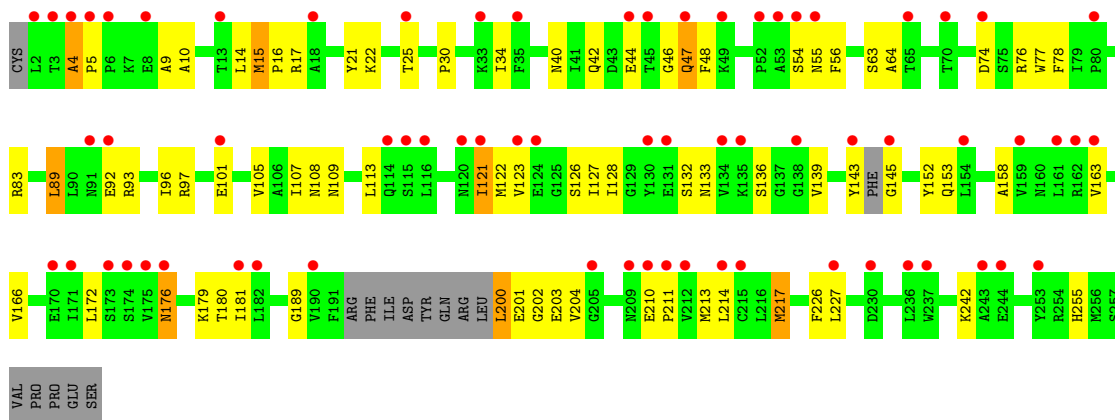


• Molecule 1: CURLI PRODUCTION ASSEMBLY/TRANSPORT COMPONENT CSGG

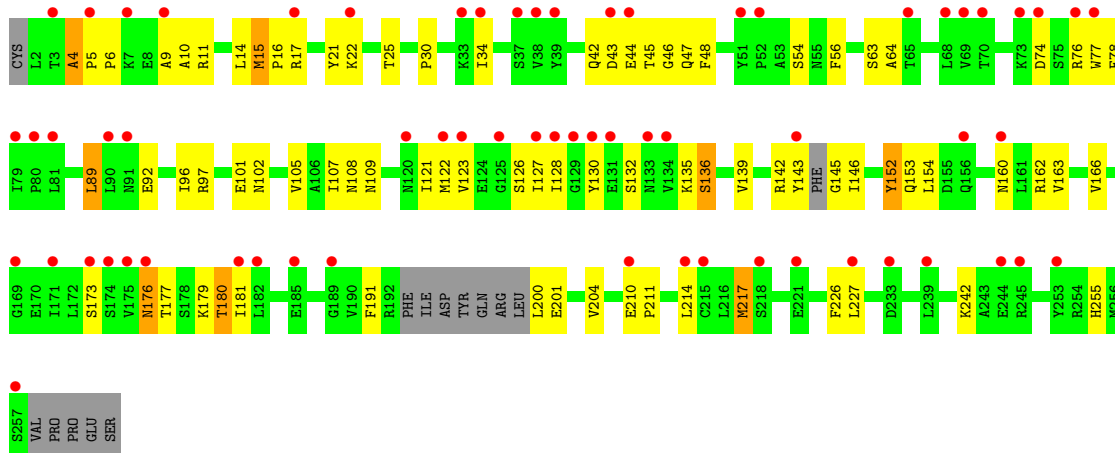


• Molecule 1: CURLI PRODUCTION ASSEMBLY/TRANSPORT COMPONENT CSGG

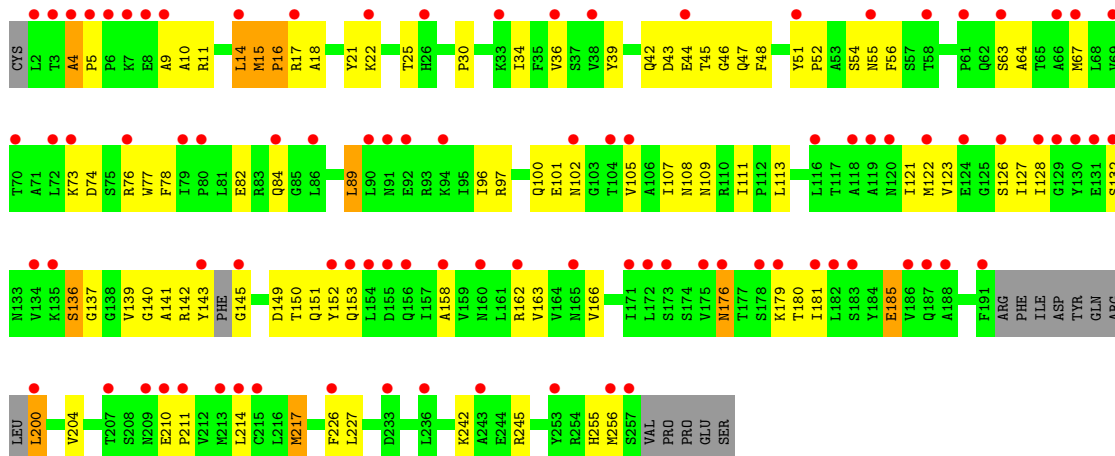




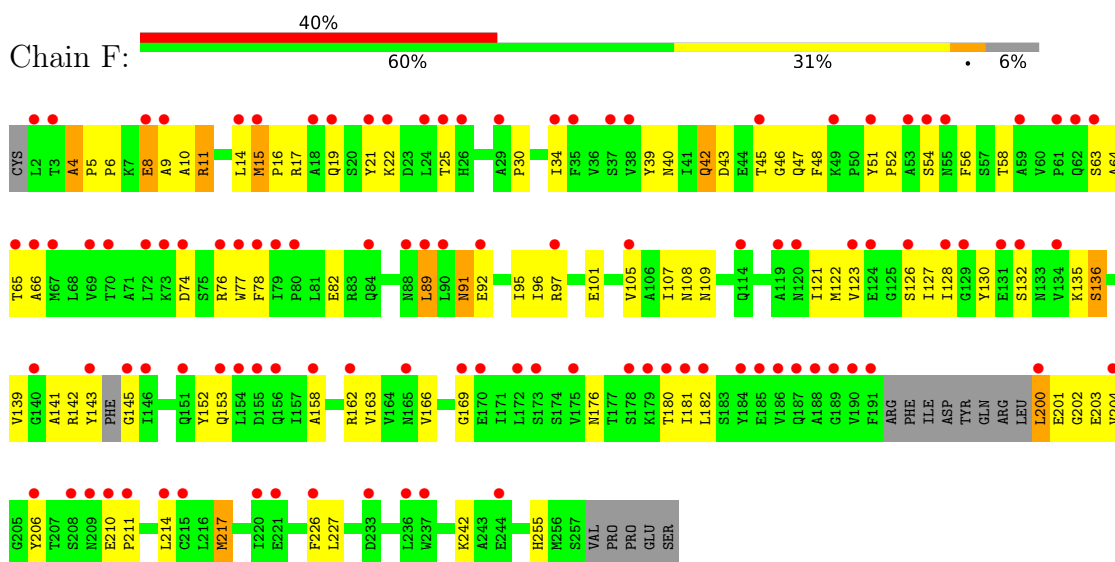
● Molecule 1: CURLI PRODUCTION ASSEMBLY/TRANSPORT COMPONENT CSGG



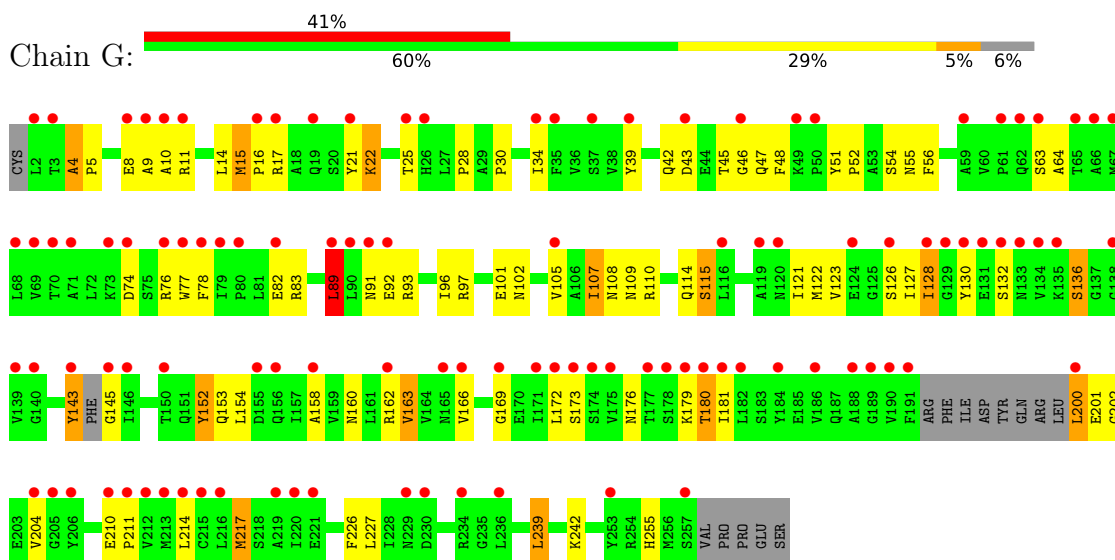
● Molecule 1: CURLI PRODUCTION ASSEMBLY/TRANSPORT COMPONENT CSGG



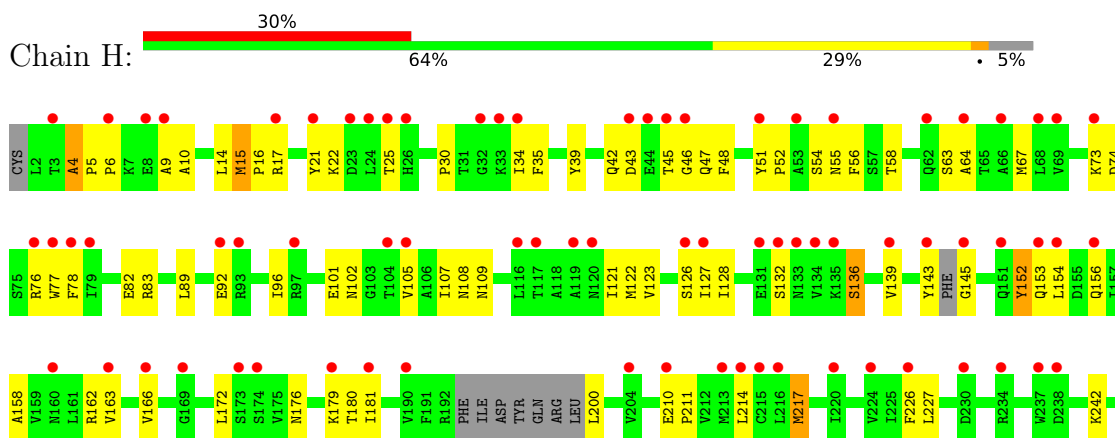
● Molecule 1: CURLI PRODUCTION ASSEMBLY/TRANSPORT COMPONENT CSGG

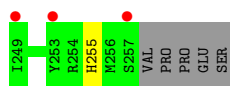


• Molecule 1: CURLI PRODUCTION ASSEMBLY/TRANSPORT COMPONENT CSGG

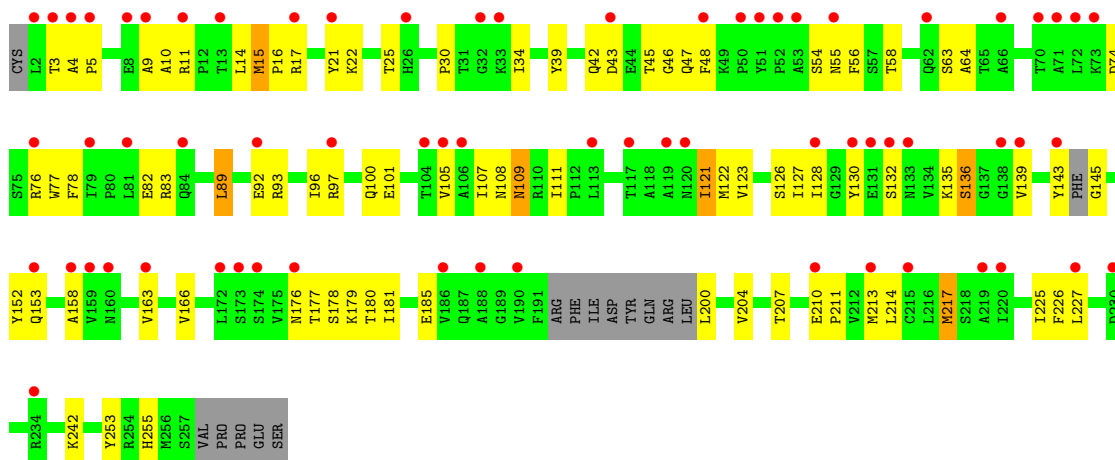


• Molecule 1: CURLI PRODUCTION ASSEMBLY/TRANSPORT COMPONENT CSGG

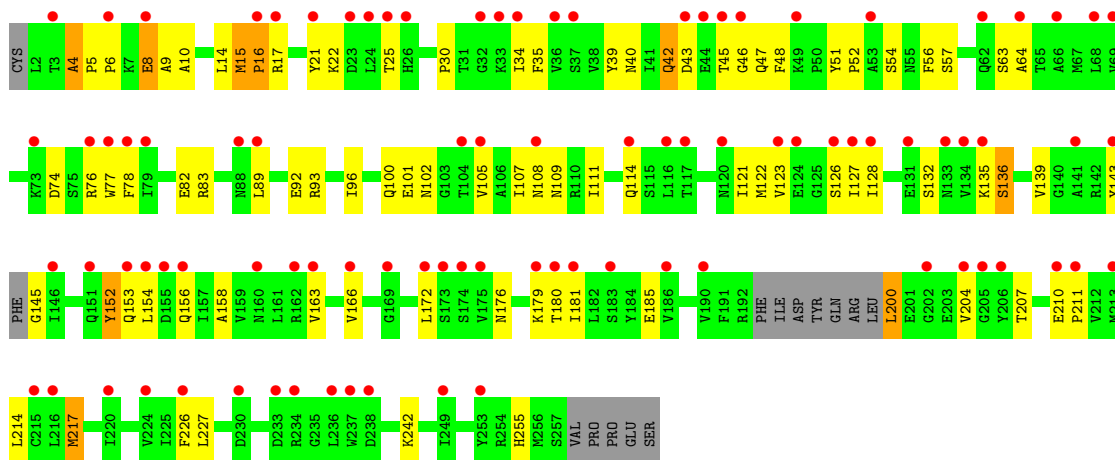




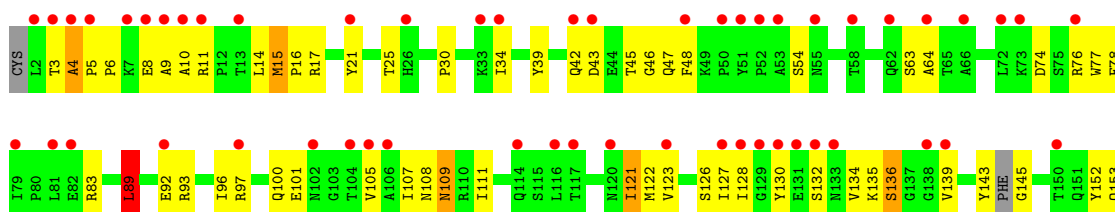
• Molecule 1: CURLI PRODUCTION ASSEMBLY/TRANSPORT COMPONENT CSGG

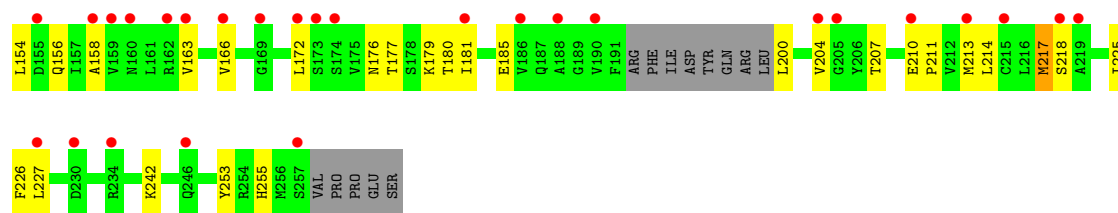


• Molecule 1: CURLI PRODUCTION ASSEMBLY/TRANSPORT COMPONENT CSGG

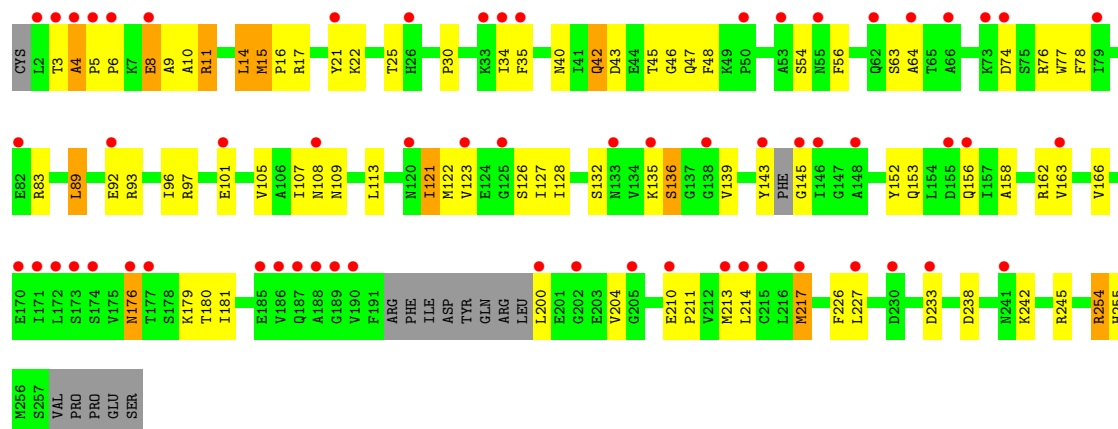


• Molecule 1: CURLI PRODUCTION ASSEMBLY/TRANSPORT COMPONENT CSGG

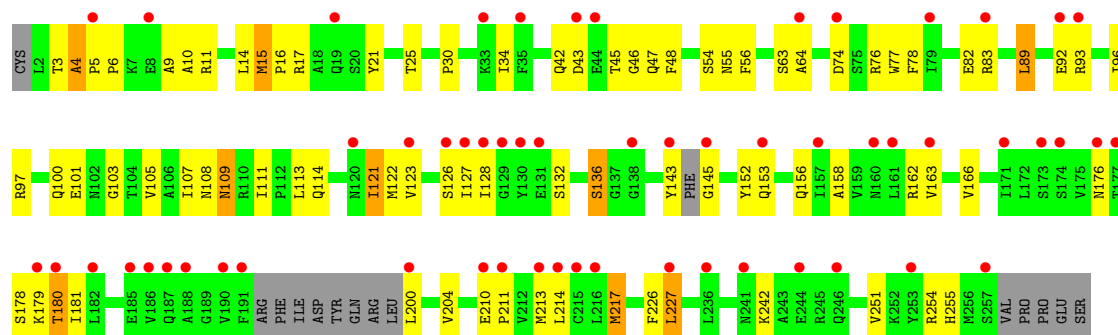




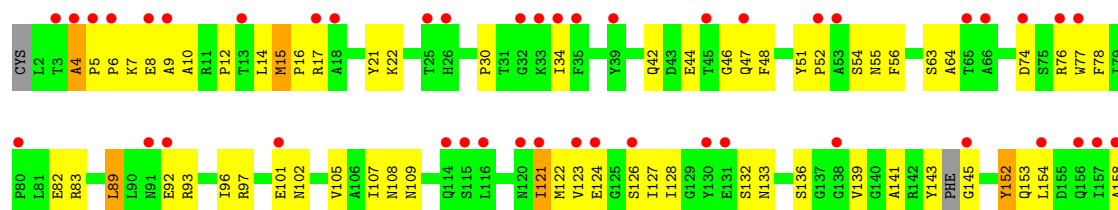
● Molecule 1: CURLI PRODUCTION ASSEMBLY/TRANSPORT COMPONENT CSGG

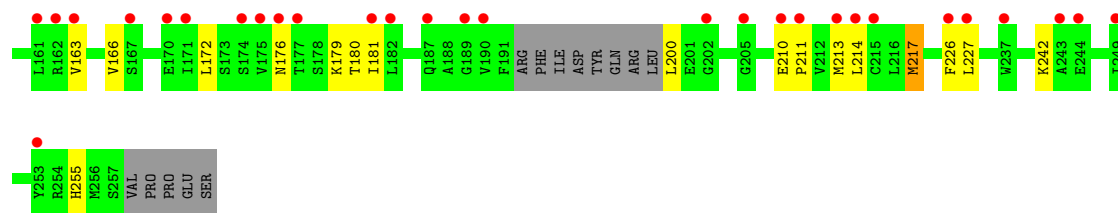


● Molecule 1: CURLI PRODUCTION ASSEMBLY/TRANSPORT COMPONENT CSGG

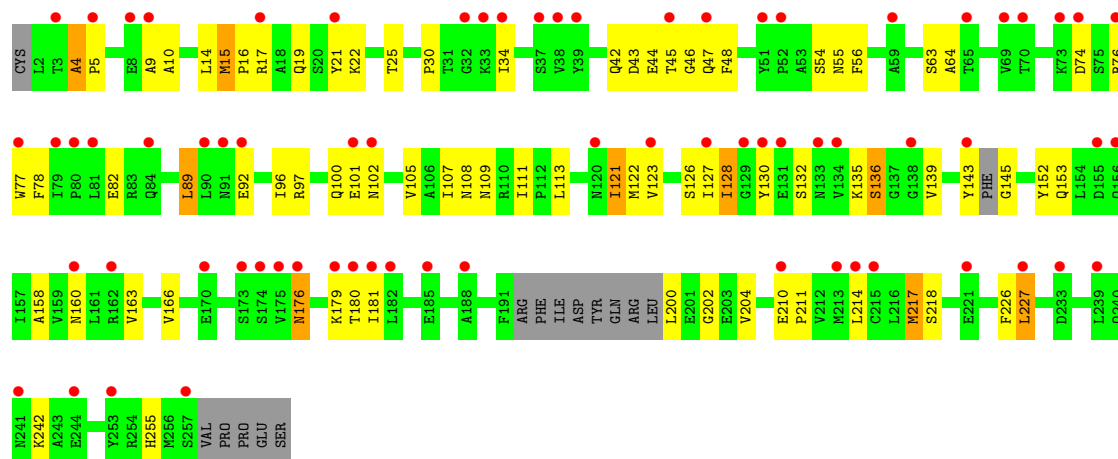


● Molecule 1: CURLI PRODUCTION ASSEMBLY/TRANSPORT COMPONENT CSGG

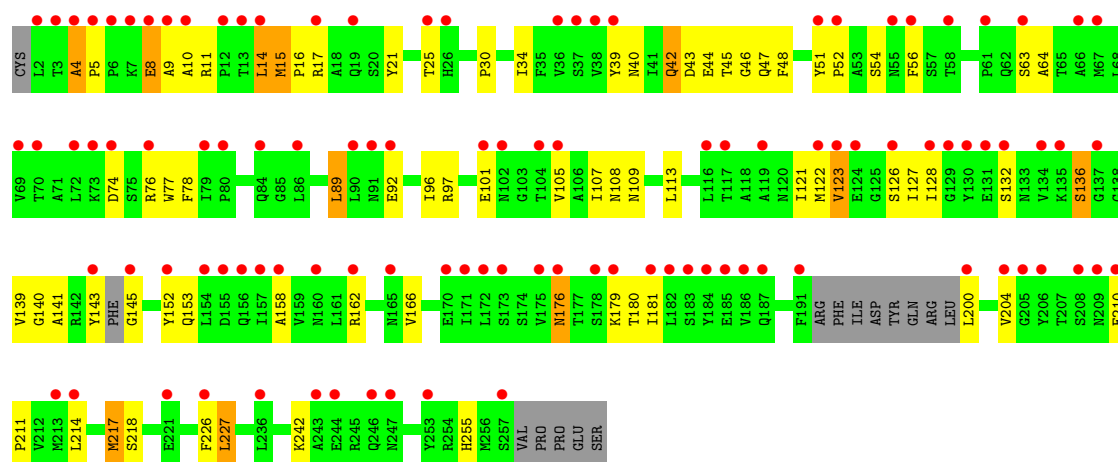
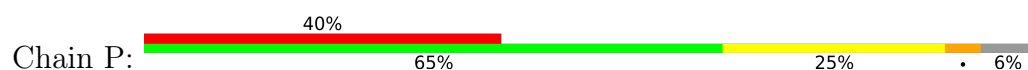




