



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 02:35 PM GMT

PDB ID : 3ZWJ
Title : CRYSTAL STRUCTURE OF THE PORE-FORMING TOXIN FRAC FROM ACTINIA FRAGACEA (Form 3)
Authors : Mechaly, A.E.; Bellomioa, A.; Morantea, K.; Gonzalez-Manas, J.M.; Guerin, D.M.A.
Deposited on : 2011-08-01
Resolution : 2.37 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
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467
Mogul : 1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026688
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

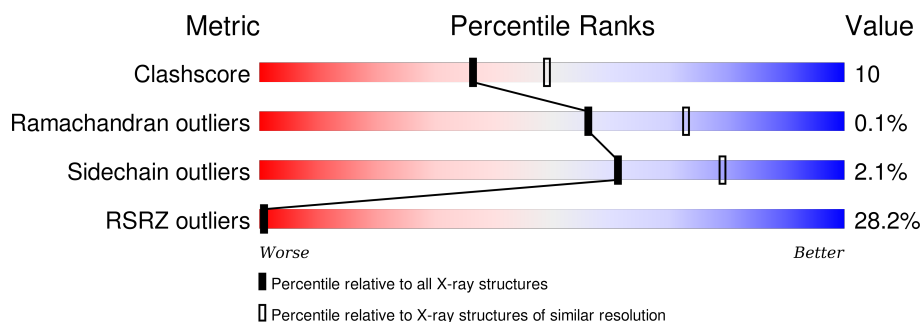
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.37 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))
Clashscore	102246	4595 (2.40-2.36)
Ramachandran outliers	100387	4520 (2.40-2.36)
Sidechain outliers	100360	4522 (2.40-2.36)
RSRZ outliers	91569	4034 (2.40-2.36)

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 on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. 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	179	<div> <div>3%</div> <div>83%</div> <div>15%</div> <div>..</div> </div>
1	B	179	<div> <div>6%</div> <div>79%</div> <div>18%</div> <div>..</div> </div>
1	C	179	<div> <div>4%</div> <div>80%</div> <div>17%</div> <div>..</div> </div>
1	D	179	<div> <div>5%</div> <div>82%</div> <div>16%</div> <div>..</div> </div>
1	E	179	<div> <div>5%</div> <div>79%</div> <div>19%</div> <div>..</div> </div>
1	F	179	<div> <div>6%</div> <div>83%</div> <div>15%</div> <div>..</div> </div>
1	G	179	<div> <div>72%</div> <div>80%</div> <div>18%</div> <div>..</div> </div>

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
1	H	179	<div><div></div><div>79%</div><div></div><div>19%</div><div>..</div></div>
1	I	179	<div><div></div><div>72%</div><div></div><div>20%</div><div>..</div></div>

2 Entry composition [i](#)

There are 2 unique types of molecules in this entry. The entry contains 12794 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 FRAGACEATOXIN C.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	177	Total	C	N	O	S	0	0	0
			1384	880	249	251	4			
1	B	177	Total	C	N	O	S	0	0	0
			1384	880	249	251	4			
1	C	177	Total	C	N	O	S	0	0	0
			1384	880	249	251	4			
1	D	177	Total	C	N	O	S	0	0	0
			1384	880	249	251	4			
1	E	177	Total	C	N	O	S	0	0	0
			1384	880	249	251	4			
1	F	177	Total	C	N	O	S	0	0	0
			1384	880	249	251	4			
1	G	177	Total	C	N	O	S	0	0	0
			1384	880	249	251	4			
1	H	177	Total	C	N	O	S	0	0	0
			1384	880	249	251	4			
1	I	177	Total	C	N	O	S	0	0	0
			1384	880	249	251	4			

- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	54	Total	O	0	0
			54	54		
2	B	46	Total	O	0	0
			46	46		
2	C	42	Total	O	0	0
			42	42		
2	D	42	Total	O	0	0
			42	42		
2	E	38	Total	O	0	0
			38	38		

Continued on next page...

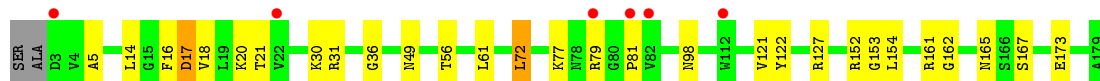
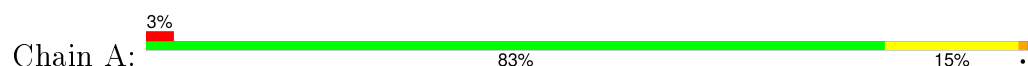
Continued from previous page...

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	F	39	Total 39	O 39	0	0
2	G	26	Total 26	O 26	0	0
2	H	20	Total 20	O 20	0	0
2	I	31	Total 31	O 31	0	0

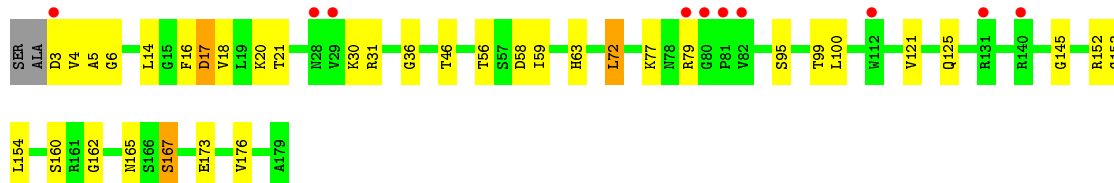
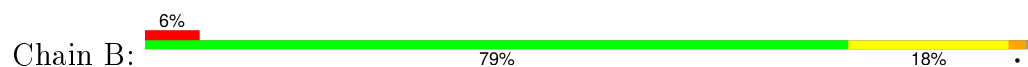
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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.