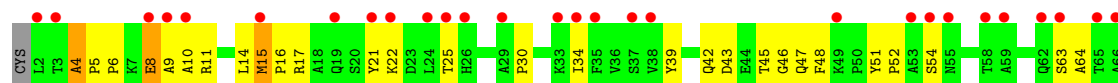
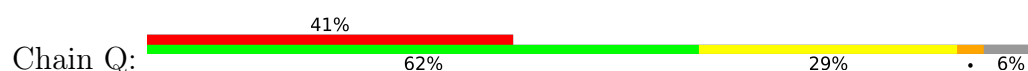
• Molecule 1: CURLI PRODUCTION ASSEMBLY/TRANSPORT COMPONENT CSGG

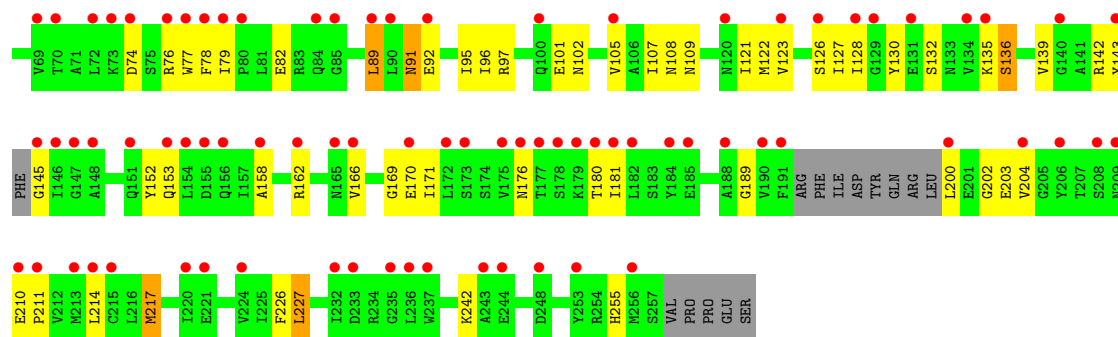


• Molecule 1: CURLI PRODUCTION ASSEMBLY/TRANSPORT COMPONENT CSGG

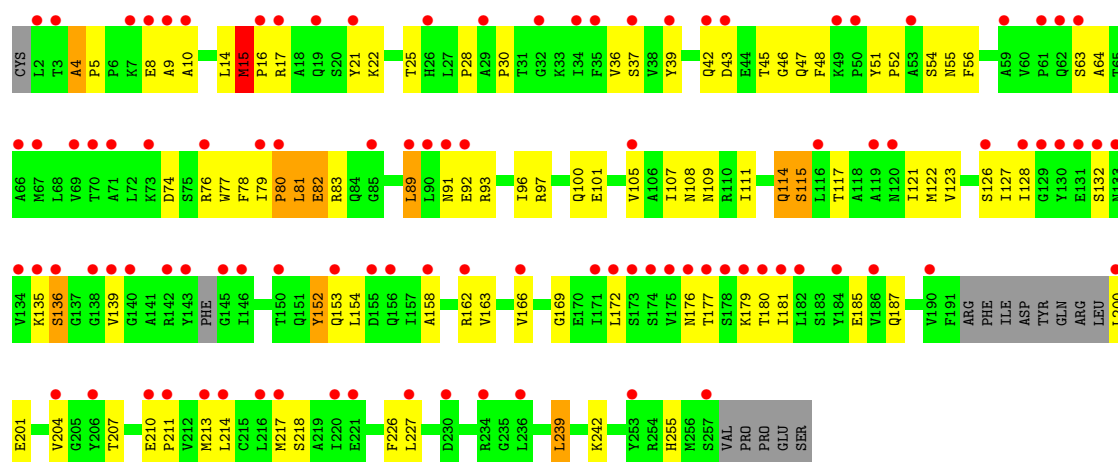
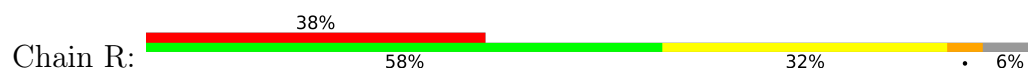


• Molecule 1: CURLI PRODUCTION ASSEMBLY/TRANSPORT COMPONENT CSGG





● Molecule 1: CURLI PRODUCTION ASSEMBLY/TRANSPORT COMPONENT CSGG



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	161.93Å 372.85Å 161.97Å 90.00° 92.90° 90.00°	Depositor
Resolution (Å)	30.00 – 3.59 30.00 – 3.59	Depositor EDS
% Data completeness (in resolution range)	91.5 (30.00-3.59) 91.6 (30.00-3.59)	Depositor EDS
R_{merge}	0.16	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.93 (at 3.57Å)	Xtriage
Refinement program	REFMAC 5.7.0029	Depositor
R, R_{free}	0.297 , 0.349 0.296 , 0.344	Depositor DCC
R_{free} test set	5110 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	101.0	Xtriage
Anisotropy	0.225	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.26 , 73.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.45$, $\langle L^2 \rangle = 0.28$	Xtriage
Estimated twinning fraction	0.029 for h,-k,-l	Xtriage
F_o, F_c correlation	0.83	EDS
Total number of atoms	34255	wwPDB-VP
Average B, all atoms (Å ²)	116.0	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 53.94 % 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 3.9236e-05. 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

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	0.84	1/1941 (0.1%)	0.98	3/2633 (0.1%)
1	B	0.77	1/1941 (0.1%)	0.97	7/2633 (0.3%)
1	C	0.68	1/1930 (0.1%)	0.91	2/2619 (0.1%)
1	D	0.70	0/1941	0.93	2/2633 (0.1%)
1	E	0.79	0/1930	0.96	3/2619 (0.1%)
1	F	0.78	0/1930	0.96	3/2619 (0.1%)
1	G	0.78	1/1930 (0.1%)	0.99	10/2619 (0.4%)
1	H	0.73	0/1941	0.93	2/2633 (0.1%)
1	I	0.72	0/1930	0.92	2/2619 (0.1%)
1	J	0.72	0/1941	0.93	2/2633 (0.1%)
1	K	0.73	0/1930	0.92	3/2619 (0.1%)
1	L	0.84	1/1930 (0.1%)	0.99	2/2619 (0.1%)
1	M	0.75	0/1930	0.95	2/2619 (0.1%)
1	N	0.68	0/1930	0.92	2/2619 (0.1%)
1	O	0.68	0/1930	0.94	3/2619 (0.1%)
1	P	0.77	0/1930	0.94	3/2619 (0.1%)
1	Q	0.78	0/1930	0.95	4/2619 (0.2%)
1	R	0.88	5/1930 (0.3%)	1.06	12/2619 (0.5%)
All	All	0.76	10/34795 (0.0%)	0.95	67/47212 (0.1%)

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	E	0	1
1	L	0	1
1	P	0	1
1	R	0	1
All	All	0	4

All (10) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	R	115	SER	C-O	-8.66	1.13	1.24
1	G	115	SER	C-O	-7.81	1.14	1.24
1	R	82	GLU	N-CA	6.76	1.54	1.46
1	R	80	PRO	CA-C	-6.38	1.43	1.52
1	R	79	ILE	CA-C	-6.38	1.46	1.53
1	B	33	LYS	CA-C	6.27	1.60	1.52
1	L	245	ARG	CA-CB	5.30	1.61	1.53
1	A	245	ARG	CA-CB	5.07	1.61	1.53
1	R	15	MET	CG-SD	-5.07	1.68	1.80
1	C	47	GLN	N-CA	-5.01	1.39	1.46

All (67) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	R	81	LEU	CA-C-N	9.81	136.02	122.19
1	R	81	LEU	C-N-CA	9.81	136.02	122.19
1	R	79	ILE	N-CA-C	-9.16	99.97	108.95
1	O	128	ILE	CB-CA-C	-9.02	100.24	111.88
1	D	4	ALA	CA-C-N	-8.31	111.82	120.38
1	D	4	ALA	C-N-CA	-8.31	111.82	120.38
1	O	4	ALA	CA-C-N	-8.24	111.90	120.38
1	O	4	ALA	C-N-CA	-8.24	111.90	120.38
1	F	4	ALA	CA-C-N	-8.13	112.00	120.38
1	F	4	ALA	C-N-CA	-8.13	112.00	120.38
1	L	4	ALA	CA-C-N	-8.00	112.14	120.38
1	L	4	ALA	C-N-CA	-8.00	112.14	120.38
1	A	4	ALA	CA-C-N	-7.96	112.18	120.38
1	A	4	ALA	C-N-CA	-7.96	112.18	120.38
1	G	128	ILE	CB-CA-C	-7.95	101.63	111.88
1	R	4	ALA	CA-C-N	-7.91	112.23	120.38
1	R	4	ALA	C-N-CA	-7.91	112.23	120.38
1	G	4	ALA	CA-C-N	-7.83	112.31	120.38
1	G	4	ALA	C-N-CA	-7.83	112.31	120.38
1	J	4	ALA	CA-C-N	-7.77	112.38	120.38
1	J	4	ALA	C-N-CA	-7.77	112.38	120.38
1	H	4	ALA	CA-C-N	-7.63	112.52	120.38
1	H	4	ALA	C-N-CA	-7.63	112.52	120.38
1	B	15	MET	N-CA-C	7.57	120.46	109.71
1	Q	4	ALA	CA-C-N	-7.51	112.64	120.38
1	Q	4	ALA	C-N-CA	-7.51	112.64	120.38
1	P	4	ALA	CA-C-N	-7.06	113.11	120.38
1	P	4	ALA	C-N-CA	-7.06	113.11	120.38
1	E	4	ALA	CA-C-N	-6.99	113.19	120.38

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	E	4	ALA	C-N-CA	-6.99	113.19	120.38
1	C	4	ALA	CA-C-N	-6.89	113.28	120.38
1	C	4	ALA	C-N-CA	-6.89	113.28	120.38
1	N	4	ALA	CA-C-N	-6.77	113.41	120.38
1	N	4	ALA	C-N-CA	-6.77	113.41	120.38
1	B	4	ALA	CA-C-N	-6.73	113.44	120.38
1	B	4	ALA	C-N-CA	-6.73	113.44	120.38
1	A	128	ILE	N-CA-C	6.66	123.20	109.34
1	M	4	ALA	CA-C-N	-6.56	113.62	120.38
1	M	4	ALA	C-N-CA	-6.56	113.62	120.38
1	K	4	ALA	CA-C-N	-6.01	114.19	120.38
1	K	4	ALA	C-N-CA	-6.01	114.19	120.38
1	B	15	MET	CB-CA-C	-5.82	100.82	109.60
1	B	128	ILE	N-CA-C	5.70	121.20	109.34
1	R	163	VAL	CB-CA-C	-5.68	104.09	110.96
1	G	89	LEU	N-CA-C	-5.62	105.24	111.36
1	F	169	GLY	N-CA-C	-5.60	107.64	114.92
1	G	163	VAL	CB-CA-C	-5.56	104.23	110.96
1	R	80	PRO	CB-CA-C	-5.54	102.42	111.56
1	K	89	LEU	N-CA-C	-5.46	105.33	111.28
1	G	22	LYS	CG-CD-CE	5.44	123.81	111.30
1	G	115	SER	CA-C-N	5.38	128.49	120.95
1	G	115	SER	C-N-CA	5.38	128.49	120.95
1	R	81	LEU	O-C-N	5.34	129.49	122.93
1	I	4	ALA	CA-C-N	-5.32	114.90	120.38
1	I	4	ALA	C-N-CA	-5.32	114.90	120.38
1	G	143	TYR	N-CA-C	-5.30	106.70	114.39
1	E	11	ARG	CB-CA-C	5.28	116.76	108.63
1	B	70	THR	N-CA-C	5.23	116.67	111.07
1	R	82	GLU	N-CA-C	5.23	118.14	109.46
1	R	82	GLU	CA-C-N	5.23	131.53	121.54
1	R	82	GLU	C-N-CA	5.23	131.53	121.54
1	R	169	GLY	N-CA-C	-5.23	108.42	115.21
1	P	123	VAL	N-CA-C	5.15	115.32	108.11
1	B	33	LYS	CB-CA-C	5.14	118.44	109.65
1	Q	79	ILE	CA-C-N	-5.11	113.35	120.25
1	Q	79	ILE	C-N-CA	-5.11	113.35	120.25
1	G	169	GLY	N-CA-C	-5.01	108.41	114.92

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	E	14	LEU	Peptide
1	L	14	LEU	Peptide
1	P	14	LEU	Peptide
1	R	78	PHE	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	1911	0	1930	73	0
1	B	1911	0	1930	65	0
1	C	1900	0	1917	64	0
1	D	1911	0	1930	69	0
1	E	1900	0	1917	84	0
1	F	1900	0	1917	90	0
1	G	1900	0	1917	88	0
1	H	1911	0	1930	88	0
1	I	1900	0	1917	70	0
1	J	1911	0	1930	92	0
1	K	1900	0	1917	73	0
1	L	1900	0	1917	87	0
1	M	1900	0	1917	74	0
1	N	1900	0	1917	71	0
1	O	1900	0	1917	69	0
1	P	1900	0	1917	67	0
1	Q	1900	0	1917	69	0
1	R	1900	0	1917	81	0
All	All	34255	0	34571	937	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 14.

All (937) 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:F:107:ILE:HD13	1:N:107:ILE:HD13	1.33	1.09
1:E:107:ILE:HD13	1:O:107:ILE:HD13	1.38	1.05

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:84:GLN:O	1:E:84:GLN:HG3	1.57	0.99
1:D:107:ILE:HD13	1:P:107:ILE:HD13	1.44	0.99
1:F:182:LEU:HD22	1:G:9:ALA:HB1	1.43	0.99
1:C:107:ILE:HD13	1:Q:107:ILE:HD13	1.46	0.96
1:J:54:SER:HB3	1:R:48:PHE:HB2	1.49	0.94
1:A:107:ILE:HD13	1:J:107:ILE:HD13	1.49	0.94
1:N:226:PHE:CZ	1:O:14:LEU:HD22	2.05	0.92
1:F:182:LEU:HD22	1:G:9:ALA:CB	1.98	0.92
1:J:200:LEU:HD23	1:J:200:LEU:O	1.69	0.92
1:F:162:ARG:NH2	1:G:82:GLU:OE1	2.03	0.92
1:C:226:PHE:CZ	1:D:14:LEU:HD22	2.06	0.90
1:L:233:ASP:OD2	1:L:254:ARG:NH2	2.03	0.90
1:H:107:ILE:HD13	1:L:107:ILE:HD13	1.54	0.90
1:G:48:PHE:HB2	1:H:54:SER:HB3	1.54	0.89
1:J:48:PHE:HB2	1:K:54:SER:HB3	1.55	0.89
1:G:128:ILE:HD11	1:G:160:ASN:HB2	1.55	0.89
1:D:226:PHE:CZ	1:E:14:LEU:HD22	2.08	0.88
1:O:128:ILE:HD11	1:O:160:ASN:HB2	1.58	0.86
1:A:14:LEU:HD22	1:I:226:PHE:CZ	2.11	0.86
1:R:36:VAL:HG12	1:R:80:PRO:HA	1.58	0.86
1:K:3:THR:HA	1:R:154:LEU:HD22	1.58	0.85
1:N:16:PRO:HG3	1:O:5:PRO:HG3	1.58	0.84
1:M:55:ASN:ND2	1:N:56:PHE:CE2	2.46	0.83
1:H:16:PRO:HG3	1:I:5:PRO:HG3	1.61	0.82
1:B:107:ILE:HD13	1:R:107:ILE:HD13	1.61	0.82
1:K:226:PHE:CZ	1:L:14:LEU:HD22	2.15	0.82
1:H:48:PHE:HB2	1:I:54:SER:HB3	1.59	0.81
1:J:154:LEU:HD22	1:L:3:THR:HB	1.63	0.80
1:O:226:PHE:CZ	1:P:14:LEU:HD22	2.17	0.80
1:Q:189:GLY:HA3	1:Q:203:GLU:OE2	1.82	0.80
1:A:92:GLU:OE2	1:I:83:ARG:NE	2.14	0.79
1:Q:171:ILE:HG13	1:R:82:GLU:HB2	1.65	0.78
1:J:14:LEU:HD22	1:R:226:PHE:CZ	2.18	0.78
1:B:145:GLY:N	1:B:191:PHE:O	2.18	0.77
1:E:48:PHE:HB2	1:F:54:SER:HB3	1.65	0.77
1:Q:226:PHE:CZ	1:R:14:LEU:HD22	2.20	0.76
1:B:15:MET:HE1	1:B:217:MET:HG3	1.67	0.76
1:A:3:THR:O	1:H:180:THR:HG21	1.86	0.76
1:I:107:ILE:HD13	1:K:107:ILE:HD13	1.67	0.76
1:J:152:TYR:CE2	1:L:3:THR:HG22	2.21	0.75
1:N:48:PHE:HB2	1:O:54:SER:HB3	1.69	0.75

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:16:PRO:HG3	1:D:5:PRO:HG3	1.67	0.75
1:G:226:PHE:CZ	1:H:14:LEU:HD22	2.21	0.74
1:J:48:PHE:HB2	1:K:54:SER:CB	2.17	0.74
1:Q:15:MET:HE1	1:Q:217:MET:HG3	1.69	0.74
1:J:54:SER:CB	1:R:48:PHE:HB2	2.17	0.74
1:A:226:PHE:CZ	1:B:14:LEU:HD22	2.22	0.74
1:F:226:PHE:CZ	1:G:14:LEU:HD22	2.23	0.74
1:F:139:VAL:HG22	1:G:204:VAL:HG22	1.70	0.73
1:M:226:PHE:CZ	1:N:14:LEU:HD22	2.23	0.73
1:D:48:PHE:HB2	1:E:54:SER:HB3	1.70	0.73
1:D:128:ILE:HG23	1:E:63:SER:OG	1.89	0.72
1:P:136:SER:HB2	1:P:153:GLN:HG3	1.71	0.72
1:P:48:PHE:HB2	1:Q:54:SER:HB3	1.70	0.72
1:F:15:MET:HE1	1:F:217:MET:HG3	1.70	0.72
1:K:83:ARG:NE	1:L:92:GLU:OE2	2.18	0.72
1:M:210:GLU:OE1	1:N:9:ALA:HB3	1.90	0.72
1:D:136:SER:HB2	1:D:153:GLN:HG3	1.72	0.72
1:B:226:PHE:CZ	1:C:14:LEU:HD22	2.25	0.71
1:E:136:SER:HB2	1:E:153:GLN:HG3	1.71	0.71
1:R:28:PRO:HB2	1:R:239:LEU:HD21	1.73	0.71
1:O:136:SER:HB2	1:O:153:GLN:HG3	1.73	0.70
1:G:136:SER:HB2	1:G:153:GLN:HG2	1.73	0.70
1:M:15:MET:HE1	1:M:217:MET:HG3	1.72	0.70
1:R:136:SER:HB2	1:R:153:GLN:HG2	1.74	0.70
1:L:15:MET:HE1	1:L:217:MET:HG3	1.74	0.70
1:L:226:PHE:CE2	1:M:14:LEU:HG	2.27	0.70
1:N:15:MET:HE1	1:N:217:MET:HG3	1.72	0.70
1:C:48:PHE:HB2	1:D:54:SER:HB3	1.72	0.70
1:F:136:SER:HB2	1:F:153:GLN:HG2	1.74	0.70
1:G:28:PRO:HB2	1:G:239:LEU:HD21	1.72	0.70
1:P:15:MET:HE1	1:P:217:MET:HG3	1.74	0.70
1:D:15:MET:HE1	1:D:217:MET:HG3	1.74	0.70
1:O:15:MET:HE1	1:O:217:MET:HG3	1.73	0.70
1:D:191:PHE:HD1	1:D:201:GLU:HG3	1.56	0.70
1:G:48:PHE:HB2	1:H:54:SER:CB	2.22	0.70
1:O:48:PHE:HB2	1:P:54:SER:HB3	1.74	0.70
1:C:133:ASN:OD1	1:C:153:GLN:CD	2.34	0.69
1:G:15:MET:HE1	1:G:217:MET:HG3	1.72	0.69
1:H:136:SER:HB2	1:H:153:GLN:HG2	1.74	0.69
1:M:136:SER:HB2	1:M:153:GLN:HG2	1.72	0.69
1:J:136:SER:HB2	1:J:153:GLN:HG2	1.74	0.69

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:136:SER:HB2	1:I:153:GLN:HG2	1.75	0.69
1:C:15:MET:HE1	1:C:217:MET:HG3	1.72	0.69
1:E:15:MET:HE1	1:E:217:MET:HG3	1.74	0.69
1:A:136:SER:HB2	1:A:153:GLN:HG2	1.74	0.69
1:Q:48:PHE:HB2	1:R:54:SER:HB3	1.73	0.69
1:Q:136:SER:HB2	1:Q:153:GLN:HG2	1.74	0.69
1:B:16:PRO:HG3	1:C:5:PRO:HG3	1.72	0.68
1:B:136:SER:HB2	1:B:153:GLN:HG2	1.74	0.68
1:A:15:MET:HE3	1:A:214:LEU:HD12	1.75	0.68
1:I:15:MET:HE1	1:I:217:MET:HG3	1.75	0.68
1:N:226:PHE:CZ	1:O:14:LEU:CD2	2.76	0.68
1:G:107:ILE:HG21	1:M:107:ILE:HD13	1.74	0.68
1:L:233:ASP:CG	1:L:254:ARG:HH22	2.01	0.68
1:J:15:MET:HE1	1:J:217:MET:HG3	1.75	0.68
1:O:16:PRO:HG3	1:P:5:PRO:HG3	1.76	0.68
1:N:55:ASN:ND2	1:O:56:PHE:CE2	2.62	0.67
1:E:139:VAL:HG22	1:F:204:VAL:HG22	1.77	0.67
1:L:136:SER:HB2	1:L:153:GLN:HG2	1.74	0.67
1:K:136:SER:HB2	1:K:153:GLN:HG2	1.75	0.67
1:F:48:PHE:HB2	1:G:54:SER:HB3	1.77	0.67
1:L:176:ASN:O	1:M:15:MET:HB2	1.95	0.67
1:K:15:MET:HE1	1:K:217:MET:HG3	1.76	0.67
1:A:176:ASN:O	1:B:15:MET:HB2	1.95	0.66
1:R:81:LEU:HD11	1:R:117:THR:HG22	1.77	0.66
1:H:226:PHE:CZ	1:I:14:LEU:HD22	2.30	0.66
1:B:55:ASN:ND2	1:C:56:PHE:CE2	2.64	0.66
1:A:3:THR:HA	1:H:154:LEU:CD2	2.25	0.66
1:H:15:MET:HE1	1:H:217:MET:HG3	1.76	0.66
1:O:218:SER:HB2	1:P:8:GLU:OE2	1.95	0.66
1:E:141:ALA:HA	1:F:202:GLY:HA2	1.77	0.66
1:D:128:ILE:HD12	1:D:160:ASN:HB2	1.78	0.65
1:P:139:VAL:HG22	1:Q:204:VAL:HG22	1.77	0.65
1:F:182:LEU:CD2	1:G:9:ALA:HB1	2.23	0.65
1:O:139:VAL:HG22	1:P:204:VAL:HG22	1.77	0.65
1:K:3:THR:HA	1:R:154:LEU:CD2	2.26	0.65
1:C:226:PHE:CZ	1:D:14:LEU:CD2	2.80	0.65
1:D:143:TYR:O	1:D:145:GLY:N	2.30	0.64
1:C:40:ASN:OD1	1:C:42:GLN:NE2	2.30	0.64
1:J:152:TYR:HE2	1:L:3:THR:HG22	1.60	0.64
1:B:15:MET:HE3	1:B:214:LEU:HD12	1.80	0.64
1:H:48:PHE:HB2	1:I:54:SER:CB	2.26	0.64

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:226:PHE:CZ	1:K:14:LEU:HD22	2.33	0.63
1:R:185:GLU:OE2	1:R:187:GLN:NE2	2.31	0.63
1:H:39:TYR:HE1	1:I:92:GLU:HG2	1.63	0.63
1:E:84:GLN:O	1:E:84:GLN:CG	2.38	0.63
1:N:176:ASN:O	1:O:15:MET:HB2	1.98	0.63
1:Q:139:VAL:HG22	1:R:204:VAL:HG22	1.79	0.63
1:M:251:VAL:HG12	1:M:254:ARG:NH2	2.14	0.63
1:D:16:PRO:HG3	1:E:5:PRO:HG3	1.81	0.62
1:L:143:TYR:O	1:L:145:GLY:N	2.31	0.62
1:K:166:VAL:HA	1:L:89:LEU:HD21	1.82	0.62
1:J:56:PHE:CE2	1:R:55:ASN:ND2	2.68	0.62
1:K:176:ASN:O	1:L:15:MET:N	2.31	0.62
1:O:166:VAL:HG11	1:P:96:ILE:CD1	2.29	0.62
1:K:48:PHE:HB2	1:L:54:SER:HB3	1.82	0.62
1:A:166:VAL:HG11	1:B:96:ILE:HD11	1.82	0.61
1:R:15:MET:SD	1:R:213:MET:HE3	2.41	0.61
1:F:162:ARG:HH21	1:G:82:GLU:CD	2.08	0.61
1:J:39:TYR:HE1	1:K:92:GLU:HG2	1.66	0.61
1:N:143:TYR:O	1:N:145:GLY:N	2.34	0.60
1:N:139:VAL:HG22	1:O:204:VAL:HG22	1.83	0.60
1:B:176:ASN:O	1:C:15:MET:HB2	2.01	0.60
1:Q:143:TYR:O	1:Q:145:GLY:N	2.35	0.60
1:F:19:GLN:HB2	1:G:8:GLU:OE2	2.02	0.60
1:A:233:ASP:OD1	1:A:254:ARG:NH2	2.33	0.60
1:G:16:PRO:HG3	1:H:5:PRO:HG3	1.84	0.60
1:A:204:VAL:HG22	1:I:139:VAL:HG22	1.83	0.60
1:D:166:VAL:HG11	1:E:96:ILE:CD1	2.31	0.60
1:A:166:VAL:HG11	1:B:96:ILE:CD1	2.32	0.60
1:A:46:GLY:O	1:A:47:GLN:NE2	2.34	0.60
1:F:143:TYR:O	1:F:145:GLY:N	2.35	0.60
1:O:166:VAL:HG11	1:P:96:ILE:HD11	1.82	0.60
1:K:139:VAL:HG22	1:L:204:VAL:HG22	1.84	0.59
1:L:46:GLY:O	1:L:47:GLN:NE2	2.35	0.59
1:A:3:THR:CA	1:H:154:LEU:HD22	2.33	0.59
1:R:15:MET:CE	1:R:213:MET:HE3	2.32	0.59
1:D:4:ALA:HB1	1:D:5:PRO:CD	2.33	0.59
1:H:154:LEU:HD13	1:H:180:THR:CG2	2.33	0.59
1:M:176:ASN:O	1:N:15:MET:HB2	2.02	0.59
1:O:143:TYR:O	1:O:145:GLY:N	2.35	0.59
1:D:180:THR:HG21	1:F:4:ALA:HA	1.85	0.59
1:J:154:LEU:HD22	1:L:3:THR:O	2.02	0.59

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:154:LEU:HD13	1:J:180:THR:CG2	2.32	0.59
1:F:176:ASN:O	1:G:15:MET:HB2	2.02	0.58
1:L:128:ILE:HG22	1:M:63:SER:HB2	1.85	0.58
1:L:166:VAL:HG11	1:M:96:ILE:CD1	2.33	0.58
1:D:226:PHE:CZ	1:E:14:LEU:CD2	2.83	0.58
1:P:16:PRO:HG3	1:Q:5:PRO:HG3	1.85	0.58
1:O:56:PHE:CE1	1:P:56:PHE:CE2	2.92	0.58
1:O:4:ALA:HB1	1:O:5:PRO:CD	2.34	0.58
1:C:176:ASN:O	1:D:15:MET:HB2	2.03	0.58
1:A:163:VAL:HG23	1:A:227:LEU:HD22	1.86	0.58
1:O:176:ASN:O	1:P:15:MET:HB2	2.03	0.58
1:G:4:ALA:HB1	1:G:5:PRO:CD	2.34	0.58
1:A:15:MET:CE	1:A:214:LEU:HD12	2.34	0.57
1:A:15:MET:N	1:I:176:ASN:O	2.34	0.57
1:A:89:LEU:HD21	1:I:166:VAL:HA	1.84	0.57
1:A:4:ALA:HB1	1:A:5:PRO:CD	2.34	0.57
1:L:226:PHE:CZ	1:M:14:LEU:HG	2.40	0.57
1:M:166:VAL:HG11	1:N:96:ILE:CD1	2.34	0.57
1:A:14:LEU:CD2	1:I:226:PHE:CZ	2.86	0.57
1:B:166:VAL:HA	1:C:89:LEU:HD21	1.85	0.57
1:K:177:THR:HA	1:L:14:LEU:HA	1.87	0.57
1:L:4:ALA:HB1	1:L:5:PRO:CD	2.35	0.57
1:C:189:GLY:HA3	1:C:203:GLU:OE2	2.04	0.57
1:D:166:VAL:HG11	1:E:96:ILE:HD11	1.85	0.57
1:L:166:VAL:HG11	1:M:96:ILE:HD11	1.85	0.57
1:H:4:ALA:HB1	1:H:5:PRO:CD	2.35	0.57
1:G:162:ARG:HH21	1:H:82:GLU:CD	2.13	0.57
1:K:154:LEU:HD13	1:K:180:THR:CG2	2.35	0.57
1:L:163:VAL:HG23	1:L:227:LEU:HD22	1.87	0.57
1:N:166:VAL:HA	1:O:89:LEU:HD21	1.86	0.57
1:M:4:ALA:HB1	1:M:5:PRO:CD	2.34	0.57
1:R:4:ALA:HB1	1:R:5:PRO:CD	2.34	0.57
1:C:139:VAL:HG22	1:D:204:VAL:HG22	1.86	0.57
1:J:176:ASN:O	1:K:15:MET:HB2	2.05	0.57
1:R:37:SER:HA	1:R:81:LEU:O	2.05	0.57
1:B:163:VAL:HG23	1:B:227:LEU:HD22	1.87	0.57
1:D:46:GLY:O	1:D:47:GLN:NE2	2.38	0.57
1:J:154:LEU:HD22	1:L:3:THR:CB	2.34	0.57
1:E:139:VAL:O	1:E:149:ASP:OD1	2.23	0.56
1:J:4:ALA:HB1	1:J:5:PRO:CD	2.35	0.56
1:A:128:ILE:HG22	1:B:63:SER:HB2	1.87	0.56

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:46:GLY:O	1:C:47:GLN:NE2	2.38	0.56
1:H:176:ASN:O	1:I:15:MET:HB2	2.05	0.56
1:P:46:GLY:O	1:P:47:GLN:NE2	2.38	0.56
1:K:64:ALA:HB2	1:K:127:ILE:HD11	1.88	0.56
1:Q:4:ALA:HB1	1:Q:5:PRO:CD	2.35	0.56
1:C:4:ALA:HB1	1:C:5:PRO:CD	2.35	0.56
1:D:176:ASN:O	1:E:15:MET:HB2	2.06	0.56
1:L:64:ALA:HB2	1:L:127:ILE:HD11	1.88	0.56
1:B:166:VAL:HG11	1:C:96:ILE:CD1	2.36	0.56
1:B:4:ALA:HB1	1:B:5:PRO:CD	2.36	0.56
1:G:83:ARG:NE	1:H:92:GLU:OE2	2.30	0.56
1:P:226:PHE:CZ	1:Q:14:LEU:HD22	2.41	0.56
1:B:46:GLY:O	1:B:47:GLN:NE2	2.38	0.56
1:C:143:TYR:O	1:C:145:GLY:N	2.39	0.56
1:K:4:ALA:HB1	1:K:5:PRO:CD	2.36	0.56
1:A:48:PHE:HB2	1:B:54:SER:HB3	1.87	0.56
1:K:30:PRO:HB3	1:K:77:TRP:CZ3	2.41	0.56
1:N:176:ASN:O	1:O:15:MET:N	2.38	0.56
1:I:64:ALA:HB2	1:I:127:ILE:HD11	1.88	0.55
1:M:166:VAL:HA	1:N:89:LEU:HD21	1.87	0.55
1:E:176:ASN:O	1:F:15:MET:HB2	2.06	0.55
1:F:135:LYS:HE3	1:H:6:PRO:HD3	1.86	0.55
1:G:107:ILE:CG2	1:M:107:ILE:HD13	2.36	0.55
1:H:166:VAL:HG11	1:I:96:ILE:CD1	2.36	0.55
1:F:4:ALA:HB1	1:F:5:PRO:CD	2.36	0.55
1:M:46:GLY:O	1:M:47:GLN:NE2	2.39	0.55
1:R:25:THR:O	1:R:76:ARG:NH2	2.37	0.55
1:F:176:ASN:O	1:G:15:MET:N	2.38	0.55
1:G:180:THR:HG21	1:I:3:THR:O	2.06	0.55
1:I:30:PRO:HB3	1:I:77:TRP:CZ3	2.42	0.55
1:M:143:TYR:O	1:M:145:GLY:N	2.38	0.55
1:B:64:ALA:HB2	1:B:127:ILE:HD11	1.89	0.55
1:C:166:VAL:HA	1:D:89:LEU:HD21	1.88	0.55
1:G:128:ILE:HG23	1:H:63:SER:OG	2.06	0.55
1:M:180:THR:HG23	1:N:10:ALA:HB3	1.89	0.55
1:O:46:GLY:O	1:O:47:GLN:NE2	2.40	0.55
1:I:143:TYR:O	1:I:145:GLY:N	2.39	0.55
1:N:4:ALA:HB1	1:N:5:PRO:CD	2.37	0.55
1:J:166:VAL:HG11	1:K:96:ILE:CD1	2.36	0.55
1:N:30:PRO:HB3	1:N:77:TRP:CZ3	2.42	0.55
1:E:4:ALA:HB1	1:E:5:PRO:CD	2.37	0.55

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:15:MET:HG2	1:I:16:PRO:HD2	1.89	0.55
1:K:143:TYR:O	1:K:145:GLY:N	2.39	0.55
1:N:128:ILE:HG22	1:O:63:SER:HB2	1.89	0.55
1:A:3:THR:HB	1:H:154:LEU:HD22	1.89	0.55
1:H:128:ILE:HG22	1:I:63:SER:HB2	1.89	0.55
1:J:54:SER:HB3	1:R:48:PHE:CB	2.31	0.55
1:M:15:MET:HG2	1:M:16:PRO:HD2	1.89	0.55
1:M:30:PRO:HB3	1:M:77:TRP:CZ3	2.41	0.55
1:D:64:ALA:HB2	1:D:127:ILE:HD11	1.89	0.55
1:P:4:ALA:HB1	1:P:5:PRO:CD	2.37	0.55
1:L:15:MET:HG2	1:L:16:PRO:HD2	1.90	0.54
1:L:48:PHE:HB2	1:M:54:SER:HB3	1.89	0.54
1:A:64:ALA:HB2	1:A:127:ILE:HD11	1.88	0.54
1:B:128:ILE:HG22	1:C:63:SER:HB2	1.90	0.54
1:F:142:ARG:O	1:G:201:GLU:N	2.31	0.54
1:K:180:THR:HG21	1:M:3:THR:O	2.07	0.54
1:Q:64:ALA:HB2	1:Q:127:ILE:HD11	1.89	0.54
1:D:48:PHE:HB2	1:E:54:SER:CB	2.37	0.54
1:F:16:PRO:HG3	1:G:5:PRO:HG3	1.89	0.54
1:G:166:VAL:HG11	1:H:96:ILE:CD1	2.37	0.54
1:O:64:ALA:HB2	1:O:127:ILE:HD11	1.88	0.54
1:E:101:GLU:HB2	1:O:97:ARG:HG2	1.89	0.54
1:J:64:ALA:HB2	1:J:127:ILE:HD11	1.89	0.54
1:B:30:PRO:HB3	1:B:77:TRP:CZ3	2.42	0.54
1:C:64:ALA:HB2	1:C:127:ILE:HD11	1.89	0.54
1:D:135:LYS:HE3	1:F:6:PRO:HD3	1.89	0.54
1:A:54:SER:HB3	1:I:48:PHE:HB2	1.89	0.54
1:E:143:TYR:O	1:E:145:GLY:N	2.41	0.54
1:J:5:PRO:HG3	1:R:16:PRO:HG3	1.90	0.54
1:N:64:ALA:HB2	1:N:127:ILE:HD11	1.90	0.54
1:F:15:MET:HG2	1:F:16:PRO:HD2	1.89	0.54
1:F:64:ALA:HB2	1:F:127:ILE:HD11	1.89	0.54
1:L:83:ARG:NE	1:M:92:GLU:OE2	2.36	0.54
1:P:143:TYR:O	1:P:145:GLY:N	2.41	0.54
1:G:39:TYR:HE1	1:H:92:GLU:HG2	1.73	0.54
1:H:30:PRO:HB3	1:H:77:TRP:CZ3	2.43	0.54
1:H:46:GLY:O	1:H:47:GLN:NE2	2.41	0.54
1:M:64:ALA:HB2	1:M:127:ILE:HD11	1.88	0.54
1:Q:30:PRO:HB3	1:Q:77:TRP:CZ3	2.42	0.54
1:D:128:ILE:HG12	1:E:63:SER:HB2	1.89	0.54
1:F:141:ALA:HA	1:G:202:GLY:HA2	1.90	0.54

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:143:TYR:HD1	1:F:200:LEU:CD1	2.21	0.54
1:F:163:VAL:HG23	1:F:227:LEU:HD22	1.90	0.54
1:H:64:ALA:HB2	1:H:127:ILE:HD11	1.89	0.54
1:I:163:VAL:HG23	1:I:227:LEU:HD22	1.89	0.54
1:N:46:GLY:O	1:N:47:GLN:NE2	2.41	0.54
1:J:96:ILE:CD1	1:R:166:VAL:HG11	2.38	0.53
1:Q:15:MET:HG2	1:Q:16:PRO:HD2	1.89	0.53
1:H:163:VAL:HG23	1:H:227:LEU:HD22	1.90	0.53
1:E:30:PRO:HB3	1:E:77:TRP:CZ3	2.43	0.53
1:J:163:VAL:HG23	1:J:227:LEU:HD22	1.90	0.53
1:F:166:VAL:HG11	1:G:96:ILE:CD1	2.38	0.53
1:E:149:ASP:OD1	1:E:150:THR:N	2.41	0.53
1:N:163:VAL:HG23	1:N:227:LEU:HD22	1.91	0.53
1:H:39:TYR:CE1	1:I:92:GLU:HG2	2.43	0.53
1:L:30:PRO:HB3	1:L:77:TRP:CZ3	2.44	0.53
1:O:128:ILE:O	1:O:158:ALA:HB3	2.08	0.53
1:J:43:ASP:C	1:J:45:THR:H	2.17	0.53
1:J:54:SER:CB	1:R:48:PHE:CB	2.86	0.53
1:P:176:ASN:O	1:Q:15:MET:HB2	2.07	0.53
1:C:128:ILE:HG22	1:D:63:SER:HB2	1.90	0.53
1:F:30:PRO:HB3	1:F:77:TRP:CZ3	2.43	0.53
1:J:82:GLU:CD	1:R:162:ARG:HH21	2.16	0.53
1:E:139:VAL:HG13	1:F:204:VAL:HG22	1.91	0.53
1:J:15:MET:N	1:R:176:ASN:O	2.38	0.53
1:R:36:VAL:CG1	1:R:80:PRO:HA	2.35	0.53
1:R:64:ALA:HB2	1:R:127:ILE:HD11	1.91	0.53
1:J:166:VAL:HA	1:K:89:LEU:HD21	1.91	0.53
1:K:226:PHE:CZ	1:L:14:LEU:CD2	2.90	0.53
1:H:154:LEU:HD13	1:H:180:THR:HG23	1.91	0.52
1:O:30:PRO:HB3	1:O:77:TRP:CZ3	2.44	0.52
1:E:64:ALA:HB2	1:E:127:ILE:HD11	1.91	0.52
1:E:163:VAL:HG23	1:E:227:LEU:HD22	1.91	0.52
1:J:92:GLU:OE2	1:R:83:ARG:NE	2.28	0.52
1:A:56:PHE:CE1	1:B:56:PHE:HE2	2.28	0.52
1:C:30:PRO:HB3	1:C:77:TRP:CZ3	2.44	0.52
1:F:46:GLY:O	1:F:47:GLN:NE2	2.42	0.52
1:G:93:ARG:HH22	1:G:115:SER:HA	1.75	0.52
1:J:39:TYR:CE1	1:K:92:GLU:HG2	2.44	0.52
1:J:154:LEU:HD13	1:J:180:THR:HG23	1.90	0.52
1:K:163:VAL:HG23	1:K:227:LEU:HD22	1.90	0.52
1:P:141:ALA:HA	1:Q:202:GLY:HA2	1.92	0.52

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:15:MET:HB2	1:I:176:ASN:O	2.10	0.52
1:J:25:THR:O	1:J:76:ARG:NH2	2.42	0.52
1:N:83:ARG:NE	1:O:92:GLU:OE2	2.34	0.52
1:D:163:VAL:HG23	1:D:227:LEU:HD22	1.92	0.52
1:J:30:PRO:HB3	1:J:77:TRP:CZ3	2.44	0.52
1:R:93:ARG:HH22	1:R:115:SER:HA	1.75	0.52
1:C:128:ILE:O	1:C:158:ALA:HB3	2.10	0.52
1:C:163:VAL:HG23	1:C:227:LEU:HD22	1.91	0.52
1:G:64:ALA:HB2	1:G:127:ILE:HD11	1.91	0.52
1:M:128:ILE:HG22	1:N:63:SER:HB2	1.90	0.52
1:P:30:PRO:HB3	1:P:77:TRP:CZ3	2.45	0.52
1:L:139:VAL:HG22	1:M:204:VAL:HG22	1.91	0.52
1:E:97:ARG:HG2	1:O:101:GLU:HB2	1.91	0.52
1:H:143:TYR:O	1:H:145:GLY:N	2.42	0.52
1:D:30:PRO:HB3	1:D:77:TRP:CZ3	2.45	0.52
1:G:25:THR:O	1:G:76:ARG:NH2	2.40	0.52
1:J:15:MET:HB2	1:R:176:ASN:O	2.10	0.52
1:L:25:THR:O	1:L:76:ARG:NH2	2.42	0.52
1:A:30:PRO:HB3	1:A:77:TRP:CZ3	2.44	0.52
1:E:18:ALA:HB3	1:F:8:GLU:HG3	1.91	0.52
1:E:25:THR:O	1:E:76:ARG:NH2	2.42	0.52
1:J:204:VAL:HG22	1:R:139:VAL:HG22	1.92	0.52
1:H:102:ASN:OD1	1:L:97:ARG:NH1	2.42	0.51
1:A:15:MET:HE3	1:A:214:LEU:CD1	2.39	0.51
1:B:181:ILE:HG23	1:B:210:GLU:HB3	1.93	0.51
1:G:163:VAL:HG23	1:G:227:LEU:HD22	1.92	0.51
1:H:43:ASP:C	1:H:45:THR:H	2.18	0.51
1:I:45:THR:OG1	1:I:130:TYR:N	2.43	0.51
1:J:46:GLY:O	1:J:47:GLN:NE2	2.43	0.51
1:P:166:VAL:HA	1:Q:89:LEU:HD21	1.92	0.51
1:Q:176:ASN:O	1:R:15:MET:N	2.41	0.51
1:G:56:PHE:CE1	1:H:56:PHE:CE2	2.98	0.51
1:N:76:ARG:O	1:N:76:ARG:HG3	2.10	0.51
1:D:25:THR:O	1:D:76:ARG:NH2	2.40	0.51
1:J:83:ARG:NE	1:K:92:GLU:OE2	2.25	0.51
1:L:226:PHE:CE1	1:M:14:LEU:HD11	2.45	0.51
1:M:25:THR:O	1:M:76:ARG:NH2	2.43	0.51
1:M:181:ILE:HG23	1:M:210:GLU:HB3	1.92	0.51
1:A:56:PHE:CE1	1:B:56:PHE:CE2	2.98	0.51
1:E:46:GLY:O	1:E:47:GLN:NE2	2.43	0.51
1:G:55:ASN:ND2	1:H:56:PHE:CE2	2.78	0.51