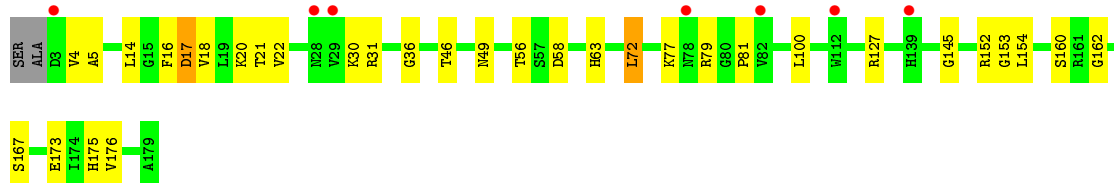
- Molecule 1: FRAGACEATOXIN C



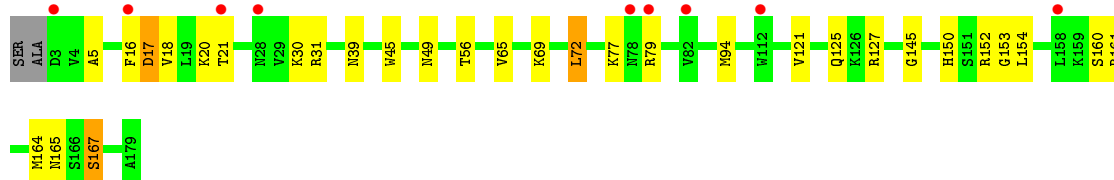
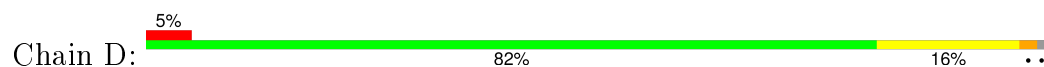
- Molecule 1: FRAGACEATOXIN C



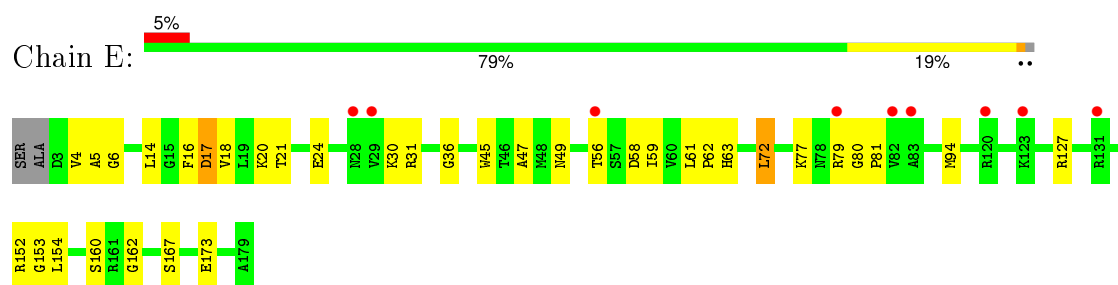
- Molecule 1: FRAGACEATOXIN C



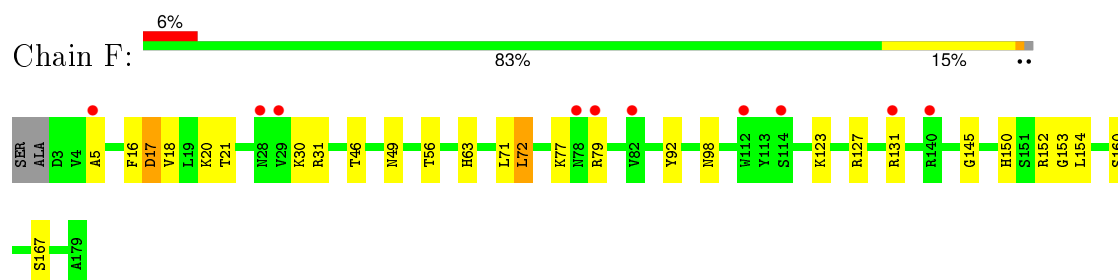
- Molecule 1: FRAGACEATOXIN C



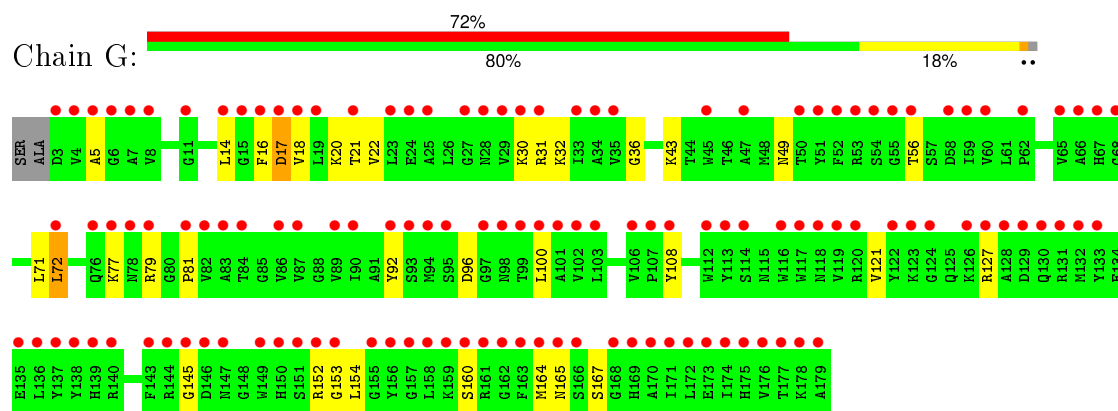
- Molecule 1: FRAGACEATOXIN C



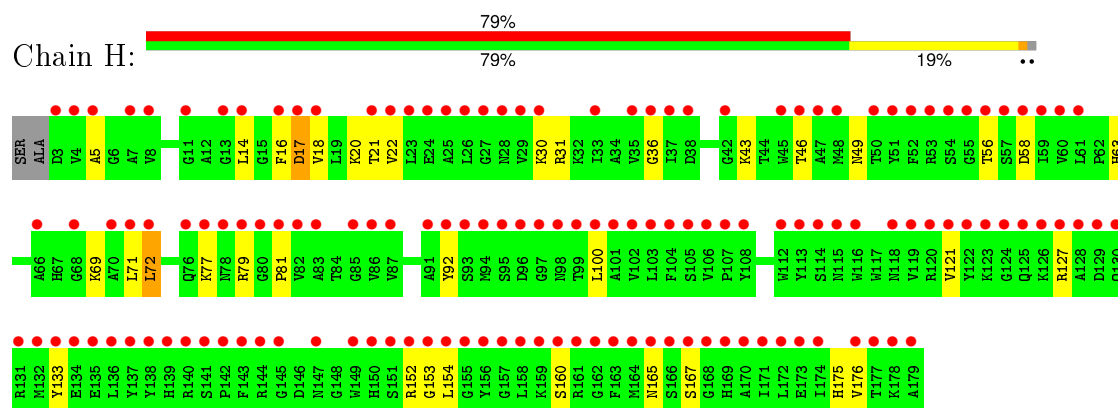
• Molecule 1: FRAGACEATOXIN C



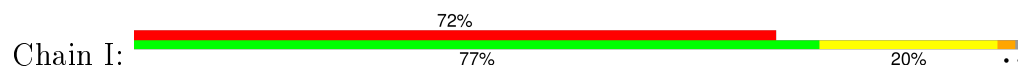
• Molecule 1: FRAGACEATOXIN C

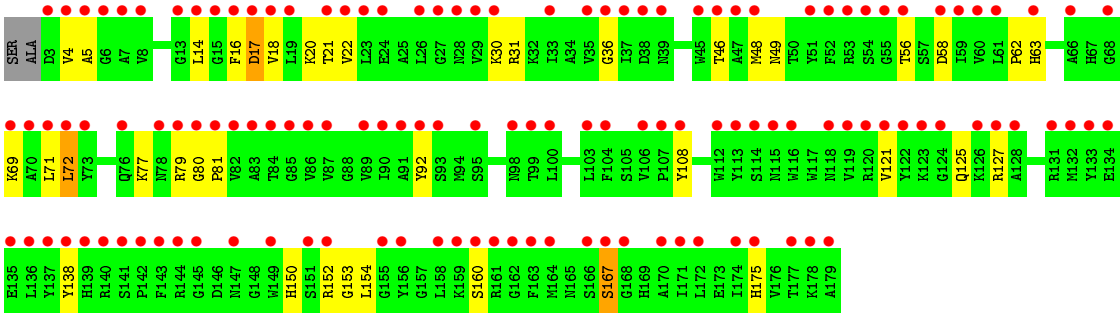


• Molecule 1: FRAGACEATOXIN C



• Molecule 1: FRAGACEATOXIN C





4 Data and refinement statistics

Property	Value	Source
Space group	P 3 2 1	Depositor
Cell constants a, b, c, α , β , γ	117.97Å 117.97Å 256.01Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	57.48 – 2.37 57.48 – 2.37	Depositor EDS
% Data completeness (in resolution range)	93.6 (57.48-2.37) 93.3 (57.48-2.37)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.98 (at 2.37Å)	Xtriage
Refinement program	PHENIX (PHENIX.REFINE)	Depositor
R, R_{free}	0.192 , 0.215 (Not available) , (Not available)	Depositor DCC
R_{free} test set	NotAvailable	DCC
Wilson B-factor (Å ²)	24.4	Xtriage
Anisotropy	0.320	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 64.8	EDS
Estimated twinning fraction	0.499 for -H,-K,L 0.468 for -h,-k,l	Xtriage
Reported twinning fraction	0.499 for -H,-K,L	Depositor
L-test for twinning ²	$\langle L \rangle = 0.40$, $\langle L^2 \rangle = 0.22$	Xtriage
Outliers	3 of 78787 reflections (0.004%)	Xtriage
F_o, F_c correlation	0.82	EDS
Total number of atoms	12794	wwPDB-VP
Average B, all atoms (Å ²)	52.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 17.15% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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	0.61	0/1419	0.54	0/1919
1	B	0.58	0/1419	0.54	0/1919
1	C	0.62	0/1419	0.54	0/1919
1	D	0.62	0/1419	0.54	0/1919
1	E	0.58	0/1419	0.52	0/1919
1	F	0.61	0/1419	0.54	0/1919
1	G	0.44	0/1419	0.49	0/1919
1	H	0.42	0/1419	0.48	0/1919
1	I	0.44	0/1419	0.49	0/1919
All	All	0.55	0/12771	0.52	0/17271

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1384	0	1353	30	0
1	B	1384	0	1353	32	0
1	C	1384	0	1353	25	0
1	D	1384	0	1353	32	0
1	E	1384	0	1353	30	0
1	F	1384	0	1353	17	0
1	G	1384	0	1353	34	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	H	1384	0	1353	30	0
1	I	1384	0	1353	38	0
2	A	54	0	0	1	0
2	B	46	0	0	4	0
2	C	42	0	0	4	0
2	D	42	0	0	7	0
2	E	38	0	0	2	0
2	F	39	0	0	2	0
2	G	26	0	0	12	0
2	H	20	0	0	5	0
2	I	31	0	0	12	0
All	All	12794	0	12177	234	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 10.

All (234) 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:E:77:LYS:NZ	2:E:2012:HOH:O	1.86	1.08
1:F:131:ARG:NH1	2:F:2029:HOH:O	2.04	0.91
1:D:164:MET:SD	2:D:2027:HOH:O	2.33	0.86
1:I:138:TYR:HB3	2:I:2022:HOH:O	1.78	0.82
1:E:79:ARG:NH2	2:E:2016:HOH:O	2.14	0.79
1:B:95:SER:HB3	2:B:2015:HOH:O	1.84	0.78
1:G:121:VAL:HG22	2:G:2013:HOH:O	1.85	0.77
1:D:17:ASP:OD1	1:E:4:VAL:HG21	1.88	0.74
1:G:79:ARG:HG2	2:G:2011:HOH:O	1.86	0.74
1:I:175:HIS:O	2:I:2029:HOH:O	2.05	0.73
1:G:14:LEU:O	2:G:2002:HOH:O	2.05	0.73
1:D:167:SER:HB3	2:D:2040:HOH:O	1.89	0.71
1:A:17:ASP:OD1	1:B:4:VAL:HG21	1.93	0.69
1:A:30:LYS:NZ	1:I:81:PRO:HB3	2.09	0.68
1:G:100:LEU:HA	2:G:2013:HOH:O	1.93	0.67
1:D:17:ASP:CG	1:E:4:VAL:HG21	2.15	0.67
1:A:17:ASP:CG	1:B:4:VAL:HG21	2.16	0.65
1:A:30:LYS:HZ1	1:I:81:PRO:HB3	1.62	0.65
1:G:43:LYS:HB3	2:G:2012:HOH:O	1.97	0.64
1:H:63:HIS:HB3	2:H:2007:HOH:O	1.97	0.64
1:I:167:SER:HB3	2:I:2031:HOH:O	1.99	0.62
1:G:165:ASN:HD22	1:H:58:ASP:HB3	1.63	0.61