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:83:ARG:NE	1:I:92:GLU:OE2	2.25	0.51
1:H:128:ILE:O	1:H:158:ALA:HB3	2.11	0.51
1:A:93:ARG:NH1	1:A:97:ARG:HH22	2.09	0.51
1:E:142:ARG:N	1:F:201:GLU:O	2.30	0.51
1:P:25:THR:O	1:P:76:ARG:NH2	2.40	0.51
1:R:46:GLY:O	1:R:47:GLN:NE2	2.44	0.51
1:J:128:ILE:O	1:J:158:ALA:HB3	2.11	0.51
1:E:39:TYR:HE1	1:F:92:GLU:HG2	1.76	0.51
1:G:176:ASN:O	1:H:15:MET:HB2	2.10	0.51
1:K:15:MET:HG2	1:K:16:PRO:HD2	1.93	0.51
1:N:128:ILE:O	1:N:158:ALA:HB3	2.11	0.51
1:M:143:TYR:C	1:M:145:GLY:N	2.69	0.51
1:Q:171:ILE:CG1	1:R:82:GLU:HB2	2.38	0.51
1:A:3:THR:HA	1:H:154:LEU:HD22	1.90	0.50
1:D:142:ARG:O	1:E:200:LEU:HD12	2.11	0.50
1:K:25:THR:O	1:K:76:ARG:NH2	2.42	0.50
1:M:128:ILE:O	1:M:158:ALA:HB3	2.11	0.50
1:F:43:ASP:C	1:F:45:THR:H	2.19	0.50
1:J:35:PHE:HE2	1:K:109:ASN:OD1	1.92	0.50
1:J:154:LEU:CD2	1:L:3:THR:HA	2.41	0.50
1:P:64:ALA:HB2	1:P:127:ILE:HD11	1.92	0.50
1:A:63:SER:HB2	1:I:128:ILE:HG22	1.92	0.50
1:G:15:MET:HG2	1:G:16:PRO:HD2	1.92	0.50
1:G:46:GLY:O	1:G:47:GLN:NE2	2.44	0.50
1:Q:25:THR:O	1:Q:76:ARG:NH2	2.40	0.50
1:A:5:PRO:HG3	1:I:16:PRO:HG3	1.94	0.50
1:D:135:LYS:HE3	1:F:6:PRO:CD	2.41	0.50
1:E:166:VAL:HG11	1:F:96:ILE:CD1	2.42	0.50
1:G:128:ILE:O	1:G:158:ALA:HB3	2.11	0.50
1:H:166:VAL:HG11	1:I:96:ILE:HD11	1.93	0.50
1:K:154:LEU:HD13	1:K:180:THR:HG23	1.92	0.50
1:P:16:PRO:HG3	1:Q:5:PRO:CG	2.42	0.50
1:F:162:ARG:NH2	1:G:82:GLU:CD	2.65	0.50
1:L:135:LYS:HE3	1:N:6:PRO:HD3	1.93	0.50
1:M:166:VAL:HG11	1:N:96:ILE:HD11	1.94	0.50
1:Q:128:ILE:O	1:Q:158:ALA:HB3	2.11	0.50
1:B:166:VAL:HG11	1:C:96:ILE:HD11	1.94	0.50
1:J:139:VAL:HG22	1:K:204:VAL:HG22	1.94	0.50
1:N:226:PHE:CE1	1:O:14:LEU:HD22	2.47	0.50
1:O:128:ILE:HG23	1:P:63:SER:OG	2.11	0.50
1:A:17:ARG:NH1	1:A:74:ASP:OD2	2.45	0.50

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:162:ARG:HH21	1:B:82:GLU:CD	2.20	0.50
1:J:6:PRO:HD3	1:Q:135:LYS:HE3	1.92	0.50
1:O:48:PHE:HB2	1:P:54:SER:CB	2.41	0.50
1:R:128:ILE:O	1:R:158:ALA:HB3	2.12	0.50
1:G:30:PRO:HB3	1:G:77:TRP:CZ3	2.46	0.50
1:H:166:VAL:HA	1:I:89:LEU:HD21	1.93	0.50
1:J:128:ILE:HG22	1:K:63:SER:HB2	1.94	0.50
1:A:181:ILE:HG23	1:A:210:GLU:HB3	1.94	0.50
1:D:176:ASN:O	1:E:15:MET:N	2.44	0.50
1:G:17:ARG:NH1	1:G:74:ASP:OD2	2.44	0.50
1:G:128:ILE:CG2	1:H:67:MET:HE3	2.42	0.50
1:L:181:ILE:HG23	1:L:210:GLU:HB3	1.93	0.50
1:C:25:THR:O	1:C:76:ARG:NH2	2.43	0.49
1:E:15:MET:HG2	1:E:16:PRO:HD2	1.93	0.49
1:E:143:TYR:C	1:E:145:GLY:N	2.70	0.49
1:Q:166:VAL:HG11	1:R:96:ILE:CD1	2.42	0.49
1:G:181:ILE:HG23	1:G:210:GLU:HB3	1.94	0.49
1:J:14:LEU:CD2	1:R:226:PHE:CZ	2.94	0.49
1:J:166:VAL:HG11	1:K:96:ILE:HD11	1.93	0.49
1:C:17:ARG:NH1	1:C:74:ASP:OD2	2.45	0.49
1:E:181:ILE:HG23	1:E:210:GLU:HB3	1.95	0.49
1:F:128:ILE:O	1:F:158:ALA:HB3	2.12	0.49
1:C:181:ILE:HG23	1:C:210:GLU:HB3	1.94	0.49
1:I:128:ILE:O	1:I:158:ALA:HB3	2.12	0.49
1:N:9:ALA:O	1:N:10:ALA:HB3	2.13	0.49
1:N:143:TYR:C	1:N:145:GLY:N	2.70	0.49
1:O:16:PRO:HG3	1:P:5:PRO:CG	2.40	0.49
1:Q:43:ASP:C	1:Q:45:THR:H	2.21	0.49
1:Q:128:ILE:HG22	1:R:63:SER:HB2	1.94	0.49
1:G:166:VAL:HG11	1:H:96:ILE:HD11	1.93	0.49
1:P:128:ILE:HG22	1:Q:63:SER:HB2	1.94	0.49
1:D:143:TYR:C	1:D:145:GLY:N	2.71	0.49
1:G:162:ARG:NH2	1:H:82:GLU:OE2	2.44	0.49
1:L:211:PRO:HB2	1:L:214:LEU:HB2	1.94	0.49
1:B:4:ALA:O	1:I:135:LYS:HE3	2.13	0.49
1:E:128:ILE:HG22	1:F:63:SER:HB2	1.94	0.49
1:G:143:TYR:C	1:G:145:GLY:N	2.71	0.49
1:I:128:ILE:O	1:I:128:ILE:HG13	2.13	0.49
1:K:45:THR:OG1	1:K:130:TYR:N	2.46	0.49
1:L:143:TYR:C	1:L:145:GLY:N	2.70	0.49
1:C:15:MET:HG2	1:C:16:PRO:HD2	1.94	0.49

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:139:VAL:HG22	1:E:204:VAL:HG22	1.95	0.49
1:H:15:MET:HG2	1:H:16:PRO:HD2	1.95	0.49
1:I:25:THR:O	1:I:76:ARG:NH2	2.43	0.49
1:K:128:ILE:HG22	1:L:63:SER:HB2	1.94	0.49
1:L:17:ARG:NH1	1:L:74:ASP:OD2	2.45	0.49
1:Q:189:GLY:HA3	1:Q:203:GLU:CD	2.36	0.49
1:G:48:PHE:CB	1:H:54:SER:HB3	2.36	0.49
1:J:48:PHE:CB	1:K:54:SER:CB	2.90	0.49
1:P:143:TYR:C	1:P:145:GLY:N	2.71	0.49
1:Q:39:TYR:CE1	1:R:92:GLU:HG2	2.48	0.49
1:A:40:ASN:ND2	1:A:42:GLN:HG3	2.28	0.49
1:C:55:ASN:ND2	1:D:56:PHE:CE2	2.81	0.49
1:E:162:ARG:HH21	1:F:82:GLU:CD	2.21	0.49
1:K:43:ASP:C	1:K:45:THR:H	2.21	0.49
1:N:93:ARG:NH1	1:N:97:ARG:HH22	2.11	0.49
1:J:96:ILE:HD11	1:R:166:VAL:HG11	1.95	0.48
1:A:93:ARG:HH12	1:A:97:ARG:HH22	1.62	0.48
1:B:15:MET:HE2	1:B:17:ARG:HG3	1.94	0.48
1:K:128:ILE:HG13	1:K:128:ILE:O	2.12	0.48
1:P:15:MET:HG2	1:P:16:PRO:HD2	1.94	0.48
1:P:43:ASP:C	1:P:45:THR:H	2.21	0.48
1:Q:128:ILE:O	1:Q:128:ILE:HG13	2.13	0.48
1:R:181:ILE:HG23	1:R:210:GLU:HB3	1.93	0.48
1:G:39:TYR:CE1	1:H:92:GLU:HG2	2.48	0.48
1:I:181:ILE:HG23	1:I:210:GLU:HB3	1.95	0.48
1:K:128:ILE:O	1:K:158:ALA:HB3	2.13	0.48
1:M:128:ILE:O	1:M:128:ILE:HG13	2.13	0.48
1:O:25:THR:O	1:O:76:ARG:NH2	2.41	0.48
1:O:143:TYR:C	1:O:145:GLY:N	2.72	0.48
1:P:211:PRO:HB2	1:P:214:LEU:HB2	1.95	0.48
1:Q:143:TYR:C	1:Q:145:GLY:N	2.72	0.48
1:R:17:ARG:NH1	1:R:74:ASP:OD2	2.45	0.48
1:A:14:LEU:HA	1:I:177:THR:HA	1.94	0.48
1:B:192:ARG:HA	1:B:192:ARG:HD3	1.61	0.48
1:E:43:ASP:C	1:E:45:THR:H	2.20	0.48
1:H:9:ALA:O	1:H:10:ALA:HB3	2.13	0.48
1:H:181:ILE:HG23	1:H:210:GLU:HB3	1.95	0.48
1:L:128:ILE:O	1:L:158:ALA:HB3	2.13	0.48
1:D:97:ARG:HG2	1:P:101:GLU:HB2	1.96	0.48
1:E:17:ARG:NH1	1:E:74:ASP:OD2	2.46	0.48
1:G:9:ALA:O	1:G:10:ALA:HB3	2.14	0.48