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:16:PHE:HE2	2:I:2004:HOH:O	1.84	0.60
1:A:165:ASN:ND2	1:B:58:ASP:HB3	2.17	0.60
1:A:30:LYS:NZ	1:I:81:PRO:CB	2.66	0.59
1:A:16:PHE:CZ	1:B:59:ILE:HD13	2.38	0.58
1:I:69:LYS:NZ	2:I:2002:HOH:O	2.35	0.58
1:D:16:PHE:CZ	1:E:59:ILE:HD13	2.39	0.58
1:I:56:THR:CG2	1:I:79:ARG:HH12	2.18	0.57
1:I:152:ARG:HG2	1:I:153:GLY:O	2.05	0.57
1:C:16:PHE:N	2:C:2006:HOH:O	2.36	0.56
1:A:81:PRO:HB2	1:I:108:TYR:OH	2.06	0.56
1:C:152:ARG:HG2	1:C:153:GLY:O	2.06	0.56
1:C:81:PRO:HB2	1:G:108:TYR:OH	2.05	0.56
1:G:56:THR:CG2	1:G:79:ARG:HH12	2.18	0.56
1:C:56:THR:CG2	1:C:79:ARG:HH12	2.19	0.56
1:B:56:THR:CG2	1:B:79:ARG:HH12	2.18	0.56
1:A:56:THR:CG2	1:A:79:ARG:HH12	2.19	0.56
1:I:48:MET:SD	2:I:2008:HOH:O	2.58	0.55
1:B:152:ARG:HG2	1:B:153:GLY:O	2.06	0.55
1:D:17:ASP:O	1:D:21:THR:HG23	2.07	0.55
1:A:165:ASN:HD22	1:B:58:ASP:HB3	1.72	0.55
1:A:30:LYS:HZ1	1:I:81:PRO:CB	2.19	0.55
1:D:165:ASN:ND2	1:E:58:ASP:HB3	2.21	0.55
1:D:152:ARG:HG2	1:D:153:GLY:O	2.07	0.55
1:I:150:HIS:ND1	2:I:2027:HOH:O	2.23	0.54
1:D:165:ASN:HD22	1:E:58:ASP:HB3	1.73	0.54
1:G:18:VAL:HG11	1:G:72:LEU:HD21	1.90	0.54
1:H:56:THR:CG2	1:H:79:ARG:HH12	2.21	0.53
1:H:152:ARG:HG2	1:H:153:GLY:O	2.09	0.53
1:H:17:ASP:O	1:H:21:THR:HG23	2.09	0.53
1:B:17:ASP:OD1	1:C:4:VAL:HG21	2.08	0.53
1:D:16:PHE:CE1	1:E:59:ILE:HA	2.44	0.52
1:C:153:GLY:O	2:C:2038:HOH:O	2.19	0.52
1:I:17:ASP:O	1:I:21:THR:HG23	2.10	0.52
1:G:16:PHE:CZ	1:G:20:LYS:HD2	2.45	0.52
1:D:5:ALA:O	1:D:72:LEU:O	2.27	0.52
1:G:152:ARG:HG2	1:G:153:GLY:O	2.10	0.52
1:C:30:LYS:NZ	1:G:81:PRO:HB3	2.25	0.52
1:F:5:ALA:O	1:F:72:LEU:O	2.28	0.52
1:A:17:ASP:O	1:A:21:THR:HG23	2.11	0.51
1:E:152:ARG:HG2	1:E:153:GLY:O	2.11	0.51
1:D:56:THR:CG2	1:D:79:ARG:HH12	2.22	0.51

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:56:THR:HG22	1:H:79:ARG:HH12	1.76	0.51
1:D:165:ASN:ND2	1:E:58:ASP:CB	2.74	0.51
1:A:5:ALA:O	1:A:72:LEU:O	2.29	0.51
1:E:56:THR:CG2	1:E:79:ARG:HH12	2.23	0.51
1:G:56:THR:HG22	1:G:79:ARG:HH12	1.76	0.51
1:A:16:PHE:CZ	1:A:20:LYS:HD2	2.46	0.51
1:C:17:ASP:O	1:C:21:THR:HG23	2.11	0.51
1:F:56:THR:CG2	1:F:79:ARG:HH12	2.23	0.50
1:B:3:ASP:N	2:B:2001:HOH:O	2.44	0.50
1:B:165:ASN:HD22	1:C:58:ASP:HB3	1.76	0.50
1:I:56:THR:HG22	1:I:79:ARG:HH12	1.76	0.50
1:F:16:PHE:CZ	1:F:20:LYS:HD2	2.46	0.50
1:A:152:ARG:HG2	1:A:153:GLY:O	2.11	0.50
1:H:16:PHE:CZ	1:H:20:LYS:HD2	2.46	0.50
1:G:165:ASN:ND2	1:H:58:ASP:HB3	2.24	0.50
1:C:16:PHE:CZ	1:C:20:LYS:HD2	2.47	0.50
1:C:18:VAL:CG1	1:C:72:LEU:HD21	2.42	0.50
1:G:121:VAL:HA	2:G:2013:HOH:O	2.11	0.50
1:E:17:ASP:O	1:E:21:THR:HG23	2.12	0.50
1:F:154:LEU:HD11	1:F:160:SER:HB3	1.94	0.50
1:I:18:VAL:HG11	1:I:72:LEU:HD21	1.94	0.49
1:G:18:VAL:CG1	1:G:72:LEU:HD21	2.41	0.49
1:B:30:LYS:HD2	1:B:77:LYS:NZ	2.27	0.49
1:A:16:PHE:CE1	1:B:59:ILE:HA	2.47	0.49
1:B:16:PHE:CZ	1:B:20:LYS:HD2	2.48	0.49
1:C:5:ALA:O	1:C:72:LEU:O	2.31	0.49
1:A:165:ASN:ND2	1:B:58:ASP:CB	2.75	0.49
1:G:17:ASP:O	1:G:21:THR:HG23	2.13	0.49
1:C:18:VAL:HG11	1:C:72:LEU:HD21	1.94	0.49
1:F:17:ASP:O	1:F:21:THR:HG23	2.12	0.49
1:A:14:LEU:HD11	1:A:36:GLY:HA3	1.94	0.49
1:B:56:THR:HG22	1:B:79:ARG:HH12	1.78	0.48
1:G:121:VAL:HG23	1:G:154:LEU:HB3	1.95	0.48
1:A:30:LYS:HD2	1:A:77:LYS:NZ	2.28	0.48
1:G:165:ASN:ND2	1:H:58:ASP:CB	2.77	0.48
1:D:16:PHE:CZ	1:D:20:LYS:HD2	2.48	0.48
1:D:56:THR:HG22	1:D:79:ARG:HH12	1.79	0.48
1:E:30:LYS:HD2	1:E:77:LYS:NZ	2.27	0.48
1:H:69:LYS:NZ	2:H:2002:HOH:O	2.30	0.48
1:I:154:LEU:HD11	1:I:160:SER:HB3	1.95	0.48
1:H:30:LYS:HD2	1:H:77:LYS:NZ	2.28	0.48