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:10:ALA:HB2	1:I:3:THR:OG1	2.13	0.48
1:J:143:TYR:O	1:J:145:GLY:N	2.47	0.48
1:J:154:LEU:HD22	1:L:3:THR:CA	2.44	0.48
1:N:17:ARG:NH1	1:N:74:ASP:OD2	2.46	0.48
1:P:17:ARG:NH1	1:P:74:ASP:OD2	2.46	0.48
1:R:30:PRO:HB3	1:R:77:TRP:CZ3	2.49	0.48
1:E:36:VAL:CG1	1:E:78:PHE:CD1	2.97	0.48
1:F:9:ALA:O	1:F:10:ALA:HB3	2.14	0.48
1:I:17:ARG:NH1	1:I:74:ASP:OD2	2.47	0.48
1:N:15:MET:HG2	1:N:16:PRO:HD2	1.96	0.48
1:A:211:PRO:HB2	1:A:214:LEU:HB2	1.96	0.48
1:A:226:PHE:CZ	1:B:14:LEU:CD2	2.96	0.48
1:C:166:VAL:HG11	1:D:96:ILE:CD1	2.43	0.48
1:E:128:ILE:O	1:E:158:ALA:HB3	2.13	0.48
1:K:134:VAL:HG12	1:M:6:PRO:CD	2.44	0.48
1:M:156:GLN:HG2	1:N:213:MET:HE1	1.95	0.48
1:O:176:ASN:O	1:P:15:MET:N	2.44	0.48
1:P:128:ILE:O	1:P:158:ALA:HB3	2.14	0.48
1:Q:46:GLY:O	1:Q:47:GLN:NE2	2.46	0.48
1:J:154:LEU:CD2	1:L:3:THR:CA	2.91	0.48
1:K:9:ALA:O	1:K:10:ALA:HB3	2.14	0.48
1:M:83:ARG:NE	1:N:92:GLU:OE2	2.44	0.48
1:I:46:GLY:O	1:I:47:GLN:NE2	2.47	0.48
1:J:15:MET:HG2	1:J:16:PRO:HD2	1.95	0.48
1:Q:169:GLY:O	1:R:82:GLU:HB3	2.13	0.48
1:Q:181:ILE:HG23	1:Q:210:GLU:HB3	1.95	0.48
1:A:83:ARG:NE	1:B:92:GLU:OE2	2.38	0.48
1:B:48:PHE:HB2	1:C:54:SER:HB3	1.96	0.48
1:D:43:ASP:C	1:D:45:THR:H	2.22	0.48
1:E:39:TYR:CE1	1:F:92:GLU:HG2	2.48	0.48
1:F:181:ILE:HG23	1:F:210:GLU:HB3	1.94	0.48
1:M:17:ARG:NH1	1:M:74:ASP:OD2	2.47	0.48
1:O:19:GLN:HG2	1:P:11:ARG:HH21	1.78	0.48
1:P:181:ILE:HG23	1:P:210:GLU:HB3	1.96	0.48
1:B:180:THR:HG23	1:C:10:ALA:HB3	1.94	0.47
1:E:128:ILE:O	1:E:128:ILE:HG13	2.14	0.47
1:E:140:GLY:O	1:F:203:GLU:N	2.33	0.47
1:H:17:ARG:NH1	1:H:74:ASP:OD2	2.47	0.47
1:C:9:ALA:O	1:C:10:ALA:HB3	2.14	0.47
1:H:156:GLN:HG2	1:I:213:MET:HE1	1.95	0.47
1:L:93:ARG:NH1	1:L:97:ARG:HH22	2.11	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:181:ILE:HG23	1:D:210:GLU:HB3	1.95	0.47
1:H:25:THR:O	1:H:76:ARG:NH2	2.43	0.47
1:L:40:ASN:ND2	1:L:42:GLN:HG3	2.29	0.47
1:R:36:VAL:O	1:R:81:LEU:N	2.47	0.47
1:F:25:THR:O	1:F:76:ARG:NH2	2.41	0.47
1:F:143:TYR:C	1:F:145:GLY:N	2.72	0.47
1:J:200:LEU:HD23	1:J:200:LEU:C	2.35	0.47
1:L:226:PHE:CD2	1:M:14:LEU:HD21	2.49	0.47
1:E:48:PHE:HB2	1:F:54:SER:CB	2.40	0.47
1:E:55:ASN:ND2	1:F:56:PHE:CE2	2.82	0.47
1:F:65:THR:HG23	1:F:66:ALA:N	2.30	0.47
1:H:128:ILE:O	1:H:128:ILE:HG13	2.15	0.47
1:I:43:ASP:C	1:I:45:THR:H	2.23	0.47
1:N:128:ILE:O	1:N:128:ILE:HG13	2.15	0.47
1:P:39:TYR:HE1	1:Q:92:GLU:HG2	1.78	0.47
1:Q:226:PHE:CZ	1:R:14:LEU:CD2	2.95	0.47
1:R:43:ASP:C	1:R:45:THR:H	2.22	0.47
1:A:3:THR:HG22	1:H:152:TYR:HE2	1.80	0.47
1:B:17:ARG:NH1	1:B:74:ASP:OD2	2.47	0.47
1:B:176:ASN:O	1:C:15:MET:N	2.44	0.47
1:C:176:ASN:O	1:D:15:MET:N	2.47	0.47
1:C:211:PRO:HB2	1:C:214:LEU:HB2	1.97	0.47
1:E:9:ALA:O	1:E:10:ALA:HB3	2.15	0.47
1:F:17:ARG:NH1	1:F:74:ASP:OD2	2.48	0.47
1:H:176:ASN:O	1:I:15:MET:N	2.44	0.47
1:J:128:ILE:O	1:J:128:ILE:HG13	2.15	0.47
1:K:17:ARG:NH1	1:K:74:ASP:OD2	2.48	0.47
1:R:128:ILE:O	1:R:128:ILE:HG13	2.15	0.47
1:J:176:ASN:O	1:K:15:MET:N	2.42	0.47
1:M:9:ALA:O	1:M:10:ALA:HB3	2.15	0.47
1:M:227:LEU:HD12	1:M:227:LEU:HA	1.73	0.47
1:O:43:ASP:C	1:O:45:THR:H	2.22	0.47
1:A:9:ALA:O	1:A:10:ALA:HB3	2.15	0.47
1:E:151:GLN:HB2	1:E:185:GLU:HG3	1.96	0.47
1:K:46:GLY:O	1:K:47:GLN:NE2	2.48	0.47
1:Q:9:ALA:O	1:Q:10:ALA:HB3	2.14	0.47
1:Q:39:TYR:HE1	1:R:92:GLU:HG2	1.79	0.47
1:R:9:ALA:O	1:R:10:ALA:HB3	2.14	0.47
1:A:76:ARG:HA	1:A:76:ARG:HH11	1.80	0.47
1:B:40:ASN:ND2	1:B:42:GLN:HG3	2.30	0.47
1:F:19:GLN:HG2	1:G:11:ARG:NH2	2.29	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:16:PRO:HG3	1:I:5:PRO:CG	2.39	0.47
1:H:47:GLN:NE2	1:I:58:THR:O	2.44	0.47
1:J:9:ALA:O	1:J:10:ALA:HB3	2.14	0.47
1:O:181:ILE:HG23	1:O:210:GLU:HB3	1.96	0.47
1:B:135:LYS:HE3	1:D:6:PRO:HD3	1.96	0.46
1:D:9:ALA:O	1:D:10:ALA:HB3	2.15	0.46
1:G:176:ASN:O	1:H:15:MET:N	2.41	0.46
1:J:40:ASN:ND2	1:J:42:GLN:HG3	2.30	0.46
1:N:76:ARG:O	1:N:76:ARG:CG	2.63	0.46
1:O:9:ALA:O	1:O:10:ALA:HB3	2.14	0.46
1:A:3:THR:O	1:H:154:LEU:HD13	2.15	0.46
1:C:93:ARG:NH1	1:C:97:ARG:HH22	2.12	0.46
1:D:17:ARG:NH1	1:D:74:ASP:OD2	2.48	0.46
1:J:154:LEU:HD21	1:L:3:THR:HA	1.96	0.46
1:K:17:ARG:HB3	1:K:21:TYR:HB2	1.97	0.46
1:P:166:VAL:HG11	1:Q:96:ILE:CD1	2.45	0.46
1:E:102:ASN:O	1:O:113:LEU:N	2.34	0.46
1:E:211:PRO:HB2	1:E:214:LEU:HB2	1.96	0.46
1:A:3:THR:HA	1:H:154:LEU:HD21	1.96	0.46
1:A:3:THR:CB	1:H:154:LEU:HD22	2.45	0.46
1:J:17:ARG:NH1	1:J:74:ASP:OD2	2.49	0.46
1:K:39:TYR:CE1	1:L:92:GLU:HG2	2.51	0.46
1:K:176:ASN:O	1:L:15:MET:HB2	2.16	0.46
1:K:181:ILE:HG23	1:K:210:GLU:HB3	1.96	0.46
1:O:15:MET:HG2	1:O:16:PRO:HD2	1.98	0.46
1:P:39:TYR:CE1	1:Q:92:GLU:HG2	2.50	0.46
1:C:128:ILE:O	1:C:128:ILE:HG13	2.15	0.46
1:D:15:MET:HG2	1:D:16:PRO:HD2	1.96	0.46
1:D:128:ILE:HG23	1:E:63:SER:CB	2.45	0.46
1:N:133:ASN:OD1	1:N:153:GLN:NE2	2.48	0.46
1:P:128:ILE:O	1:P:128:ILE:HG13	2.14	0.46
1:A:92:GLU:HG2	1:I:39:TYR:CE1	2.50	0.46
1:F:40:ASN:ND2	1:F:42:GLN:HG3	2.30	0.46
1:G:48:PHE:CB	1:H:54:SER:CB	2.91	0.46
1:J:181:ILE:HG23	1:J:210:GLU:HB3	1.96	0.46
1:M:211:PRO:HB2	1:M:214:LEU:HB2	1.98	0.46
1:O:226:PHE:CZ	1:P:14:LEU:CD2	2.92	0.46
1:A:176:ASN:HB3	1:B:15:MET:HB2	1.97	0.46
1:D:101:GLU:HB2	1:P:97:ARG:HG2	1.98	0.46
1:F:128:ILE:O	1:F:128:ILE:HG13	2.14	0.46
1:N:211:PRO:HB2	1:N:214:LEU:HB2	1.97	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:P:17:ARG:HB3	1:P:21:TYR:HB2	1.98	0.46
1:F:130:TYR:CD1	1:F:130:TYR:C	2.93	0.46
1:F:166:VAL:HG11	1:G:96:ILE:HD11	1.96	0.46
1:I:9:ALA:O	1:I:10:ALA:HB3	2.16	0.46
1:J:82:GLU:OE2	1:R:162:ARG:NH2	2.48	0.46
1:P:9:ALA:O	1:P:10:ALA:HB3	2.15	0.46
1:P:162:ARG:HH21	1:Q:82:GLU:CD	2.24	0.46
1:A:92:GLU:HG2	1:I:39:TYR:HE1	1.81	0.46
1:C:97:ARG:HG2	1:Q:101:GLU:HB2	1.97	0.46
1:C:143:TYR:C	1:C:145:GLY:N	2.74	0.46
1:C:113:LEU:N	1:Q:102:ASN:O	2.42	0.45
1:E:143:TYR:HD1	1:F:200:LEU:HD12	1.80	0.45
1:L:9:ALA:O	1:L:10:ALA:HB3	2.16	0.45
1:L:128:ILE:O	1:L:128:ILE:HG13	2.15	0.45
1:N:181:ILE:HG23	1:N:210:GLU:HB3	1.97	0.45
1:O:17:ARG:NH1	1:O:74:ASP:OD2	2.48	0.45
1:O:130:TYR:C	1:O:130:TYR:CD1	2.94	0.45
1:R:211:PRO:HB2	1:R:214:LEU:HB2	1.98	0.45
1:A:33:LYS:HE2	1:A:76:ARG:HH22	1.81	0.45
1:B:211:PRO:HB2	1:B:214:LEU:HB2	1.97	0.45
1:F:107:ILE:HD13	1:N:107:ILE:CD1	2.24	0.45
1:J:154:LEU:CD2	1:L:3:THR:O	2.65	0.45
1:L:11:ARG:HG2	1:L:11:ARG:O	2.15	0.45
1:L:17:ARG:HB3	1:L:21:TYR:HB2	1.97	0.45
1:C:83:ARG:NE	1:D:92:GLU:OE2	2.34	0.45
1:G:211:PRO:HB2	1:G:214:LEU:HB2	1.98	0.45
1:O:211:PRO:HB2	1:O:214:LEU:HB2	1.99	0.45
1:Q:17:ARG:NH1	1:Q:74:ASP:OD2	2.49	0.45
1:Q:211:PRO:HB2	1:Q:214:LEU:HB2	1.98	0.45
1:A:15:MET:HG3	1:I:178:SER:HB2	1.97	0.45
1:B:17:ARG:HB3	1:B:21:TYR:HB2	1.99	0.45
1:B:156:GLN:HG2	1:C:213:MET:HE1	1.98	0.45
1:D:173:SER:HA	1:E:73:LYS:NZ	2.31	0.45
1:D:211:PRO:HB2	1:D:214:LEU:HB2	1.98	0.45
1:Q:16:PRO:HG3	1:R:5:PRO:HG3	1.98	0.45
1:F:211:PRO:HB2	1:F:214:LEU:HB2	1.98	0.45
1:I:211:PRO:HB2	1:I:214:LEU:HB2	1.99	0.45
1:O:166:VAL:HA	1:P:89:LEU:HD21	1.98	0.45
1:A:16:PRO:HG3	1:B:5:PRO:HG3	1.99	0.45
1:E:17:ARG:HB3	1:E:21:TYR:HB2	1.98	0.45
1:F:17:ARG:HB3	1:F:21:TYR:HB2	1.99	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:97:ARG:HG2	1:N:101:GLU:HB2	1.98	0.45
1:I:143:TYR:C	1:I:145:GLY:N	2.75	0.45
1:K:143:TYR:C	1:K:145:GLY:N	2.74	0.45
1:M:166:VAL:HG11	1:N:96:ILE:HD12	1.98	0.45
1:Q:17:ARG:HB3	1:Q:21:TYR:HB2	1.99	0.45
1:C:92:GLU:O	1:C:96:ILE:HG13	2.17	0.45
1:E:166:VAL:HA	1:F:89:LEU:HD21	1.97	0.45
1:O:166:VAL:HG11	1:P:96:ILE:HD12	1.99	0.45
1:Q:162:ARG:NH2	1:R:82:GLU:OE2	2.49	0.45
1:A:17:ARG:HB3	1:A:21:TYR:HB2	1.97	0.45
1:B:93:ARG:NH1	1:B:97:ARG:HH22	2.15	0.45
1:B:142:ARG:O	1:C:201:GLU:N	2.36	0.45
1:D:130:TYR:CD1	1:D:130:TYR:C	2.95	0.45
1:F:101:GLU:HB2	1:N:97:ARG:HG2	1.98	0.45
1:J:8:GLU:OE2	1:R:218:SER:HB2	2.16	0.45
1:K:100:GLN:NE2	1:K:111:ILE:O	2.32	0.45
1:L:121:ILE:HD13	1:L:163:VAL:HG13	1.99	0.45
1:M:17:ARG:HB3	1:M:21:TYR:HB2	1.99	0.45
1:O:128:ILE:HG23	1:P:63:SER:CB	2.47	0.45
1:A:97:ARG:NH1	1:J:102:ASN:OD1	2.50	0.45
1:B:139:VAL:HG22	1:C:204:VAL:HG22	1.99	0.45
1:C:101:GLU:HB2	1:Q:97:ARG:HG2	1.98	0.45
1:G:43:ASP:C	1:G:45:THR:H	2.24	0.45
1:H:211:PRO:HB2	1:H:214:LEU:HB2	1.99	0.45
1:J:211:PRO:HB2	1:J:214:LEU:HB2	1.99	0.45
1:K:135:LYS:HE3	1:M:4:ALA:O	2.17	0.45
1:O:56:PHE:CE1	1:P:56:PHE:HE2	2.35	0.45
1:A:100:GLN:NE2	1:A:111:ILE:O	2.34	0.45
1:B:141:ALA:HA	1:C:202:GLY:HA2	1.98	0.45
1:H:55:ASN:ND2	1:I:56:PHE:CE2	2.85	0.45
1:K:166:VAL:HG11	1:L:96:ILE:CD1	2.47	0.45
1:K:179:LYS:NZ	1:L:8:GLU:CG	2.80	0.45
1:K:211:PRO:HB2	1:K:214:LEU:HB2	1.99	0.45
1:K:218:SER:HB2	1:L:8:GLU:OE2	2.17	0.45
1:Q:166:VAL:HA	1:R:89:LEU:HD21	1.99	0.45
1:I:17:ARG:HB3	1:I:21:TYR:HB2	1.98	0.44
1:N:56:PHE:CE1	1:O:56:PHE:CE2	3.05	0.44
1:B:9:ALA:O	1:B:10:ALA:HB3	2.17	0.44
1:B:131:GLU:OE1	1:C:213:MET:HB2	2.18	0.44
1:B:15:MET:HE1	1:B:217:MET:CG	2.41	0.44
1:G:110:ARG:NH1	1:M:103:GLY:HA2	2.31	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:P:176:ASN:O	1:Q:15:MET:N	2.50	0.44
1:G:152:TYR:CE2	1:G:154:LEU:HD23	2.52	0.44
1:K:156:GLN:HG2	1:L:213:MET:HE1	1.99	0.44
1:Q:166:VAL:HG11	1:R:96:ILE:HD11	2.00	0.44
1:Q:170:GLU:HA	1:R:81:LEU:HD23	1.99	0.44
1:F:97:ARG:NH1	1:N:102:ASN:OD1	2.51	0.44
1:N:48:PHE:HB2	1:O:54:SER:CB	2.43	0.44
1:L:16:PRO:HG3	1:M:5:PRO:HG3	1.99	0.44
1:P:218:SER:HB2	1:Q:8:GLU:OE2	2.17	0.44
1:F:166:VAL:HA	1:G:89:LEU:HD21	1.99	0.44
1:P:40:ASN:ND2	1:P:42:GLN:HG3	2.33	0.44
1:C:48:PHE:HB2	1:D:54:SER:CB	2.43	0.44
1:E:176:ASN:O	1:F:15:MET:N	2.50	0.44
1:H:143:TYR:C	1:H:145:GLY:N	2.75	0.44
1:E:226:PHE:CZ	1:F:14:LEU:HD22	2.53	0.44
1:F:143:TYR:HA	1:G:200:LEU:HA	1.99	0.44
1:E:51:TYR:CG	1:E:52:PRO:HA	2.53	0.43
1:F:39:TYR:CE1	1:G:92:GLU:HG2	2.53	0.43
1:E:47:GLN:NE2	1:F:58:THR:O	2.45	0.43
1:E:137:GLY:HA2	1:F:206:TYR:HA	1.99	0.43
1:J:154:LEU:CD2	1:L:3:THR:HB	2.40	0.43
1:O:55:ASN:ND2	1:P:56:PHE:CE2	2.86	0.43
1:Q:45:THR:OG1	1:Q:130:TYR:N	2.51	0.43
1:B:143:TYR:HA	1:C:200:LEU:HA	2.00	0.43
1:D:17:ARG:HB3	1:D:21:TYR:HB2	2.00	0.43
1:M:178:SER:HB2	1:N:15:MET:HG3	2.00	0.43
1:N:166:VAL:HG11	1:O:96:ILE:CD1	2.48	0.43
1:A:176:ASN:O	1:B:15:MET:N	2.38	0.43
1:J:154:LEU:HD13	1:L:3:THR:O	2.18	0.43
1:L:166:VAL:HA	1:M:89:LEU:HD21	2.00	0.43
1:C:93:ARG:HH12	1:C:97:ARG:HH22	1.67	0.43
1:F:45:THR:OG1	1:F:130:TYR:N	2.52	0.43
1:G:56:PHE:CD1	1:H:56:PHE:CE2	3.07	0.43
1:R:152:TYR:CE2	1:R:154:LEU:HD23	2.53	0.43
1:B:166:VAL:HG11	1:C:96:ILE:HD12	2.00	0.43
1:D:166:VAL:HA	1:E:89:LEU:HD21	1.99	0.43
1:E:36:VAL:HG11	1:E:78:PHE:CD1	2.53	0.43
1:Q:227:LEU:HD12	1:Q:227:LEU:HA	1.77	0.43
1:F:128:ILE:HG22	1:G:63:SER:HB2	1.99	0.43
1:J:63:SER:HB2	1:R:128:ILE:HG22	2.00	0.43
1:N:8:GLU:OE2	1:N:12:PRO:HD3	2.19	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:R:17:ARG:HB3	1:R:21:TYR:HB2	2.01	0.43
1:R:185:GLU:HG3	1:R:207:THR:HG22	2.01	0.43
1:G:97:ARG:HG2	1:M:101:GLU:HB2	2.01	0.43
1:G:128:ILE:HG23	1:H:63:SER:CB	2.48	0.43
1:L:93:ARG:HH12	1:L:97:ARG:HH22	1.67	0.43
1:M:55:ASN:ND2	1:N:56:PHE:HE2	2.12	0.43
1:P:139:VAL:HG13	1:Q:204:VAL:HG22	2.00	0.43
1:P:227:LEU:HD12	1:P:227:LEU:HA	1.78	0.43
1:C:14:LEU:HD23	1:C:14:LEU:H	1.83	0.43
1:D:173:SER:HA	1:E:73:LYS:HZ1	1.83	0.43
1:I:179:LYS:NZ	1:I:210:GLU:OE2	2.51	0.43
1:I:185:GLU:HG3	1:I:207:THR:HG22	2.01	0.43
1:J:92:GLU:HG2	1:R:39:TYR:HE1	1.83	0.43
1:K:121:ILE:HD13	1:K:163:VAL:HG13	2.01	0.43
1:K:179:LYS:NZ	1:K:210:GLU:OE2	2.51	0.43
1:N:92:GLU:O	1:N:96:ILE:HG13	2.18	0.43
1:N:141:ALA:HA	1:O:202:GLY:HA2	2.00	0.43
1:Q:34:ILE:O	1:Q:78:PHE:HA	2.19	0.43
1:A:192:ARG:N	1:A:200:LEU:O	2.50	0.43
1:H:179:LYS:NZ	1:H:210:GLU:OE2	2.52	0.43
1:L:56:PHE:CE1	1:M:56:PHE:HE2	2.36	0.43
1:I:100:GLN:NE2	1:I:111:ILE:O	2.32	0.42
1:J:57:SER:HG	1:R:48:PHE:H	1.60	0.42
1:B:185:GLU:HG3	1:B:207:THR:HG22	2.00	0.42
1:F:14:LEU:H	1:F:14:LEU:HD23	1.84	0.42
1:F:162:ARG:CZ	1:G:82:GLU:OE1	2.67	0.42
1:G:34:ILE:O	1:G:78:PHE:HA	2.19	0.42
1:H:162:ARG:HH21	1:I:82:GLU:CD	2.27	0.42
1:J:34:ILE:O	1:J:78:PHE:HA	2.18	0.42
1:K:39:TYR:HE1	1:L:92:GLU:HG2	1.83	0.42
1:K:185:GLU:HG3	1:K:207:THR:HG22	2.01	0.42
1:L:179:LYS:NZ	1:L:210:GLU:OE2	2.52	0.42
1:O:17:ARG:HB3	1:O:21:TYR:HB2	2.00	0.42
1:P:51:TYR:CG	1:P:52:PRO:HA	2.55	0.42
1:R:100:GLN:NE2	1:R:111:ILE:O	2.32	0.42
1:A:43:ASP:C	1:A:45:THR:H	2.28	0.42
1:A:179:LYS:NZ	1:A:210:GLU:OE2	2.52	0.42
1:B:179:LYS:NZ	1:B:210:GLU:OE2	2.52	0.42
1:D:128:ILE:CG2	1:E:67:MET:HE3	2.49	0.42
1:E:34:ILE:O	1:E:78:PHE:HA	2.19	0.42
1:F:142:ARG:N	1:G:201:GLU:O	2.50	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:101:GLU:HA	1:K:101:GLU:HA	2.00	0.42
1:I:121:ILE:HD13	1:I:163:VAL:HG13	2.02	0.42
1:N:93:ARG:HH12	1:N:97:ARG:HH22	1.67	0.42
1:A:139:VAL:HG22	1:B:204:VAL:HG22	2.02	0.42
1:B:97:ARG:HG2	1:R:101:GLU:HB2	2.01	0.42
1:H:34:ILE:O	1:H:78:PHE:HA	2.20	0.42
1:J:92:GLU:HG2	1:R:39:TYR:CE1	2.54	0.42
1:N:14:LEU:HD23	1:N:14:LEU:H	1.83	0.42
1:N:179:LYS:NZ	1:N:210:GLU:OE2	2.52	0.42
1:O:92:GLU:O	1:O:96:ILE:HG13	2.19	0.42
1:R:51:TYR:CG	1:R:52:PRO:HA	2.55	0.42
1:A:56:PHE:CE2	1:I:55:ASN:ND2	2.87	0.42
1:C:17:ARG:HB3	1:C:21:TYR:HB2	1.99	0.42
1:E:179:LYS:NZ	1:E:210:GLU:OE2	2.52	0.42
1:F:34:ILE:O	1:F:78:PHE:HA	2.19	0.42
1:H:92:GLU:O	1:H:96:ILE:HG13	2.19	0.42
1:J:16:PRO:HG3	1:K:5:PRO:HG3	2.01	0.42
1:L:162:ARG:HH21	1:M:82:GLU:CD	2.26	0.42
1:M:180:THR:HG23	1:N:10:ALA:CB	2.49	0.42
1:N:17:ARG:HB3	1:N:21:TYR:HB2	2.01	0.42
1:N:51:TYR:CG	1:N:52:PRO:HA	2.55	0.42
1:R:92:GLU:O	1:R:96:ILE:HG13	2.18	0.42
1:D:152:TYR:CE2	1:D:154:LEU:HD23	2.55	0.42
1:D:166:VAL:HG11	1:E:96:ILE:HD12	2.01	0.42
1:G:102:ASN:O	1:M:113:LEU:N	2.47	0.42
1:I:93:ARG:NH1	1:I:97:ARG:HH22	2.17	0.42
1:M:210:GLU:CD	1:N:9:ALA:H	2.26	0.42
1:N:124:GLU:OE2	1:O:82:GLU:OE2	2.38	0.42
1:B:178:SER:HB2	1:C:15:MET:HG3	2.02	0.42
1:D:102:ASN:OD1	1:P:97:ARG:NH1	2.53	0.42
1:D:179:LYS:NZ	1:D:210:GLU:OE2	2.53	0.42
1:E:256:MET:O	1:F:14:LEU:HD21	2.19	0.42
1:H:166:VAL:HG11	1:I:96:ILE:HD12	2.02	0.42
1:J:14:LEU:HD23	1:J:14:LEU:H	1.84	0.42
1:M:48:PHE:HB2	1:N:54:SER:HB3	2.02	0.42
1:O:135:LYS:HE3	1:Q:6:PRO:HD3	2.01	0.42
1:Q:14:LEU:HD23	1:Q:14:LEU:H	1.84	0.42
1:A:96:ILE:CD1	1:I:166:VAL:HG11	2.49	0.42
1:G:17:ARG:HB3	1:G:21:TYR:HB2	2.00	0.42
1:H:35:PHE:HE2	1:I:109:ASN:OD1	2.02	0.42
1:I:34:ILE:O	1:I:78:PHE:HA	2.20	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M:34:ILE:O	1:M:78:PHE:HA	2.20	0.42
1:M:179:LYS:NZ	1:M:210:GLU:OE2	2.53	0.42
1:C:121:ILE:HD13	1:C:163:VAL:HG13	2.02	0.42
1:F:51:TYR:CG	1:F:52:PRO:HA	2.55	0.42
1:K:6:PRO:HD3	1:R:135:LYS:HE3	2.02	0.42
1:K:93:ARG:NH1	1:K:97:ARG:HH22	2.17	0.42
1:L:43:ASP:C	1:L:45:THR:H	2.28	0.42
1:L:176:ASN:O	1:M:15:MET:N	2.46	0.42
1:M:93:ARG:NH1	1:M:97:ARG:HH22	2.18	0.42
1:Q:51:TYR:CG	1:Q:52:PRO:HA	2.55	0.42
1:D:34:ILE:O	1:D:78:PHE:HA	2.20	0.42
1:F:39:TYR:HE1	1:G:92:GLU:HG2	1.85	0.42
1:G:107:ILE:HG21	1:M:107:ILE:CD1	2.47	0.42
1:N:121:ILE:HD13	1:N:163:VAL:HG13	2.02	0.42
1:O:100:GLN:NE2	1:O:111:ILE:O	2.34	0.42
1:O:179:LYS:NZ	1:O:210:GLU:OE2	2.52	0.42
1:P:34:ILE:O	1:P:78:PHE:HA	2.20	0.42
1:P:179:LYS:NZ	1:P:210:GLU:OE2	2.52	0.42
1:R:82:GLU:C	1:R:83:ARG:HG2	2.45	0.42
1:D:14:LEU:H	1:D:14:LEU:HD23	1.85	0.41
1:E:151:GLN:HB2	1:E:185:GLU:CG	2.50	0.41
1:H:51:TYR:CG	1:H:52:PRO:HA	2.55	0.41
1:L:135:LYS:CE	1:N:6:PRO:HD3	2.51	0.41
1:Q:158:ALA:CB	1:R:15:MET:SD	3.08	0.41
1:E:107:ILE:CD1	1:O:107:ILE:HD13	2.28	0.41
1:F:226:PHE:CZ	1:G:14:LEU:CD2	2.98	0.41
1:K:166:VAL:HG11	1:L:96:ILE:HD11	2.03	0.41
1:L:56:PHE:CE1	1:M:56:PHE:CE2	3.08	0.41
1:B:121:ILE:HD13	1:B:163:VAL:HG13	2.02	0.41
1:C:166:VAL:HG11	1:D:96:ILE:HD11	2.01	0.41
1:H:139:VAL:HG22	1:I:204:VAL:HG22	2.02	0.41
1:J:143:TYR:C	1:J:145:GLY:N	2.78	0.41
1:A:121:ILE:HD13	1:A:163:VAL:HG13	2.02	0.41
1:G:92:GLU:O	1:G:96:ILE:HG13	2.20	0.41
1:G:101:GLU:HB2	1:M:97:ARG:HG2	2.02	0.41
1:H:17:ARG:HB3	1:H:21:TYR:HB2	2.01	0.41
1:J:152:TYR:CE2	1:J:154:LEU:HD23	2.54	0.41
1:M:93:ARG:NH2	1:M:114:GLN:O	2.53	0.41
1:G:51:TYR:CG	1:G:52:PRO:HA	2.55	0.41
1:K:225:ILE:HG21	1:K:253:TYR:CD2	2.56	0.41
1:P:92:GLU:O	1:P:96:ILE:HG13	2.20	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:92:GLU:O	1:D:96:ILE:HG13	2.20	0.41
1:F:19:GLN:HG2	1:G:11:ARG:CZ	2.51	0.41
1:R:179:LYS:NZ	1:R:210:GLU:OE2	2.54	0.41
1:H:14:LEU:HD23	1:H:14:LEU:H	1.85	0.41
1:J:156:GLN:HG2	1:K:213:MET:HE1	2.02	0.41
1:L:226:PHE:CZ	1:M:14:LEU:HD11	2.56	0.41
1:M:100:GLN:NE2	1:M:111:ILE:O	2.36	0.41
1:P:14:LEU:H	1:P:14:LEU:HD23	1.86	0.41
1:D:56:PHE:CE1	1:E:56:PHE:CE2	3.09	0.41
1:E:166:VAL:HG11	1:F:96:ILE:HD11	2.01	0.41
1:G:47:GLN:NE2	1:H:58:THR:O	2.49	0.41
1:G:179:LYS:NZ	1:G:210:GLU:OE2	2.54	0.41
1:J:14:LEU:HA	1:R:177:THR:HA	2.03	0.41
1:L:34:ILE:O	1:L:78:PHE:HA	2.21	0.41
1:L:92:GLU:O	1:L:96:ILE:HG13	2.20	0.41
1:O:227:LEU:HA	1:O:227:LEU:HD12	1.75	0.41
1:A:125:GLY:HA3	1:A:160:ASN:O	2.21	0.41
1:A:231:GLY:HA2	1:A:236:LEU:HD13	2.03	0.41
1:E:113:LEU:N	1:O:102:ASN:O	2.39	0.41
1:G:45:THR:OG1	1:G:130:TYR:N	2.54	0.41
1:G:226:PHE:CZ	1:H:14:LEU:CD2	2.98	0.41
1:J:56:PHE:CE2	1:R:56:PHE:CE1	3.09	0.41
1:J:179:LYS:NZ	1:J:210:GLU:OE2	2.53	0.41
1:J:185:GLU:HG3	1:J:207:THR:HG22	2.01	0.41
1:M:121:ILE:HD13	1:M:163:VAL:HG13	2.02	0.41
1:M:162:ARG:HH21	1:N:82:GLU:CD	2.28	0.41
1:N:152:TYR:CE2	1:N:154:LEU:HD23	2.56	0.41
1:O:121:ILE:HD13	1:O:163:VAL:HG13	2.03	0.41
1:P:113:LEU:HD23	1:P:113:LEU:HA	1.97	0.41
1:P:140:GLY:O	1:Q:203:GLU:N	2.47	0.41
1:Q:91:ASN:O	1:Q:95:ILE:HG13	2.21	0.41
1:R:93:ARG:NH2	1:R:114:GLN:O	2.54	0.41
1:B:43:ASP:C	1:B:45:THR:H	2.29	0.41
1:E:100:GLN:NE2	1:E:111:ILE:O	2.34	0.41
1:F:56:PHE:CE1	1:G:56:PHE:HE2	2.38	0.41
1:G:166:VAL:HG11	1:H:96:ILE:HD12	2.02	0.41
1:G:173:SER:HA	1:H:73:LYS:NZ	2.36	0.41
1:H:48:PHE:CB	1:I:54:SER:CB	2.96	0.41
1:J:100:GLN:NE2	1:J:111:ILE:O	2.34	0.41
1:J:135:LYS:HE3	1:L:6:PRO:HD3	2.02	0.41
1:K:34:ILE:O	1:K:78:PHE:HA	2.21	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:O:34:ILE:O	1:O:78:PHE:HA	2.20	0.41
1:A:166:VAL:HA	1:B:89:LEU:HD21	2.03	0.40
1:B:83:ARG:NE	1:C:92:GLU:OE2	2.46	0.40
1:B:101:GLU:HB2	1:R:97:ARG:HG2	2.02	0.40
1:E:14:LEU:HD23	1:E:14:LEU:H	1.86	0.40
1:J:51:TYR:CG	1:J:52:PRO:HA	2.55	0.40
1:J:135:LYS:HE3	1:L:4:ALA:O	2.21	0.40
1:J:180:THR:HG21	1:L:3:THR:O	2.21	0.40
1:N:34:ILE:O	1:N:78:PHE:HA	2.21	0.40
1:B:34:ILE:O	1:B:78:PHE:HA	2.21	0.40
1:C:34:ILE:O	1:C:78:PHE:HA	2.21	0.40
1:D:162:ARG:HH21	1:E:82:GLU:CD	2.30	0.40
1:F:11:ARG:HB3	1:F:11:ARG:HH11	1.86	0.40
1:F:91:ASN:O	1:F:95:ILE:HG13	2.21	0.40
1:L:156:GLN:HG2	1:M:213:MET:HE1	2.02	0.40
1:M:43:ASP:C	1:M:45:THR:H	2.29	0.40
1:A:92:GLU:O	1:A:96:ILE:HG13	2.22	0.40
1:A:130:TYR:CD1	1:A:130:TYR:C	3.00	0.40
1:I:92:GLU:O	1:I:96:ILE:HG13	2.22	0.40
1:I:225:ILE:HG21	1:I:253:TYR:CD2	2.57	0.40
1:J:166:VAL:HG11	1:K:96:ILE:HD12	2.02	0.40
1:R:36:VAL:O	1:R:81:LEU:O	2.39	0.40
1:F:48:PHE:HB2	1:G:54:SER:CB	2.50	0.40
1:J:93:ARG:NH2	1:J:114:GLN:O	2.55	0.40
1:K:92:GLU:O	1:K:96:ILE:HG13	2.21	0.40
1:L:35:PHE:HE2	1:M:109:ASN:OD1	2.04	0.40
1:Q:130:TYR:CD1	1:Q:130:TYR:C	3.00	0.40
1:A:97:ARG:HG2	1:J:101:GLU:HB2	2.03	0.40
1:D:177:THR:HA	1:E:14:LEU:HA	2.02	0.40
1:H:101:GLU:HA	1:L:101:GLU:HA	2.04	0.40
1:H:102:ASN:O	1:L:113:LEU:N	2.43	0.40
1:J:17:ARG:HB3	1:J:21:TYR:HB2	2.02	0.40
1:Q:142:ARG:O	1:R:201:GLU:N	2.39	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all 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	242/262 (92%)	225 (93%)	16 (7%)	1 (0%)	30	61
1	B	242/262 (92%)	227 (94%)	15 (6%)	0	100	100
1	C	241/262 (92%)	225 (93%)	15 (6%)	1 (0%)	30	61
1	D	242/262 (92%)	227 (94%)	14 (6%)	1 (0%)	30	61
1	E	241/262 (92%)	226 (94%)	13 (5%)	2 (1%)	16	49
1	F	241/262 (92%)	228 (95%)	13 (5%)	0	100	100
1	G	241/262 (92%)	227 (94%)	14 (6%)	0	100	100
1	H	242/262 (92%)	226 (93%)	16 (7%)	0	100	100
1	I	241/262 (92%)	229 (95%)	12 (5%)	0	100	100
1	J	242/262 (92%)	225 (93%)	16 (7%)	1 (0%)	30	61
1	K	241/262 (92%)	227 (94%)	14 (6%)	0	100	100
1	L	241/262 (92%)	226 (94%)	15 (6%)	0	100	100
1	M	241/262 (92%)	226 (94%)	15 (6%)	0	100	100
1	N	241/262 (92%)	224 (93%)	16 (7%)	1 (0%)	30	61
1	O	241/262 (92%)	226 (94%)	14 (6%)	1 (0%)	30	61
1	P	241/262 (92%)	227 (94%)	13 (5%)	1 (0%)	30	61
1	Q	241/262 (92%)	228 (95%)	13 (5%)	0	100	100
1	R	241/262 (92%)	225 (93%)	16 (7%)	0	100	100
All	All	4343/4716 (92%)	4074 (94%)	260 (6%)	9 (0%)	43	72