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:56:THR:HG22	1:E:79:ARG:HH12	1.79	0.48
1:H:165:ASN:HD22	1:I:58:ASP:HB3	1.79	0.48
1:D:30:LYS:HD2	1:D:77:LYS:NZ	2.29	0.47
1:I:167:SER:N	2:I:2031:HOH:O	2.46	0.47
1:H:18:VAL:HG11	1:H:72:LEU:HD21	1.96	0.47
1:H:31:ARG:HB2	1:H:77:LYS:HB3	1.96	0.47
1:I:30:LYS:HD2	1:I:77:LYS:NZ	2.29	0.47
1:C:56:THR:HG22	1:C:79:ARG:HH12	1.78	0.47
1:A:18:VAL:HG11	1:A:72:LEU:HD21	1.97	0.47
1:A:56:THR:HG22	1:A:79:ARG:HH12	1.80	0.47
1:G:152:ARG:HD3	2:G:2024:HOH:O	2.15	0.47
1:F:56:THR:HG22	1:F:79:ARG:HH12	1.79	0.47
1:G:49:ASN:HB3	1:G:127:ARG:NH2	2.30	0.47
1:F:18:VAL:CG1	1:F:72:LEU:HD21	2.45	0.47
1:E:18:VAL:CG1	1:E:72:LEU:HD21	2.45	0.47
1:G:17:ASP:OD1	2:G:2003:HOH:O	2.21	0.47
1:H:17:ASP:OD1	1:I:4:VAL:HG21	2.15	0.46
1:I:31:ARG:HB2	1:I:77:LYS:HB3	1.97	0.46
1:C:49:ASN:HB3	1:C:127:ARG:NH2	2.30	0.46
1:G:96:ASP:N	2:G:2012:HOH:O	2.30	0.46
1:I:18:VAL:CG1	1:I:72:LEU:HD21	2.45	0.46
1:A:49:ASN:HB3	1:A:127:ARG:NH2	2.30	0.46
1:I:125:GLN:HB3	2:I:2008:HOH:O	2.14	0.46
1:H:5:ALA:O	1:H:72:LEU:O	2.34	0.46
1:E:49:ASN:HB3	1:E:127:ARG:NH2	2.31	0.46
1:E:31:ARG:HB2	1:E:77:LYS:HB3	1.97	0.46
1:I:16:PHE:CZ	1:I:20:LYS:HD2	2.50	0.46
1:H:18:VAL:CG1	1:H:72:LEU:HD21	2.46	0.46
1:D:150:HIS:HD2	2:D:2028:HOH:O	1.97	0.46
1:C:162:GLY:HA2	1:C:173:GLU:O	2.16	0.46
1:G:43:LYS:HD2	2:G:2012:HOH:O	2.15	0.46
1:C:154:LEU:HD11	1:C:160:SER:HB3	1.97	0.46
1:I:5:ALA:O	1:I:72:LEU:O	2.34	0.46
1:B:121:VAL:HG23	1:B:154:LEU:HB3	1.97	0.46
1:H:175:HIS:CE1	2:H:2018:HOH:O	2.69	0.46
1:B:17:ASP:O	1:B:21:THR:HG23	2.16	0.45
1:I:14:LEU:HD11	1:I:36:GLY:HA3	1.98	0.45
1:C:81:PRO:HA	2:C:2008:HOH:O	2.15	0.45
1:C:30:LYS:HD2	1:C:77:LYS:NZ	2.31	0.45
1:A:18:VAL:CG1	1:A:72:LEU:HD21	2.47	0.45
1:E:16:PHE:CZ	1:E:20:LYS:HD2	2.51	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:152:ARG:HG2	1:F:153:GLY:O	2.16	0.45
1:E:18:VAL:HG11	1:E:72:LEU:HD21	1.99	0.45
1:G:31:ARG:HB2	1:G:77:LYS:HB3	1.98	0.45
1:I:121:VAL:HG23	1:I:154:LEU:HB3	1.98	0.45
1:D:121:VAL:HG23	1:D:154:LEU:HB3	1.99	0.45
1:D:18:VAL:HG11	1:D:72:LEU:HD21	1.99	0.44
1:H:71:LEU:HD22	1:H:92:TYR:CZ	2.52	0.44
1:G:154:LEU:HD11	1:G:160:SER:HB3	1.99	0.44
1:A:16:PHE:HB3	1:B:6:GLY:HA3	1.99	0.44
1:D:16:PHE:HB3	1:E:6:GLY:HA3	1.99	0.44
1:C:18:VAL:O	1:C:22:VAL:HG23	2.17	0.44
1:F:49:ASN:HB3	1:F:127:ARG:NH2	2.32	0.44
1:I:79:ARG:HG2	2:I:2012:HOH:O	2.17	0.44
1:F:31:ARG:HB2	1:F:77:LYS:HB3	1.99	0.44
1:A:161:ARG:HD2	1:B:63:HIS:NE2	2.33	0.44
1:A:31:ARG:HB2	1:A:77:LYS:HB3	1.99	0.44
1:D:161:ARG:HD2	1:E:63:HIS:NE2	2.32	0.44
1:B:145:GLY:O	2:B:2029:HOH:O	2.20	0.44
1:B:31:ARG:HB2	1:B:77:LYS:HB3	1.99	0.44
1:H:154:LEU:HD11	1:H:160:SER:HB3	1.99	0.44
1:C:14:LEU:HD11	1:C:36:GLY:HA3	2.00	0.44
1:E:154:LEU:HD11	1:E:160:SER:HB3	2.00	0.44
1:E:47:ALA:HB3	1:E:63:HIS:HA	2.00	0.43
1:B:154:LEU:HD11	1:B:160:SER:HB3	1.99	0.43
1:F:71:LEU:HD22	1:F:92:TYR:CZ	2.53	0.43
1:H:133:TYR:HE2	2:H:2005:HOH:O	2.01	0.43
1:I:71:LEU:HD22	1:I:92:TYR:CZ	2.53	0.43
1:G:20:LYS:HD3	2:G:2003:HOH:O	2.18	0.43
1:F:18:VAL:HG11	1:F:72:LEU:HD21	2.00	0.43
1:D:45:TRP:CD1	1:D:94:MET:HG2	2.53	0.43
1:A:162:GLY:HA2	1:A:173:GLU:O	2.19	0.43
1:G:30:LYS:HD2	1:G:77:LYS:NZ	2.33	0.43
1:I:46:THR:HA	1:I:63:HIS:O	2.19	0.43
1:D:49:ASN:HB3	1:D:127:ARG:NH2	2.34	0.43
1:F:30:LYS:HD2	1:F:77:LYS:NZ	2.33	0.43
1:I:62:PRO:HA	2:I:2010:HOH:O	2.17	0.43
1:G:18:VAL:O	1:G:22:VAL:HG23	2.19	0.42
1:H:14:LEU:HD11	1:H:36:GLY:HA3	2.00	0.42
1:D:69:LYS:NZ	2:D:2021:HOH:O	2.51	0.42
1:D:145:GLY:N	2:D:2027:HOH:O	2.52	0.42
1:H:165:ASN:ND2	1:I:58:ASP:HB3	2.34	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:175:HIS:HE1	2:C:2005:HOH:O	2.02	0.42
1:I:49:ASN:HB3	1:I:127:ARG:NH2	2.34	0.42
1:G:5:ALA:O	1:G:72:LEU:O	2.37	0.42
1:B:5:ALA:O	1:B:72:LEU:O	2.37	0.42
1:F:98:ASN:OD1	1:F:123:LYS:HA	2.20	0.42
1:D:31:ARG:HB2	1:D:77:LYS:HB3	2.00	0.42
1:B:18:VAL:HG11	1:B:72:LEU:HD21	2.02	0.42
1:G:32:LYS:NZ	2:G:2004:HOH:O	2.51	0.42
1:A:121:VAL:HG23	1:A:154:LEU:HB3	2.00	0.42
1:F:150:HIS:HA	2:F:2036:HOH:O	2.18	0.42
1:E:80:GLY:HA2	1:E:81:PRO:HD3	1.89	0.42
1:D:145:GLY:CA	2:D:2027:HOH:O	2.66	0.42
1:D:18:VAL:CG1	1:D:72:LEU:HD21	2.49	0.42
1:H:121:VAL:HG23	1:H:154:LEU:HB3	2.01	0.42
1:B:14:LEU:HD11	1:B:36:GLY:HA3	2.02	0.42
1:B:30:LYS:NZ	1:H:81:PRO:HB3	2.35	0.41
1:E:5:ALA:O	1:E:72:LEU:O	2.38	0.41
1:E:45:TRP:CD1	1:E:94:MET:HG2	2.55	0.41
1:D:154:LEU:HD11	1:D:160:SER:HB3	2.02	0.41
1:B:99:THR:OG1	1:B:125:GLN:HA	2.21	0.41
1:B:100:LEU:HD21	1:B:176:VAL:HG21	2.02	0.41
1:I:80:GLY:HA2	1:I:81:PRO:HD3	1.88	0.41
1:H:46:THR:HA	1:H:63:HIS:O	2.20	0.41
1:A:98:ASN:HB3	1:A:122:TYR:O	2.21	0.41
1:D:39:ASN:ND2	1:D:65:VAL:O	2.53	0.41
1:B:167:SER:HB3	2:B:2045:HOH:O	2.19	0.41
1:I:79:ARG:HA	2:I:2011:HOH:O	2.21	0.41
1:B:46:THR:HA	1:B:63:HIS:O	2.20	0.41
1:H:43:LYS:HE3	2:H:2008:HOH:O	2.19	0.41
1:A:61:LEU:HB2	2:A:2014:HOH:O	2.20	0.41
1:D:125:GLN:NE2	2:D:2022:HOH:O	2.46	0.41
1:G:14:LEU:HD11	1:G:36:GLY:HA3	2.01	0.41
1:F:46:THR:HA	1:F:63:HIS:O	2.21	0.41
1:G:145:GLY:HA2	1:G:164:MET:HB3	2.03	0.41
1:H:18:VAL:O	1:H:22:VAL:HG23	2.20	0.41
1:H:49:ASN:HB3	1:H:127:ARG:NH2	2.36	0.41
1:E:14:LEU:HD11	1:E:36:GLY:HA3	2.01	0.41
1:G:71:LEU:HD22	1:G:92:TYR:CZ	2.55	0.41
1:B:162:GLY:HA2	1:B:173:GLU:O	2.21	0.41
1:D:145:GLY:HA2	1:D:164:MET:HB3	2.03	0.41
1:I:18:VAL:O	1:I:22:VAL:HG23	2.20	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:20:LYS:HE2	1:E:24:GLU:OE2	2.21	0.40
1:C:100:LEU:HD21	1:C:176:VAL:HG21	2.04	0.40
1:C:46:THR:HA	1:C:63:HIS:O	2.22	0.40
1:H:100:LEU:HD21	1:H:176:VAL:HG21	2.03	0.40
1:E:162:GLY:HA2	1:E:173:GLU:O	2.22	0.40
1:C:31:ARG:HB2	1:C:77:LYS:HB3	2.03	0.40
1:E:61:LEU:HD12	1:E:62:PRO:HD2	2.02	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all 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	175/179 (98%)	168 (96%)	7 (4%)	0	100	100
1	B	175/179 (98%)	168 (96%)	7 (4%)	0	100	100
1	C	175/179 (98%)	168 (96%)	6 (3%)	1 (1%)	30	40
1	D	175/179 (98%)	169 (97%)	6 (3%)	0	100	100
1	E	175/179 (98%)	169 (97%)	6 (3%)	0	100	100
1	F	175/179 (98%)	169 (97%)	5 (3%)	1 (1%)	30	40
1	G	175/179 (98%)	169 (97%)	6 (3%)	0	100	100
1	H	175/179 (98%)	168 (96%)	7 (4%)	0	100	100
1	I	175/179 (98%)	169 (97%)	6 (3%)	0	100	100
All	All	1575/1611 (98%)	1517 (96%)	56 (4%)	2 (0%)	56	73