All (9) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	E	44	GLU
1	O	44	GLU
1	P	44	GLU
1	C	44	GLU

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	D	44	GLU
1	E	16	PRO
1	N	44	GLU
1	A	128	ILE
1	J	16	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 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	209/223 (94%)	187 (90%)	22 (10%)	6	29
1	B	209/223 (94%)	186 (89%)	23 (11%)	6	27
1	C	208/223 (93%)	187 (90%)	21 (10%)	7	30
1	D	209/223 (94%)	187 (90%)	22 (10%)	6	29
1	E	208/223 (93%)	186 (89%)	22 (11%)	6	28
1	F	208/223 (93%)	186 (89%)	22 (11%)	6	28
1	G	208/223 (93%)	184 (88%)	24 (12%)	5	25
1	H	209/223 (94%)	190 (91%)	19 (9%)	9	33
1	I	208/223 (93%)	188 (90%)	20 (10%)	8	32
1	J	209/223 (94%)	189 (90%)	20 (10%)	8	32
1	K	208/223 (93%)	188 (90%)	20 (10%)	8	32
1	L	208/223 (93%)	184 (88%)	24 (12%)	5	25
1	M	208/223 (93%)	188 (90%)	20 (10%)	8	32
1	N	208/223 (93%)	187 (90%)	21 (10%)	7	30
1	O	208/223 (93%)	187 (90%)	21 (10%)	7	30
1	P	208/223 (93%)	187 (90%)	21 (10%)	7	30
1	Q	208/223 (93%)	185 (89%)	23 (11%)	6	27
1	R	208/223 (93%)	183 (88%)	25 (12%)	5	24
All	All	3749/4014 (93%)	3359 (90%)	390 (10%)	7	29

All (390) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	11	ARG
1	A	22	LYS
1	A	42	GLN
1	A	89	LEU
1	A	105	VAL
1	A	108	ASN
1	A	109	ASN
1	A	121	ILE
1	A	122	MET
1	A	123	VAL
1	A	126	SER
1	A	132	SER
1	A	136	SER
1	A	152	TYR
1	A	172	LEU
1	A	180	THR
1	A	192	ARG
1	A	200	LEU
1	A	217	MET
1	A	238	ASP
1	A	242	LYS
1	A	255	HIS
1	B	22	LYS
1	B	33	LYS
1	B	42	GLN
1	B	76	ARG
1	B	89	LEU
1	B	105	VAL
1	B	108	ASN
1	B	109	ASN
1	B	121	ILE
1	B	122	MET
1	B	123	VAL
1	B	126	SER
1	B	131	GLU
1	B	132	SER
1	B	136	SER
1	B	152	TYR
1	B	180	THR
1	B	192	ARG
1	B	200	LEU
1	B	213	MET

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	B	217	MET
1	B	242	LYS
1	B	255	HIS
1	C	15	MET
1	C	22	LYS
1	C	89	LEU
1	C	105	VAL
1	C	108	ASN
1	C	109	ASN
1	C	121	ILE
1	C	122	MET
1	C	123	VAL
1	C	126	SER
1	C	132	SER
1	C	136	SER
1	C	152	TYR
1	C	172	LEU
1	C	176	ASN
1	C	179	LYS
1	C	180	THR
1	C	200	LEU
1	C	217	MET
1	C	242	LYS
1	C	255	HIS
1	D	11	ARG
1	D	15	MET
1	D	22	LYS
1	D	42	GLN
1	D	89	LEU
1	D	105	VAL
1	D	108	ASN
1	D	109	ASN
1	D	121	ILE
1	D	122	MET
1	D	123	VAL
1	D	126	SER
1	D	132	SER
1	D	136	SER
1	D	146	ILE
1	D	152	TYR
1	D	176	ASN
1	D	180	THR

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	D	200	LEU
1	D	217	MET
1	D	242	LYS
1	D	255	HIS
1	E	15	MET
1	E	22	LYS
1	E	42	GLN
1	E	89	LEU
1	E	105	VAL
1	E	108	ASN
1	E	109	ASN
1	E	121	ILE
1	E	122	MET
1	E	123	VAL
1	E	126	SER
1	E	132	SER
1	E	136	SER
1	E	152	TYR
1	E	176	ASN
1	E	180	THR
1	E	185	GLU
1	E	200	LEU
1	E	217	MET
1	E	242	LYS
1	E	245	ARG
1	E	255	HIS
1	F	8	GLU
1	F	11	ARG
1	F	15	MET
1	F	22	LYS
1	F	42	GLN
1	F	89	LEU
1	F	91	ASN
1	F	105	VAL
1	F	108	ASN
1	F	109	ASN
1	F	121	ILE
1	F	122	MET
1	F	123	VAL
1	F	126	SER
1	F	132	SER
1	F	136	SER

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	F	152	TYR
1	F	180	THR
1	F	200	LEU
1	F	217	MET
1	F	242	LYS
1	F	255	HIS
1	G	15	MET
1	G	22	LYS
1	G	42	GLN
1	G	89	LEU
1	G	91	ASN
1	G	105	VAL
1	G	107	ILE
1	G	108	ASN
1	G	109	ASN
1	G	114	GLN
1	G	121	ILE
1	G	122	MET
1	G	123	VAL
1	G	126	SER
1	G	132	SER
1	G	136	SER
1	G	152	TYR
1	G	172	LEU
1	G	180	THR
1	G	200	LEU
1	G	217	MET
1	G	239	LEU
1	G	242	LYS
1	G	255	HIS
1	H	15	MET
1	H	22	LYS
1	H	42	GLN
1	H	89	LEU
1	H	105	VAL
1	H	108	ASN
1	H	109	ASN
1	H	121	ILE
1	H	122	MET
1	H	123	VAL
1	H	126	SER
1	H	132	SER

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	H	136	SER
1	H	152	TYR
1	H	172	LEU
1	H	200	LEU
1	H	217	MET
1	H	242	LYS
1	H	255	HIS
1	I	11	ARG
1	I	15	MET
1	I	22	LYS
1	I	42	GLN
1	I	89	LEU
1	I	105	VAL
1	I	108	ASN
1	I	109	ASN
1	I	121	ILE
1	I	122	MET
1	I	123	VAL
1	I	126	SER
1	I	132	SER
1	I	136	SER
1	I	152	TYR
1	I	180	THR
1	I	200	LEU
1	I	217	MET
1	I	242	LYS
1	I	255	HIS
1	J	8	GLU
1	J	15	MET
1	J	22	LYS
1	J	42	GLN
1	J	89	LEU
1	J	105	VAL
1	J	108	ASN
1	J	109	ASN
1	J	121	ILE
1	J	122	MET
1	J	123	VAL
1	J	126	SER
1	J	132	SER
1	J	136	SER
1	J	152	TYR

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	J	172	LEU
1	J	200	LEU
1	J	217	MET
1	J	242	LYS
1	J	255	HIS
1	K	8	GLU
1	K	11	ARG
1	K	15	MET
1	K	42	GLN
1	K	89	LEU
1	K	105	VAL
1	K	108	ASN
1	K	109	ASN
1	K	121	ILE
1	K	122	MET
1	K	123	VAL
1	K	126	SER
1	K	132	SER
1	K	136	SER
1	K	152	TYR
1	K	172	LEU
1	K	200	LEU
1	K	217	MET
1	K	242	LYS
1	K	255	HIS
1	L	8	GLU
1	L	11	ARG
1	L	15	MET
1	L	22	LYS
1	L	42	GLN
1	L	89	LEU
1	L	105	VAL
1	L	108	ASN
1	L	109	ASN
1	L	121	ILE
1	L	122	MET
1	L	123	VAL
1	L	126	SER
1	L	132	SER
1	L	136	SER
1	L	152	TYR
1	L	176	ASN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	L	180	THR
1	L	200	LEU
1	L	217	MET
1	L	238	ASP
1	L	242	LYS
1	L	254	ARG
1	L	255	HIS
1	M	11	ARG
1	M	15	MET
1	M	42	GLN
1	M	89	LEU
1	M	105	VAL
1	M	108	ASN
1	M	109	ASN
1	M	121	ILE
1	M	122	MET
1	M	123	VAL
1	M	126	SER
1	M	132	SER
1	M	136	SER
1	M	152	TYR
1	M	180	THR
1	M	200	LEU
1	M	217	MET
1	M	227	LEU
1	M	242	LYS
1	M	255	HIS
1	N	7	LYS
1	N	15	MET
1	N	22	LYS
1	N	42	GLN
1	N	89	LEU
1	N	105	VAL
1	N	108	ASN
1	N	109	ASN
1	N	121	ILE
1	N	122	MET
1	N	123	VAL
1	N	126	SER
1	N	132	SER
1	N	136	SER
1	N	152	TYR

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	N	172	LEU
1	N	180	THR
1	N	200	LEU
1	N	217	MET
1	N	242	LYS
1	N	255	HIS
1	O	15	MET
1	O	22	LYS
1	O	42	GLN
1	O	89	LEU
1	O	105	VAL
1	O	108	ASN
1	O	109	ASN
1	O	121	ILE
1	O	122	MET
1	O	123	VAL
1	O	126	SER
1	O	132	SER
1	O	136	SER
1	O	152	TYR
1	O	176	ASN
1	O	180	THR
1	O	200	LEU
1	O	217	MET
1	O	227	LEU
1	O	242	LYS
1	O	255	HIS
1	P	8	GLU
1	P	15	MET
1	P	42	GLN
1	P	89	LEU
1	P	105	VAL
1	P	108	ASN
1	P	109	ASN
1	P	121	ILE
1	P	122	MET
1	P	123	VAL
1	P	126	SER
1	P	132	SER
1	P	136	SER
1	P	152	TYR
1	P	176	ASN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	P	180	THR
1	P	200	LEU
1	P	217	MET
1	P	227	LEU
1	P	242	LYS
1	P	255	HIS
1	Q	8	GLU
1	Q	11	ARG
1	Q	15	MET
1	Q	22	LYS
1	Q	42	GLN
1	Q	89	LEU
1	Q	91	ASN
1	Q	105	VAL
1	Q	108	ASN
1	Q	109	ASN
1	Q	121	ILE
1	Q	122	MET
1	Q	123	VAL
1	Q	126	SER
1	Q	132	SER
1	Q	136	SER
1	Q	152	TYR
1	Q	180	THR
1	Q	200	LEU
1	Q	217	MET
1	Q	227	LEU
1	Q	242	LYS
1	Q	255	HIS
1	R	8	GLU
1	R	15	MET
1	R	22	LYS
1	R	42	GLN
1	R	89	LEU
1	R	91	ASN
1	R	105	VAL
1	R	108	ASN
1	R	109	ASN
1	R	114	GLN
1	R	121	ILE
1	R	122	MET
1	R	123	VAL

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	R	126	SER
1	R	132	SER
1	R	136	SER
1	R	152	TYR
1	R	172	LEU
1	R	180	THR
1	R	200	LEU
1	R	217	MET
1	R	227	LEU
1	R	239	LEU
1	R	242	LYS
1	R	255	HIS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (63) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	40	ASN
1	A	42	GLN
1	A	114	GLN
1	A	247	ASN
1	B	40	ASN
1	B	247	ASN
1	C	42	GLN
1	C	156	GLN
1	C	176	ASN
1	C	247	ASN
1	D	176	ASN
1	D	247	ASN
1	E	151	GLN
1	E	187	GLN
1	E	247	ASN
1	E	255	HIS
1	F	40	ASN
1	F	176	ASN
1	F	247	ASN
1	G	84	GLN
1	G	120	ASN
1	G	247	ASN
1	H	55	ASN
1	H	156	GLN
1	H	247	ASN
1	H	255	HIS

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	I	47	GLN
1	I	114	GLN
1	I	156	GLN
1	I	247	ASN
1	J	40	ASN
1	J	55	ASN
1	J	156	GLN
1	J	247	ASN
1	K	187	GLN
1	K	247	ASN
1	L	40	ASN
1	L	42	GLN
1	L	47	GLN
1	L	114	GLN
1	L	156	GLN
1	L	247	ASN
1	M	84	GLN
1	M	176	ASN
1	M	247	ASN
1	N	84	GLN
1	N	153	GLN
1	N	247	ASN
1	O	47	GLN
1	O	84	GLN
1	O	120	ASN
1	O	156	GLN
1	O	247	ASN
1	P	40	ASN
1	P	84	GLN
1	P	120	ASN
1	P	151	GLN
1	P	247	ASN
1	Q	114	GLN
1	Q	176	ASN
1	Q	247	ASN
1	Q	255	HIS
1	R	247	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 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	248/262 (94%)	1.39	63 (25%) 1 2	38, 94, 165, 213	0
1	B	248/262 (94%)	1.38	64 (25%) 1 2	45, 99, 162, 200	0
1	C	247/262 (94%)	1.55	68 (27%) 1 2	49, 119, 181, 226	0
1	D	248/262 (94%)	1.56	64 (25%) 1 2	58, 120, 186, 224	0
1	E	247/262 (94%)	1.84	93 (37%) 1 1	52, 118, 183, 230	0
1	F	247/262 (94%)	2.00	105 (42%) 0 1	53, 117, 184, 233	0
1	G	247/262 (94%)	1.86	108 (43%) 0 1	53, 117, 174, 236	0
1	H	248/262 (94%)	1.76	78 (31%) 1 1	57, 112, 174, 249	0
1	I	247/262 (94%)	1.50	67 (27%) 1 2	43, 105, 167, 258	0
1	J	248/262 (94%)	1.75	92 (37%) 1 1	58, 112, 184, 238	0
1	K	247/262 (94%)	1.53	80 (32%) 1 1	38, 107, 168, 229	0
1	L	247/262 (94%)	1.46	62 (25%) 1 2	29, 92, 155, 226	0
1	M	247/262 (94%)	1.35	57 (23%) 2 2	41, 102, 158, 205	0
1	N	247/262 (94%)	1.54	74 (29%) 1 1	42, 115, 173, 212	0
1	O	247/262 (94%)	1.54	70 (28%) 1 1	57, 123, 184, 229	0
1	P	247/262 (94%)	1.88	106 (42%) 0 1	51, 120, 188, 248	0
1	Q	247/262 (94%)	2.00	107 (43%) 0 1	50, 121, 184, 240	0
1	R	247/262 (94%)	1.79	100 (40%) 0 1	50, 116, 176, 204	0
All	All	4451/4716 (94%)	1.65	1458 (32%) 1 1	29, 111, 179, 258	0

All (1458) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	J	73	LYS	9.0
1	H	73	LYS	8.7
1	C	4	ALA	8.2

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	O	80	PRO	8.1
1	R	43	ASP	8.0
1	C	171	ILE	8.0
1	Q	79	ILE	7.8
1	J	237	TRP	7.5
1	G	9	ALA	7.3
1	D	80	PRO	7.2
1	C	5	PRO	7.1
1	F	79	ILE	7.0
1	N	171	ILE	6.9
1	H	237	TRP	6.8
1	P	69	VAL	6.6
1	N	4	ALA	6.6
1	K	9	ALA	6.6
1	P	9	ALA	6.6
1	A	3	THR	6.5
1	G	73	LYS	6.5
1	G	43	ASP	6.4
1	Q	69	VAL	6.3
1	R	9	ALA	6.3
1	R	73	LYS	6.1
1	E	210	GLU	6.1
1	E	51	TYR	6.1
1	I	73	LYS	6.1
1	R	67	MET	6.0
1	E	63	SER	6.0
1	G	67	MET	6.0
1	K	73	LYS	6.0
1	H	8	GLU	6.0
1	J	234	ARG	5.9
1	N	3	THR	5.8
1	D	52	PRO	5.8
1	F	182	LEU	5.8
1	P	8	GLU	5.7
1	L	3	THR	5.7
1	I	8	GLU	5.6
1	H	43	ASP	5.6
1	F	69	VAL	5.6
1	B	215	CYS	5.6
1	L	4	ALA	5.6
1	I	43	ASP	5.6
1	Q	155	ASP	5.5

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	A	4	ALA	5.5
1	E	69	VAL	5.5
1	I	9	ALA	5.5
1	A	173	SER	5.4
1	P	51	TYR	5.3
1	C	3	THR	5.3
1	I	158	ALA	5.3
1	K	3	THR	5.3
1	Q	34	ILE	5.3
1	K	8	GLU	5.2
1	E	4	ALA	5.2
1	C	6	PRO	5.2
1	D	174	SER	5.2
1	I	4	ALA	5.2
1	I	120	ASN	5.2
1	N	176	ASN	5.2
1	F	210	GLU	5.2
1	A	171	ILE	5.2
1	L	173	SER	5.1
1	C	174	SER	5.0
1	F	9	ALA	5.0
1	I	62	GLN	5.0
1	M	123	VAL	5.0
1	R	158	ALA	5.0
1	R	79	ILE	5.0
1	N	131	GLU	4.9
1	C	253	TYR	4.9
1	B	120	ASN	4.9
1	G	8	GLU	4.9
1	E	9	ALA	4.9
1	J	43	ASP	4.8
1	Q	181	ILE	4.8
1	F	155	ASP	4.8
1	H	210	GLU	4.8
1	P	210	GLU	4.8
1	C	131	GLU	4.8
1	J	230	ASP	4.8
1	L	171	ILE	4.8
1	Q	90	LEU	4.8
1	N	227	LEU	4.8
1	Q	182	LEU	4.8
1	Q	9	ALA	4.7

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	A	172	LEU	4.7
1	D	51	TYR	4.7
1	F	34	ILE	4.7
1	Q	173	SER	4.7
1	E	3	THR	4.7
1	O	38	VAL	4.7
1	F	180	THR	4.7
1	M	120	ASN	4.6
1	C	215	CYS	4.6
1	A	163	VAL	4.6
1	B	210	GLU	4.6
1	O	181	ILE	4.6
1	L	163	VAL	4.6
1	C	176	ASN	4.6
1	H	169	GLY	4.6
1	N	5	PRO	4.6
1	J	210	GLU	4.5
1	L	33	LYS	4.5
1	H	181	ILE	4.5
1	L	172	LEU	4.5
1	G	158	ALA	4.5
1	K	66	ALA	4.5
1	N	174	SER	4.5
1	F	129	GLY	4.5
1	G	180	THR	4.5
1	K	11	ARG	4.5
1	E	143	TYR	4.5
1	Q	25	THR	4.4
1	R	70	THR	4.4
1	L	143	TYR	4.4
1	O	130	TYR	4.4
1	R	210	GLU	4.4
1	E	187	GLN	4.4
1	Q	210	GLU	4.4
1	N	6	PRO	4.4
1	R	143	TYR	4.4
1	F	208	SER	4.4
1	E	129	GLY	4.4
1	F	143	TYR	4.4
1	O	210	GLU	4.4
1	O	175	VAL	4.4
1	K	174	SER	4.4

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	R	63	SER	4.4
1	Q	8	GLU	4.4
1	M	215	CYS	4.4
1	G	10	ALA	4.3
1	K	158	ALA	4.3
1	P	243	ALA	4.3
1	P	63	SER	4.3
1	B	79	ILE	4.3
1	F	181	ILE	4.3
1	J	79	ILE	4.3
1	H	234	ARG	4.3
1	Q	208	SER	4.3
1	I	227	LEU	4.3
1	P	38	VAL	4.3
1	R	8	GLU	4.3
1	G	62	GLN	4.3
1	N	181	ILE	4.3
1	K	43	ASP	4.3
1	R	80	PRO	4.3
1	F	78	PHE	4.3
1	L	174	SER	4.3
1	G	146	ILE	4.3
1	G	213	MET	4.3
1	F	237	TRP	4.3
1	B	131	GLU	4.3
1	F	89	LEU	4.2
1	E	58	THR	4.2
1	A	64	ALA	4.2
1	E	132	SER	4.2
1	F	170	GLU	4.2
1	C	120	ASN	4.2
1	K	120	ASN	4.2
1	B	127	ILE	4.2
1	P	70	THR	4.2
1	A	73	LYS	4.2
1	R	135	LYS	4.2
1	B	171	ILE	4.2
1	J	181	ILE	4.2
1	Q	70	THR	4.1
1	M	171	ILE	4.1
1	J	163	VAL	4.1
1	E	80	PRO	4.1

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	F	206	TYR	4.1
1	Q	143	TYR	4.1
1	N	215	CYS	4.1
1	Q	180	THR	4.1
1	R	175	VAL	4.1
1	E	66	ALA	4.1
1	G	145	GLY	4.1
1	L	120	ASN	4.1
1	R	69	VAL	4.1
1	P	156	GLN	4.1
1	L	210	GLU	4.1
1	H	163	VAL	4.1
1	I	186	VAL	4.1
1	F	77	TRP	4.1
1	D	129	GLY	4.1
1	R	62	GLN	4.0
1	C	227	LEU	4.0
1	D	38	VAL	4.0
1	G	184	TYR	4.0
1	J	153	GLN	4.0
1	B	123	VAL	4.0
1	E	175	VAL	4.0
1	J	8	GLU	4.0
1	H	33	LYS	4.0
1	B	92	GLU	4.0
1	F	184	TYR	4.0
1	M	92	GLU	4.0
1	I	174	SER	4.0
1	A	33	LYS	4.0
1	A	227	LEU	4.0
1	A	143	TYR	4.0
1	E	6	PRO	4.0
1	P	36	VAL	4.0
1	C	181	ILE	3.9
1	L	73	LYS	3.9
1	E	90	LEU	3.9
1	F	90	LEU	3.9
1	A	6	PRO	3.9
1	Q	156	GLN	3.9
1	Q	78	PHE	3.9
1	R	180	THR	3.9
1	H	230	ASP	3.9

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	M	138	GLY	3.9
1	G	89	LEU	3.9
1	O	17	ARG	3.9
1	O	52	PRO	3.9
1	F	128	ILE	3.8
1	G	210	GLU	3.8
1	P	154	LEU	3.8
1	Q	233	ASP	3.8
1	O	257	SER	3.8
1	B	180	THR	3.8
1	F	53	ALA	3.8
1	F	70	THR	3.8
1	F	145	GLY	3.8
1	I	11	ARG	3.8
1	E	154	LEU	3.8
1	F	131	GLU	3.8
1	D	69	VAL	3.8
1	Q	77	TRP	3.8
1	E	173	SER	3.8
1	I	230	ASP	3.8
1	B	128	ILE	3.8
1	H	32	GLY	3.8
1	P	90	LEU	3.8
1	L	6	PRO	3.8
1	L	64	ALA	3.8
1	H	6	PRO	3.8
1	E	156	GLN	3.8
1	A	120	ASN	3.8
1	M	127	ILE	3.8
1	P	79	ILE	3.8
1	Q	145	GLY	3.8
1	A	210	GLU	3.8
1	G	131	GLU	3.8
1	Q	170	GLU	3.8
1	G	69	VAL	3.8
1	Q	237	TRP	3.8
1	J	66	ALA	3.8
1	E	135	LYS	3.8
1	G	143	TYR	3.8
1	G	139	VAL	3.8
1	I	50	PRO	3.8
1	R	19	GLN	3.7

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	F	173	SER	3.7
1	E	176	ASN	3.7
1	E	181	ILE	3.7
1	H	79	ILE	3.7
1	A	174	SER	3.7
1	Q	10	ALA	3.7
1	K	128	ILE	3.7
1	P	181	ILE	3.7
1	L	92	GLU	3.7
1	P	131	GLU	3.7
1	H	153	GLN	3.7
1	K	62	GLN	3.7
1	H	66	ALA	3.7
1	J	33	LYS	3.7
1	J	120	ASN	3.7
1	O	129	GLY	3.7
1	O	79	ILE	3.7
1	D	175	VAL	3.7
1	F	92	GLU	3.7
1	I	138	GLY	3.7
1	D	128	ILE	3.7
1	O	131	GLU	3.7
1	P	257	SER	3.7
1	H	238	ASP	3.7
1	N	170	GLU	3.7
1	P	172	LEU	3.7
1	G	138	GLY	3.6
1	K	173	SER	3.6
1	A	170	GLU	3.6
1	J	143	TYR	3.6
1	P	130	TYR	3.6
1	E	91	ASN	3.6
1	I	234	ARG	3.6
1	F	19	GLN	3.6
1	M	79	ILE	3.6
1	N	210	GLU	3.6
1	O	51	TYR	3.6
1	G	206	TYR	3.6
1	E	243	ALA	3.6
1	I	66	ALA	3.6
1	K	227	LEU	3.6
1	Q	89	LEU	3.6

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	R	138	GLY	3.6
1	O	174	SER	3.6
1	Q	54	SER	3.6
1	E	79	ILE	3.6
1	I	128	ILE	3.6
1	M	244	GLU	3.6
1	R	131	GLU	3.6
1	P	158	ALA	3.6
1	F	72	LEU	3.6
1	N	182	LEU	3.6
1	E	70	THR	3.6
1	P	175	VAL	3.6
1	B	176	ASN	3.5
1	L	79	ILE	3.5
1	J	62	GLN	3.5
1	K	50	PRO	3.5
1	L	227	LEU	3.5
1	B	35	PHE	3.5
1	E	191	PHE	3.5
1	F	59	ALA	3.5
1	F	158	ALA	3.5
1	Q	59	ALA	3.5
1	B	138	GLY	3.5
1	G	70	THR	3.5
1	N	190	VAL	3.5
1	P	176	ASN	3.5
1	E	172	LEU	3.5
1	K	4	ALA	3.5
1	Q	53	ALA	3.5
1	J	169	GLY	3.5
1	K	138	GLY	3.5
1	G	91	ASN	3.5
1	H	156	GLN	3.5
1	J	216	LEU	3.5
1	Q	153	GLN	3.5
1	Q	206	TYR	3.5
1	M	128	ILE	3.5
1	G	186	VAL	3.5
1	K	163	VAL	3.5
1	Q	65	THR	3.5
1	K	79	ILE	3.5
1	N	253	TYR	3.5

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	P	143	TYR	3.5
1	D	77	TRP	3.5
1	K	186	VAL	3.5
1	D	70	THR	3.5
1	F	63	SER	3.5
1	J	3	THR	3.5
1	C	154	LEU	3.5
1	E	2	LEU	3.5
1	B	160	ASN	3.5
1	P	61	PRO	3.5
1	R	61	PRO	3.5
1	L	8	GLU	3.4
1	D	134	VAL	3.4
1	H	174	SER	3.4
1	O	214	LEU	3.4
1	F	97	ARG	3.4
1	N	17	ARG	3.4
1	O	156	GLN	3.4
1	H	120	ASN	3.4
1	R	133	ASN	3.4
1	K	105	VAL	3.4
1	L	123	VAL	3.4
1	P	155	ASP	3.4
1	M	180	THR	3.4
1	D	73	LYS	3.4
1	P	128	ILE	3.4
1	H	24	LEU	3.4
1	N	213	MET	3.4
1	E	155	ASP	3.4
1	L	215	CYS	3.4
1	K	234	ARG	3.4
1	G	135	LYS	3.4
1	C	214	LEU	3.4
1	B	163	VAL	3.4
1	F	38	VAL	3.4
1	N	101	GLU	3.4
1	R	173	SER	3.4
1	R	155	ASP	3.4
1	Q	215	CYS	3.4
1	L	5	PRO	3.4
1	R	10	ALA	3.4
1	E	186	VAL	3.4

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	I	173	SER	3.4
1	C	92	GLU	3.4
1	F	65	THR	3.4
1	H	34	ILE	3.4
1	J	34	ILE	3.4
1	Q	72	LEU	3.4
1	Q	200	LEU	3.4
1	G	178	SER	3.4
1	P	208	SER	3.4
1	Q	178	SER	3.4
1	G	234	ARG	3.4
1	F	124	GLU	3.3
1	G	79	ILE	3.3
1	P	119	ALA	3.3
1	P	209	ASN	3.3
1	K	205	GLY	3.3
1	Q	21	TYR	3.3
1	M	210	GLU	3.3
1	K	114	GLN	3.3
1	N	80	PRO	3.3
1	E	36	VAL	3.3
1	E	162	ARG	3.3
1	P	91	ASN	3.3
1	E	128	ILE	3.3
1	D	210	GLU	3.3
1	G	26	HIS	3.3
1	P	3	THR	3.3
1	G	80	PRO	3.3
1	N	243	ALA	3.3
1	D	79	ILE	3.3
1	J	174	SER	3.3
1	J	220	ILE	3.3
1	D	143	TYR	3.3
1	H	253	TYR	3.3
1	F	156	GLN	3.3
1	P	187	GLN	3.3
1	O	59	ALA	3.3
1	P	183	SER	3.3
1	Q	63	SER	3.3
1	D	130	TYR	3.3
1	F	8	GLU	3.3
1	J	156	GLN	3.3

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	B	182	LEU	3.3
1	J	105	VAL	3.3
1	L	34	ILE	3.3
1	P	162	ARG	3.3
1	B	74	ASP	3.3
1	G	63	SER	3.3
1	Q	190	VAL	3.3
1	M	176	ASN	3.3
1	C	13	THR	3.3
1	C	170	GLU	3.3
1	D	215	CYS	3.3
1	H	62	GLN	3.3
1	N	214	LEU	3.2
1	E	76	ARG	3.2
1	P	76	ARG	3.2
1	C	123	VAL	3.2
1	J	238	ASP	3.2
1	F	3	THR	3.2
1	D	185	GLU	3.2
1	E	131	GLU	3.2
1	G	132	SER	3.2
1	N	123	VAL	3.2
1	C	182	LEU	3.2
1	H	143	TYR	3.2
1	F	62	GLN	3.2
1	H	226	PHE	3.2
1	G	61	PRO	3.2
1	H	173	SER	3.2
1	R	217	MET	3.2
1	M	161	LEU	3.2
1	M	227	LEU	3.2
1	P	129	GLY	3.2
1	R	89	LEU	3.2
1	O	70	THR	3.2
1	E	226	PHE	3.2
1	F	21	TYR	3.2
1	G	220	ILE	3.2
1	Q	158	ALA	3.2
1	G	173	SER	3.2
1	J	26	HIS	3.2
1	O	34	ILE	3.2
1	Q	184	TYR	3.2

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	J	131	GLU	3.2
1	I	26	HIS	3.2
1	R	26	HIS	3.2
1	E	182	LEU	3.2
1	E	171	ILE	3.2
1	G	128	ILE	3.2
1	J	78	PHE	3.2
1	N	145	GLY	3.2
1	M	160	ASN	3.2
1	H	21	TYR	3.2
1	F	29	ALA	3.2
1	J	224	VAL	3.2
1	K	52	PRO	3.2
1	P	214	LEU	3.2
1	A	34	ILE	3.1
1	F	191	PHE	3.1
1	E	213	MET	3.1
1	F	120	ASN	3.1
1	P	213	MET	3.1
1	J	21	TYR	3.1
1	L	101	GLU	3.1
1	N	8	GLU	3.1
1	D	239	LEU	3.1
1	Q	80	PRO	3.1
1	B	179	LYS	3.1
1	H	25	THR	3.1
1	H	104	THR	3.1
1	L	177	THR	3.1
1	C	114	GLN	3.1
1	P	135	LYS	3.1
1	D	91	ASN	3.1
1	K	130	TYR	3.1
1	M	190	VAL	3.1
1	O	215	CYS	3.1
1	P	124	GLU	3.1
1	C	80	PRO	3.1
1	H	78	PHE	3.1
1	P	226	PHE	3.1
1	Q	26	HIS	3.1
1	Q	76	ARG	3.1
1	B	129	GLY	3.1
1	G	179	LYS	3.1

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	Q	3	THR	3.1
1	Q	154	LEU	3.1
1	P	173	SER	3.1
1	R	184	TYR	3.1
1	A	92	GLU	3.1
1	E	61	PRO	3.1
1	M	35	PHE	3.1
1	A	26	HIS	3.1
1	A	205	GLY	3.1
1	E	26	HIS	3.1
1	G	134	VAL	3.1
1	G	204	VAL	3.1
1	M	131	GLU	3.1
1	G	155	ASP	3.1
1	J	135	LYS	3.1
1	E	67	MET	3.1
1	Q	129	GLY	3.1
1	F	178	SER	3.1
1	J	173	SER	3.1
1	D	127	ILE	3.1
1	G	34	ILE	3.1
1	L	188	ALA	3.1
1	P	4	ALA	3.1
1	P	2	LEU	3.1
1	A	138	GLY	3.1
1	E	207	THR	3.1
1	F	25	THR	3.1
1	E	38	VAL	3.0
1	E	119	ALA	3.0
1	E	209	ASN	3.0
1	I	160	ASN	3.0
1	R	206	TYR	3.0
1	H	44	GLU	3.0
1	F	15	MET	3.0
1	P	182	LEU	3.0
1	P	58	THR	3.0
1	Q	128	ILE	3.0
1	H	105	VAL	3.0
1	L	35	PHE	3.0
1	B	241	ASN	3.0
1	N	120	ASN	3.0
1	Q	55	ASN	3.0

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	F	162	ARG	3.0
1	D	131	GLU	3.0
1	O	77	TRP	3.0
1	O	185	GLU	3.0
1	F	220	ILE	3.0
1	R	220	ILE	3.0
1	K	26	HIS	3.0
1	A	215	CYS	3.0
1	F	215	CYS	3.0
1	D	81	LEU	3.0
1	D	90	LEU	3.0
1	G	133	ASN	3.0
1	I	72	LEU	3.0
1	I	172	LEU	3.0
1	R	221	GLU	3.0
1	G	140	GLY	3.0
1	A	177	THR	3.0
1	F	153	GLN	3.0
1	L	186	VAL	3.0
1	M	174	SER	3.0
1	E	158	ALA	3.0
1	Q	214	LEU	3.0
1	R	71	ALA	3.0
1	R	213	MET	3.0
1	R	130	TYR	3.0
1	L	170	GLU	3.0
1	F	211	PRO	3.0
1	R	153	GLN	3.0
1	D	257	SER	3.0
1	G	200	LEU	3.0
1	I	139	VAL	3.0
1	D	160	ASN	3.0
1	O	170	GLU	3.0
1	M	5	PRO	3.0
1	K	33	LYS	3.0
1	Q	220	ILE	3.0
1	L	205	GLY	3.0
1	O	32	GLY	3.0
1	C	116	LEU	3.0
1	F	84	GLN	3.0
1	G	212	VAL	3.0
1	J	45	THR	3.0

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	I	106	ALA	3.0
1	B	143	TYR	2.9
1	I	92	GLU	2.9
1	N	244	GLU	2.9
1	F	200	LEU	2.9
1	M	129	GLY	2.9
1	P	205	GLY	2.9
1	E	134	VAL	2.9
1	N	13	THR	2.9
1	Q	38	VAL	2.9
1	R	178	SER	2.9
1	I	188	ALA	2.9
1	F	74	ASP	2.9
1	L	21	TYR	2.9
1	P	171	ILE	2.9
1	H	160	ASN	2.9
1	C	44	GLU	2.9
1	G	2	LEU	2.9
1	R	200	LEU	2.9
1	D	37	SER	2.9
1	I	105	VAL	2.9
1	N	162	ARG	2.9
1	R	204	VAL	2.9
1	A	53	ALA	2.9
1	R	59	ALA	2.9
1	L	155	ASP	2.9
1	L	200	LEU	2.9
1	R	214	LEU	2.9
1	G	35	PHE	2.9
1	G	221	GLU	2.9
1	B	93	ARG	2.9
1	F	54	SER	2.9
1	F	114	GLN	2.9
1	F	190	VAL	2.9
1	K	169	GLY	2.9
1	Q	126	SER	2.9
1	A	188	ALA	2.9
1	C	53	ALA	2.9
1	L	135	LYS	2.9
1	D	156	GLN	2.9
1	F	132	SER	2.9
1	J	32	GLY	2.9

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	A	135	LYS	2.9
1	P	117	THR	2.9
1	F	188	ALA	2.9
1	K	53	ALA	2.9
1	O	127	ILE	2.9
1	R	128	ILE	2.9
1	G	90	LEU	2.9
1	J	24	LEU	2.9
1	Q	236	LEU	2.9
1	P	253	TYR	2.9
1	D	74	ASP	2.9
1	L	241	ASN	2.9
1	Q	74	ASP	2.9
1	G	37	SER	2.9
1	M	126	SER	2.9
1	O	69	VAL	2.9
1	R	32	GLY	2.9
1	R	139	VAL	2.9
1	C	243	ALA	2.9
1	D	34	ILE	2.9
1	K	172	LEU	2.9
1	O	182	LEU	2.9
1	M	74	ASP	2.8
1	Q	92	GLU	2.9
1	F	186	VAL	2.8
1	N	138	GLY	2.8
1	O	47	GLN	2.8
1	O	9	ALA	2.8
1	P	80	PRO	2.8
1	J	215	CYS	2.8
1	E	257	SER	2.8
1	J	160	ASN	2.8
1	K	123	VAL	2.8
1	R	174	SER	2.8
1	C	138	GLY	2.8
1	E	72	LEU	2.8
1	H	216	LEU	2.8
1	J	151	GLN	2.8
1	K	181	ILE	2.8
1	Q	172	LEU	2.8
1	B	177	THR	2.8
1	G	119	ALA	2.8

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	L	148	ALA	2.8
1	E	5	PRO	2.8
1	I	130	TYR	2.8
1	R	211	PRO	2.8
1	E	55	ASN	2.8
1	F	236	LEU	2.8
1	L	146	ILE	2.8
1	O	91	ASN	2.8
1	P	186	VAL	2.8
1	O	138	GLY	2.8
1	D	233	ASP	2.8
1	G	230	ASP	2.8
1	J	236	LEU	2.8
1	M	182	LEU	2.8
1	C	190	VAL	2.8
1	G	174	SER	2.8
1	N	175	VAL	2.8
1	R	132	SER	2.8
1	F	165	ASN	2.8
1	L	138	GLY	2.8
1	M	44	GLU	2.8
1	G	66	ALA	2.8
1	F	73	LYS	2.8
1	B	227	LEU	2.8
1	D	182	LEU	2.8
1	I	51	TYR	2.8
1	J	186	VAL	2.8
1	P	184	TYR	2.8
1	A	32	GLY	2.8
1	K	92	GLU	2.8
1	K	210	GLU	2.8
1	Q	165	ASN	2.8
1	E	122	MET	2.8
1	J	104	THR	2.8
1	J	213	MET	2.8
1	R	3	THR	2.8
1	C	33	LYS	2.8
1	O	33	LYS	2.8
1	M	43	ASP	2.8
1	Q	162	ARG	2.8
1	Q	185	GLU	2.8
1	Q	191	PHE	2.8

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	A	241	ASN	2.8
1	H	3	THR	2.8
1	I	13	THR	2.8
1	L	53	ALA	2.8
1	M	33	LYS	2.8
1	B	161	LEU	2.7
1	F	14	LEU	2.7
1	F	24	LEU	2.7
1	R	181	ILE	2.7
1	C	54	SER	2.7
1	R	37	SER	2.7
1	N	156	GLN	2.7
1	R	21	TYR	2.7
1	B	244	GLU	2.7
1	P	66	ALA	2.7
1	E	17	ARG	2.7
1	N	116	LEU	2.7
1	N	161	LEU	2.7
1	O	90	LEU	2.7
1	F	26	HIS	2.7
1	G	126	SER	2.7
1	O	134	VAL	2.7
1	D	44	GLU	2.7
1	G	236	LEU	2.7
1	J	53	ALA	2.7
1	R	236	LEU	2.7
1	F	55	ASN	2.7
1	G	105	VAL	2.7
1	H	213	MET	2.7
1	J	77	TRP	2.7
1	P	179	LYS	2.7
1	Q	22	LYS	2.7
1	P	191	PHE	2.7
1	N	47	GLN	2.7
1	R	140	GLY	2.7
1	A	131	GLU	2.7
1	H	220	ILE	2.7
1	I	3	THR	2.7
1	P	55	ASN	2.7
1	R	91	ASN	2.7
1	H	26	HIS	2.7
1	F	37	SER	2.7

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	G	175	VAL	2.7
1	M	214	LEU	2.7
1	Q	211	PRO	2.7
1	R	172	LEU	2.7
1	G	189	GLY	2.7
1	H	53	ALA	2.7
1	J	162	ARG	2.7
1	I	220	ILE	2.7
1	Q	232	ILE	2.7
1	G	82	GLU	2.7
1	I	210	GLU	2.7
1	E	22	LYS	2.7
1	G	49	LYS	2.7
1	C	212	VAL	2.7
1	G	156	GLN	2.7
1	L	74	ASP	2.7
1	R	230	ASP	2.7
1	I	32	GLY	2.7
1	L	189	GLY	2.7
1	B	150	THR	2.7
1	P	185	GLU	2.7
1	Q	221	GLU	2.7
1	Q	176	ASN	2.7
1	A	15	MET	2.7
1	C	35	PHE	2.7
1	B	216	LEU	2.7
1	H	224	VAL	2.6
1	I	190	VAL	2.6
1	J	204	VAL	2.6
1	P	134	VAL	2.6
1	B	5	PRO	2.6
1	C	211	PRO	2.6
1	R	76	ARG	2.6
1	B	230	ASP	2.6
1	R	145	GLY	2.6
1	B	130	TYR	2.6
1	I	143	TYR	2.6
1	B	101	GLU	2.6
1	G	92	GLU	2.6
1	A	190	VAL	2.6
1	F	123	VAL	2.6
1	D	17	ARG	2.6