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	F	145	GLY
1	C	145	GLY

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	141/142 (99%)	138 (98%)	3 (2%)	61	79
1	B	141/142 (99%)	138 (98%)	3 (2%)	61	79
1	C	141/142 (99%)	138 (98%)	3 (2%)	61	79
1	D	141/142 (99%)	138 (98%)	3 (2%)	61	79
1	E	141/142 (99%)	138 (98%)	3 (2%)	61	79
1	F	141/142 (99%)	138 (98%)	3 (2%)	61	79
1	G	141/142 (99%)	138 (98%)	3 (2%)	61	79
1	H	141/142 (99%)	138 (98%)	3 (2%)	61	79
1	I	141/142 (99%)	138 (98%)	3 (2%)	61	79
All	All	1269/1278 (99%)	1242 (98%)	27 (2%)	61	79

All (27) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	17	ASP
1	A	72	LEU
1	A	167	SER
1	B	17	ASP
1	B	72	LEU
1	B	167	SER
1	C	17	ASP
1	C	72	LEU
1	C	167	SER
1	D	17	ASP
1	D	72	LEU
1	D	167	SER
1	E	17	ASP
1	E	72	LEU
1	E	167	SER
1	F	17	ASP
1	F	72	LEU
1	F	167	SER

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	G	17	ASP
1	G	72	LEU
1	G	167	SER
1	H	17	ASP
1	H	72	LEU
1	H	167	SER
1	I	17	ASP
1	I	72	LEU
1	I	167	SER

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no carbohydrates 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	177/179 (98%)	0.79	6 (3%)	49	53	16, 36, 66, 95	0
1	B	177/179 (98%)	0.69	10 (5%)	28	32	19, 37, 71, 106	0
1	C	177/179 (98%)	0.68	7 (3%)	42	47	16, 34, 66, 98	0
1	D	177/179 (98%)	0.77	9 (5%)	32	36	17, 35, 70, 101	0
1	E	177/179 (98%)	0.74	9 (5%)	32	36	18, 38, 66, 97	0
1	F	177/179 (98%)	0.75	10 (5%)	28	32	15, 35, 69, 90	0
1	G	177/179 (98%)	3.22	128 (72%)	0	0	52, 75, 99, 113	0
1	H	177/179 (98%)	3.50	141 (79%)	0	0	55, 81, 98, 116	0
1	I	177/179 (98%)	3.20	129 (72%)	0	0	49, 77, 99, 114	0
All	All	1593/1611 (98%)	1.59	449 (28%)	1	1	15, 45, 93, 116	0

All (449) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	I	138	TYR	10.7
1	H	95	SER	10.5
1	H	128	ALA	9.6
1	H	139	HIS	9.4
1	H	47	ALA	9.0
1	I	47	ALA	8.6
1	G	95	SER	8.4
1	I	27	GLY	8.3
1	G	52	PHE	8.2
1	I	116	TRP	8.0
1	H	82	VAL	7.8
1	H	140	ARG	7.8
1	I	128	ALA	7.8
1	H	143	PHE	7.7
1	H	112	TRP	7.6

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	G	177	THR	7.6
1	G	179	ALA	7.6
1	I	139	HIS	7.5
1	H	179	ALA	7.5
1	H	172	LEU	7.4
1	G	92	TYR	7.3
1	I	118	ASN	7.3
1	I	5	ALA	7.0
1	H	138	TYR	7.0
1	I	119	VAL	6.7
1	H	133	TYR	6.6
1	G	51	TYR	6.6
1	H	121	VAL	6.6
1	G	128	ALA	6.6
1	I	126	LYS	6.5
1	G	118	ASN	6.5
1	G	3	ASP	6.4
1	G	138	TYR	6.4
1	H	174	ILE	6.3
1	H	119	VAL	6.3
1	I	143	PHE	6.3
1	G	162	GLY	6.2
1	G	119	VAL	6.2
1	H	137	TYR	6.2
1	H	51	TYR	6.1
1	I	79	ARG	6.1
1	I	18	VAL	6.1
1	H	114	SER	6.1
1	I	55	GLY	6.0
1	I	113	TYR	6.0
1	G	7	ALA	6.0
1	H	86	VAL	5.9
1	G	174	ILE	5.9
1	I	140	ARG	5.9
1	G	21	THR	5.9
1	G	107	PRO	5.8
1	H	118	ASN	5.7
1	I	95	SER	5.7
1	H	158	LEU	5.7
1	G	137	TYR	5.7
1	D	79	ARG	5.6
1	H	157	GLY	5.6