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	D	181	ILE	2.6
1	F	146	ILE	2.6
1	R	50	PRO	2.6
1	G	59	ALA	2.6
1	Q	29	ALA	2.6
1	F	22	LYS	2.6
1	H	179	LYS	2.6
1	O	73	LYS	2.6
1	Q	140	GLY	2.6
1	G	21	TYR	2.6
1	J	253	TYR	2.6
1	M	143	TYR	2.6
1	R	150	THR	2.6
1	R	253	TYR	2.6
1	O	8	GLU	2.6
1	F	214	LEU	2.6
1	I	55	ASN	2.6
1	C	162	ARG	2.6
1	H	215	CYS	2.6
1	C	205	GLY	2.6
1	N	32	GLY	2.6
1	R	66	ALA	2.6
1	E	253	TYR	2.6
1	K	116	LEU	2.6
1	M	236	LEU	2.6
1	N	65	THR	2.6
1	D	43	ASP	2.6
1	Q	24	LEU	2.6
1	A	8	GLU	2.6
1	N	91	ASN	2.6
1	O	120	ASN	2.6
1	A	146	ILE	2.6
1	B	190	VAL	2.6
1	H	127	ILE	2.6
1	K	139	VAL	2.6
1	E	73	LYS	2.6
1	A	50	PRO	2.6
1	L	187	GLN	2.6
1	A	213	MET	2.6
1	E	86	LEU	2.6
1	A	21	TYR	2.6
1	C	130	TYR	2.6

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	E	124	GLU	2.6
1	K	131	GLU	2.6
1	C	209	ASN	2.6
1	C	175	VAL	2.6
1	R	17	ARG	2.6
1	D	33	LYS	2.6
1	B	200	LEU	2.6
1	C	52	PRO	2.6
1	E	14	LEU	2.6
1	F	80	PRO	2.6
1	F	172	LEU	2.6
1	I	5	PRO	2.6
1	I	119	ALA	2.6
1	J	64	ALA	2.6
1	Q	66	ALA	2.6
1	J	46	GLY	2.6
1	L	26	HIS	2.6
1	N	202	GLY	2.6
1	F	35	PHE	2.6
1	K	215	CYS	2.6
1	N	177	THR	2.6
1	A	79	ILE	2.6
1	C	101	GLU	2.6
1	C	244	GLU	2.6
1	F	126	SER	2.6
1	G	181	ILE	2.6
1	N	115	SER	2.6
1	A	186	VAL	2.6
1	D	123	VAL	2.6
1	D	133	ASN	2.6
1	F	49	LYS	2.6
1	Q	179	LYS	2.6
1	E	214	LEU	2.6
1	J	154	LEU	2.6
1	L	214	LEU	2.6
1	P	67	MET	2.6
1	G	19	GLN	2.6
1	K	188	ALA	2.6
1	N	53	ALA	2.6
1	B	3	THR	2.5
1	C	65	THR	2.5
1	G	177	THR	2.5

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	G	253	TYR	2.5
1	D	221	GLU	2.5
1	K	132	SER	2.5
1	M	173	SER	2.5
1	P	7	LYS	2.5
1	H	134	VAL	2.5
1	R	134	VAL	2.5
1	I	176	ASN	2.5
1	K	230	ASP	2.5
1	N	74	ASP	2.5
1	R	116	LEU	2.5
1	O	213	MET	2.5
1	H	64	ALA	2.5
1	K	246	GLN	2.5
1	M	191	PHE	2.5
1	E	145	GLY	2.5
1	L	125	GLY	2.5
1	R	85	GLY	2.5
1	G	171	ILE	2.5
1	D	7	LYS	2.5
1	D	253	TYR	2.5
1	P	152	TYR	2.5
1	B	126	SER	2.5
1	G	76	ARG	2.5
1	M	93	ARG	2.5
1	Q	134	VAL	2.5
1	R	186	VAL	2.5
1	P	19	GLN	2.5
1	H	46	GLY	2.5
1	N	34	ILE	2.5
1	N	157	ILE	2.5
1	K	58	THR	2.5
1	M	177	THR	2.5
1	B	82	GLU	2.5
1	E	44	GLU	2.5
1	G	214	LEU	2.5
1	H	131	GLU	2.5
1	I	81	LEU	2.5
1	P	86	LEU	2.5
1	L	213	MET	2.5
1	D	125	GLY	2.5
1	G	46	GLY	2.5

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	G	129	GLY	2.5
1	K	7	LYS	2.5
1	C	70	THR	2.5
1	K	13	THR	2.5
1	O	3	THR	2.5
1	J	116	LEU	2.5
1	J	172	LEU	2.5
1	M	253	TYR	2.5
1	N	167	SER	2.5
1	F	105	VAL	2.5
1	H	204	VAL	2.5
1	J	69	VAL	2.5
1	N	124	GLU	2.5
1	A	55	ASN	2.5
1	E	233	ASP	2.5
1	G	188	ALA	2.5
1	K	81	LEU	2.5
1	O	180	THR	2.5
1	P	178	SER	2.5
1	R	136	SER	2.5
1	C	163	VAL	2.5
1	M	163	VAL	2.5
1	I	131	GLU	2.5
1	P	244	GLU	2.5
1	O	133	ASN	2.5
1	R	120	ASN	2.5
1	F	66	ALA	2.5
1	J	114	GLN	2.5
1	K	219	ALA	2.5
1	A	5	PRO	2.5
1	D	5	PRO	2.5
1	H	68	LEU	2.5
1	H	116	LEU	2.5
1	I	2	LEU	2.5
1	I	17	ARG	2.5
1	C	115	SER	2.5
1	C	173	SER	2.5
1	O	143	TYR	2.5
1	E	92	GLU	2.4
1	E	179	LYS	2.4
1	O	244	GLU	2.4
1	F	18	ALA	2.4

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	C	2	LEU	2.4
1	H	214	LEU	2.4
1	G	17	ARG	2.4
1	I	52	PRO	2.4
1	P	5	PRO	2.4
1	P	6	PRO	2.4
1	F	189	GLY	2.4
1	L	145	GLY	2.4
1	A	74	ASP	2.4
1	Q	256	MET	2.4
1	L	190	VAL	2.4
1	O	221	GLU	2.4
1	R	146	ILE	2.4
1	A	11	ARG	2.4
1	B	83	ARG	2.4
1	C	91	ASN	2.4
1	D	176	ASN	2.4
1	E	188	ALA	2.4
1	F	154	LEU	2.4
1	N	237	TRP	2.4
1	K	106	ALA	2.4
1	R	29	ALA	2.4
1	N	52	PRO	2.4
1	P	122	MET	2.4
1	E	178	SER	2.4
1	H	132	SER	2.4
1	O	74	ASP	2.4
1	C	143	TYR	2.4
1	E	215	CYS	2.4
1	N	121	ILE	2.4
1	O	227	LEU	2.4
1	R	182	LEU	2.4
1	P	165	ASN	2.4
1	E	7	LYS	2.4
1	G	3	THR	2.4
1	J	117	THR	2.4
1	Q	73	LYS	2.4
1	A	123	VAL	2.4
1	I	48	PHE	2.4
1	J	134	VAL	2.4
1	O	233	ASP	2.4
1	D	39	TYR	2.4

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	K	51	TYR	2.4
1	P	26	HIS	2.4
1	Q	244	GLU	2.4
1	D	76	ARG	2.4
1	H	76	ARG	2.4
1	B	247	ASN	2.4
1	C	49	LYS	2.4
1	E	33	LYS	2.4
1	M	145	GLY	2.4
1	E	183	SER	2.4
1	G	25	THR	2.4
1	I	163	VAL	2.4
1	B	95	ILE	2.4
1	D	214	LEU	2.4
1	J	89	LEU	2.4
1	M	200	LEU	2.4
1	P	200	LEU	2.4
1	H	92	GLU	2.4
1	M	19	GLN	2.4
1	D	120	ASN	2.4
1	J	16	PRO	2.4
1	M	179	LYS	2.4
1	P	73	LYS	2.4
1	K	102	ASN	2.4
1	K	160	ASN	2.4
1	B	174	SER	2.4
1	Q	35	PHE	2.4
1	E	105	VAL	2.4
1	F	134	VAL	2.4
1	G	68	LEU	2.4
1	J	68	LEU	2.4
1	Q	15	MET	2.4
1	L	66	ALA	2.4
1	P	92	GLU	2.4
1	P	221	GLU	2.4
1	Q	62	GLN	2.3
1	R	42	GLN	2.3
1	M	241	ASN	2.3
1	O	37	SER	2.3
1	G	216	LEU	2.3
1	H	154	LEU	2.3
1	D	65	THR	2.3

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	J	175	VAL	2.3
1	J	190	VAL	2.3
1	P	25	THR	2.3
1	Q	175	VAL	2.3
1	O	76	ARG	2.3
1	D	122	MET	2.3
1	A	155	ASP	2.3
1	J	23	ASP	2.3
1	J	155	ASP	2.3
1	Q	49	LYS	2.3
1	A	141	ALA	2.3
1	A	148	ALA	2.3
1	D	9	ALA	2.3
1	M	8	GLU	2.3
1	O	101	GLU	2.3
1	P	10	ALA	2.3
1	Q	131	GLU	2.3
1	G	78	PHE	2.3
1	H	257	SER	2.3
1	I	79	ILE	2.3
1	J	126	SER	2.3
1	E	120	ASN	2.3
1	H	133	ASN	2.3
1	K	55	ASN	2.3
1	L	55	ASN	2.3
1	B	204	VAL	2.3
1	H	117	THR	2.3
1	K	190	VAL	2.3
1	O	45	THR	2.3
1	P	105	VAL	2.3
1	H	97	ARG	2.3
1	M	83	ARG	2.3
1	R	162	ARG	2.3
1	H	135	LYS	2.3
1	J	49	LYS	2.3
1	P	39	TYR	2.3
1	I	219	ALA	2.3
1	O	188	ALA	2.3
1	A	156	GLN	2.3
1	C	8	GLU	2.3
1	D	244	GLU	2.3
1	M	187	GLN	2.3

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	P	101	GLU	2.3
1	Q	248	ASP	2.3
1	C	161	LEU	2.3
1	D	171	ILE	2.3
1	E	236	LEU	2.3
1	I	113	LEU	2.3
1	N	35	PHE	2.3
1	H	126	SER	2.3
1	L	50	PRO	2.3
1	G	190	VAL	2.3
1	I	159	VAL	2.3
1	L	176	ASN	2.3
1	N	163	VAL	2.3
1	Q	166	VAL	2.3
1	B	25	THR	2.3
1	F	67	MET	2.3
1	I	215	CYS	2.3
1	K	97	ARG	2.3
1	K	162	ARG	2.3
1	E	130	TYR	2.3
1	A	187	GLN	2.3
1	C	236	LEU	2.3
1	Q	243	ALA	2.3
1	R	90	LEU	2.3
1	R	119	ALA	2.3
1	K	34	ILE	2.3
1	R	35	PHE	2.3
1	L	185	GLU	2.3
1	D	173	SER	2.3
1	R	126	SER	2.3
1	H	145	GLY	2.3
1	Q	204	VAL	2.3
1	B	91	ASN	2.3
1	E	165	ASN	2.3
1	J	133	ASN	2.3
1	O	176	ASN	2.3
1	E	256	MET	2.3
1	G	77	TRP	2.3
1	I	97	ARG	2.3
1	E	116	LEU	2.3
1	B	66	ALA	2.3
1	C	18	ALA	2.3

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	Q	253	TYR	2.3
1	B	170	GLU	2.3
1	R	92	GLU	2.3
1	J	183	SER	2.3
1	G	50	PRO	2.3
1	Q	135	LYS	2.3
1	R	179	LYS	2.3
1	D	3	THR	2.3
1	E	160	ASN	2.3
1	F	88	ASN	2.3
1	K	133	ASN	2.3
1	P	17	ARG	2.3
1	A	41	ILE	2.3
1	P	157	ILE	2.3
1	B	64	ALA	2.3
1	K	10	ALA	2.3
1	K	21	TYR	2.3
1	Q	188	ALA	2.3
1	L	62	GLN	2.3
1	P	84	GLN	2.3
1	C	210	GLU	2.3
1	E	8	GLU	2.3
1	G	124	GLU	2.3
1	P	126	SER	2.3
1	C	145	GLY	2.3
1	F	175	VAL	2.3
1	H	139	VAL	2.3
1	H	190	VAL	2.3
1	O	123	VAL	2.3
1	P	52	PRO	2.3
1	P	123	VAL	2.3
1	H	23	ASP	2.3
1	L	230	ASP	2.3
1	P	74	ASP	2.3
1	C	25	THR	2.2
1	E	102	ASN	2.2
1	P	104	THR	2.2
1	Q	209	ASN	2.2
1	C	237	TRP	2.2
1	K	127	ILE	2.2
1	Q	146	ILE	2.2
1	M	64	ALA	2.2

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	O	173	SER	2.2
1	R	49	LYS	2.2
1	F	185	GLU	2.2
1	A	139	VAL	2.2
1	P	137	GLY	2.2
1	F	233	ASP	2.2
1	I	104	THR	2.2
1	I	117	THR	2.2
1	J	180	THR	2.2
1	J	233	ASP	2.2
1	O	81	LEU	2.2
1	G	165	ASN	2.2
1	B	34	ILE	2.2
1	R	34	ILE	2.2
1	R	171	ILE	2.2
1	B	188	ALA	2.2
1	K	64	ALA	2.2
1	E	153	GLN	2.2
1	I	33	LYS	2.2
1	M	246	GLN	2.2
1	O	39	TYR	2.2
1	L	217	MET	2.2
1	A	204	VAL	2.2
1	F	244	GLU	2.2
1	G	11	ARG	2.2
1	J	17	ARG	2.2
1	J	124	GLU	2.2
1	E	200	LEU	2.2
1	K	129	GLY	2.2
1	G	215	CYS	2.2
1	Q	2	LEU	2.2
1	H	45	THR	2.2
1	O	160	ASN	2.2
1	B	33	LYS	2.2
1	F	179	LYS	2.2
1	H	77	TRP	2.2
1	I	71	ALA	2.2
1	M	188	ALA	2.2
1	F	151	GLN	2.2
1	Q	151	GLN	2.2
1	E	126	SER	2.2
1	I	213	MET	2.2

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	P	132	SER	2.2
1	Q	37	SER	2.2
1	C	134	VAL	2.2
1	A	189	GLY	2.2
1	F	221	GLU	2.2
1	J	166	VAL	2.2
1	N	211	PRO	2.2
1	Q	147	GLY	2.2
1	R	16	PRO	2.2
1	H	249	ILE	2.2
1	J	127	ILE	2.2
1	M	157	ILE	2.2
1	P	13	THR	2.2
1	C	230	ASP	2.2
1	J	179	LYS	2.2
1	K	155	ASP	2.2
1	P	102	ASN	2.2
1	P	160	ASN	2.2
1	R	176	ASN	2.2
1	H	9	ALA	2.2
1	N	18	ALA	2.2
1	R	53	ALA	2.2
1	H	151	GLN	2.2
1	K	218	SER	2.2
1	L	156	GLN	2.2
1	Q	84	GLN	2.2
1	Q	213	MET	2.2
1	A	162	ARG	2.2
1	D	227	LEU	2.2
1	G	116	LEU	2.2
1	I	76	ARG	2.2
1	R	227	LEU	2.2
1	J	44	GLU	2.2
1	C	121	ILE	2.2
1	J	146	ILE	2.2
1	M	211	PRO	2.2
1	N	226	PHE	2.2
1	D	22	LYS	2.2
1	I	133	ASN	2.2
1	L	108	ASN	2.2
1	G	219	ALA	2.2
1	N	66	ALA	2.2

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	G	162	ARG	2.2
1	J	37	SER	2.2
1	P	116	LEU	2.2
1	P	246	GLN	2.2
1	B	253	TYR	2.2
1	H	51	TYR	2.2
1	I	21	TYR	2.2
1	Q	123	VAL	2.2
1	A	101	GLU	2.2
1	G	205	GLY	2.2
1	K	82	GLU	2.2
1	P	145	GLY	2.2
1	A	58	THR	2.2
1	C	45	THR	2.2
1	L	133	ASN	2.2
1	E	118	ALA	2.1
1	F	119	ALA	2.1
1	G	182	LEU	2.2
1	H	119	ALA	2.1
1	N	154	LEU	2.2
1	P	72	LEU	2.2
1	C	74	ASP	2.1
1	M	153	GLN	2.1
1	O	162	ARG	2.1
1	N	77	TRP	2.1
1	F	204	VAL	2.1
1	G	130	TYR	2.1
1	B	205	GLY	2.1
1	K	48	PHE	2.1
1	N	205	GLY	2.1
1	Q	235	GLY	2.1
1	G	150	THR	2.1
1	K	72	LEU	2.1
1	F	209	ASN	2.1
1	F	76	ARG	2.1
1	H	93	ARG	2.1
1	B	26	HIS	2.1
1	N	26	HIS	2.1
1	R	156	GLN	2.1
1	B	149	ASP	2.1
1	G	166	VAL	2.1
1	H	166	VAL	2.1

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	J	249	ILE	2.1
1	E	94	LYS	2.1
1	J	206	TYR	2.1
1	N	33	LYS	2.1
1	N	130	TYR	2.1
1	O	253	TYR	2.1
1	P	206	TYR	2.1
1	A	103	GLY	2.1
1	B	202	GLY	2.1
1	C	124	GLU	2.1
1	G	16	PRO	2.1
1	I	70	THR	2.1
1	J	25	THR	2.1
1	P	14	LEU	2.1
1	P	236	LEU	2.1
1	A	209	ASN	2.1
1	B	99	ALA	2.1
1	G	229	ASN	2.1
1	H	17	ARG	2.1
1	H	55	ASN	2.1
1	K	76	ARG	2.1
1	D	218	SER	2.1
1	P	37	SER	2.1
1	I	153	GLN	2.1
1	A	7	LYS	2.1
1	H	69	VAL	2.1
1	J	123	VAL	2.1
1	R	190	VAL	2.1
1	O	155	ASP	2.1
1	F	169	GLY	2.1
1	E	211	PRO	2.1
1	K	5	PRO	2.1
1	A	2	LEU	2.1
1	B	44	GLU	2.1
1	K	2	LEU	2.1
1	O	239	LEU	2.1
1	K	117	THR	2.1
1	J	76	ARG	2.1
1	N	76	ARG	2.1
1	R	234	ARG	2.1
1	G	120	ASN	2.1
1	J	108	ASN	2.1

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	K	257	SER	2.1
1	N	187	GLN	2.1
1	C	159	VAL	2.1
1	K	204	VAL	2.1
1	Q	105	VAL	2.1
1	R	166	VAL	2.1
1	E	152	TYR	2.1
1	G	39	TYR	2.1
1	J	202	GLY	2.1
1	L	2	LEU	2.1
1	N	189	GLY	2.1
1	R	2	LEU	2.1
1	F	61	PRO	2.1
1	K	213	MET	2.1
1	O	5	PRO	2.1
1	N	158	ALA	2.1
1	Q	33	LYS	2.1
1	I	84	GLN	2.1
1	J	88	ASN	2.1
1	K	42	GLN	2.1
1	M	186	VAL	2.1
1	G	172	LEU	2.1
1	F	140	GLY	2.1
1	M	130	TYR	2.1
1	N	39	TYR	2.1
1	O	21	TYR	2.1
1	Q	85	GLY	2.1
1	P	12	PRO	2.1
1	M	185	GLU	2.1
1	N	92	GLU	2.1
1	R	7	LYS	2.1
1	I	53	ALA	2.1
1	I	132	SER	2.1
1	N	126	SER	2.1
1	A	35	PHE	2.1
1	B	19	GLN	2.1
1	F	187	GLN	2.1
1	F	226	PHE	2.1
1	J	226	PHE	2.1
1	N	114	GLN	2.1
1	O	241	ASN	2.1
1	Q	19	GLN	2.1

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	Q	100	GLN	2.1
1	F	2	LEU	2.1
1	K	159	VAL	2.1
1	K	166	VAL	2.1
1	M	213	MET	2.1
1	A	145	GLY	2.0
1	F	51	TYR	2.0
1	G	169	GLY	2.0
1	J	205	GLY	2.0
1	R	39	TYR	2.0
1	R	129	GLY	2.0
1	F	45	THR	2.0
1	K	104	THR	2.0
1	N	45	THR	2.0
1	Q	58	THR	2.0
1	R	177	THR	2.0
1	J	128	ILE	2.0
1	N	249	ILE	2.0
1	A	257	SER	2.0
1	M	257	SER	2.0
1	N	9	ALA	2.0
1	G	191	PHE	2.0
1	P	56	PHE	2.0
1	B	62	GLN	2.0
1	B	151	GLN	2.0
1	C	47	GLN	2.0
1	D	68	LEU	2.0
1	M	216	LEU	2.0
1	Q	224	VAL	2.0
1	R	105	VAL	2.0
1	C	55	ASN	2.0
1	D	169	GLY	2.0
1	D	189	GLY	2.0
1	B	211	PRO	2.0
1	B	121	ILE	2.0
1	D	245	ARG	2.0
1	J	211	PRO	2.0
1	O	179	LYS	2.0
1	K	150	THR	2.0
1	N	25	THR	2.0
1	L	82	GLU	2.0
1	L	233	ASP	2.0

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	O	92	GLU	2.0
1	A	113	LEU	2.0
1	G	71	ALA	2.0
1	G	257	SER	2.0
1	R	216	LEU	2.0
1	R	257	SER	2.0
1	B	153	GLN	2.0
1	E	84	GLN	2.0
1	J	36	VAL	2.0
1	O	84	GLN	2.0
1	P	204	VAL	2.0
1	O	102	ASN	2.0
1	P	247	ASN	2.0
1	Q	120	ASN	2.0
1	C	135	LYS	2.0
1	L	202	GLY	2.0
1	G	211	PRO	2.0
1	J	6	PRO	2.0
1	R	142	ARG	2.0
1	E	104	THR	2.0
1	G	65	THR	2.0
1	O	65	THR	2.0
1	Q	177	THR	2.0
1	P	170	GLU	2.0
1	G	74	ASP	2.0
1	J	141	ALA	2.0
1	Q	148	ALA	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](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.