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	G	116	TRP	5.6
1	G	99	THR	5.6
1	I	83	ALA	5.6
1	H	72	LEU	5.6
1	H	122	TYR	5.5
1	I	54	SER	5.5
1	H	3	ASP	5.5
1	I	29	VAL	5.5
1	H	116	TRP	5.5
1	G	139	HIS	5.5
1	G	149	TRP	5.4
1	H	60	VAL	5.4
1	I	179	ALA	5.4
1	G	60	VAL	5.4
1	I	177	THR	5.3
1	I	132	MET	5.3
1	H	92	TYR	5.3
1	G	163	PHE	5.3
1	I	84	THR	5.3
1	G	152	ARG	5.3
1	H	107	PRO	5.2
1	I	61	LEU	5.2
1	G	28	ASN	5.2
1	H	23	LEU	5.2
1	G	147	ASN	5.2
1	G	158	LEU	5.2
1	H	132	MET	5.1
1	G	101	ALA	5.1
1	H	127	ARG	5.1
1	H	120	ARG	5.0
1	I	92	TYR	5.0
1	I	112	TRP	5.0
1	H	93	SER	5.0
1	I	51	TYR	4.9
1	I	133	TYR	4.9
1	H	152	ARG	4.9
1	H	168	GLY	4.9
1	I	60	VAL	4.8
1	I	155	GLY	4.8
1	H	134	GLU	4.8
1	H	54	SER	4.8
1	I	93	SER	4.8

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	I	152	ARG	4.8
1	G	55	GLY	4.8
1	I	144	ARG	4.7
1	H	99	THR	4.7
1	G	68	GLY	4.7
1	G	66	ALA	4.7
1	I	82	VAL	4.7
1	H	79	ARG	4.7
1	H	98	ASN	4.6
1	I	36	GLY	4.6
1	G	156	TYR	4.6
1	H	101	ALA	4.6
1	G	131	ARG	4.6
1	G	29	VAL	4.6
1	G	133	TYR	4.6
1	I	168	GLY	4.6
1	I	156	TYR	4.5
1	H	52	PHE	4.5
1	I	52	PHE	4.5
1	H	169	HIS	4.5
1	G	173	GLU	4.5
1	G	19	LEU	4.5
1	G	120	ARG	4.5
1	I	127	ARG	4.5
1	I	145	GLY	4.5
1	I	163	PHE	4.5
1	I	164	MET	4.5
1	I	170	ALA	4.5
1	H	155	GLY	4.4
1	H	35	VAL	4.4
1	I	137	TYR	4.4
1	H	87	VAL	4.4
1	G	157	GLY	4.4
1	I	174	ILE	4.4
1	G	172	LEU	4.4
1	G	122	TYR	4.3
1	G	47	ALA	4.3
1	G	166	SER	4.3
1	G	161	ARG	4.3
1	H	53	ARG	4.3
1	H	25	ALA	4.3
1	I	151	SER	4.3

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	H	55	GLY	4.3
1	H	162	GLY	4.3
1	G	27	GLY	4.3
1	H	129	ASP	4.3
1	H	113	TYR	4.3
1	G	143	PHE	4.2
1	F	112	TRP	4.2
1	I	124	GLY	4.2
1	H	26	LEU	4.2
1	H	156	TYR	4.2
1	A	112	TRP	4.2
1	G	176	VAL	4.2
1	I	4	VAL	4.2
1	G	14	LEU	4.2
1	H	178	LYS	4.1
1	I	162	GLY	4.1
1	I	120	ARG	4.1
1	G	25	ALA	4.1
1	I	16	PHE	4.1
1	B	28	ASN	4.1
1	H	36	GLY	4.1
1	G	112	TRP	4.1
1	G	129	ASP	4.1
1	H	165	ASN	4.1
1	H	21	THR	4.0
1	G	97	GLY	4.0
1	H	166	SER	4.0
1	H	149	TRP	4.0
1	H	70	ALA	3.9
1	G	126	LYS	3.9
1	H	80	GLY	3.9
1	G	165	ASN	3.9
1	H	144	ARG	3.9
1	G	4	VAL	3.9
1	G	175	HIS	3.9
1	G	82	VAL	3.9
1	I	7	ALA	3.9
1	I	53	ARG	3.9
1	H	103	LEU	3.9
1	H	94	MET	3.9
1	I	166	SER	3.8
1	I	161	ARG	3.8

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	H	164	MET	3.8
1	G	98	ASN	3.8
1	G	72	LEU	3.8
1	F	82	VAL	3.8
1	G	54	SER	3.7
1	C	3	ASP	3.7
1	H	42	GLY	3.7
1	I	115	ASN	3.7
1	F	79	ARG	3.7
1	H	7	ALA	3.7
1	G	53	ARG	3.7
1	G	18	VAL	3.7
1	G	135	GLU	3.7
1	G	79	ARG	3.7
1	H	131	ARG	3.7
1	H	76	GLN	3.7
1	G	35	VAL	3.7
1	G	113	TYR	3.7
1	G	132	MET	3.6
1	G	124	GLY	3.6
1	H	177	THR	3.6
1	H	147	ASN	3.6
1	I	23	LEU	3.6
1	I	123	LYS	3.6
1	H	5	ALA	3.6
1	H	141	SER	3.6
1	G	84	THR	3.6
1	H	58	ASP	3.6
1	I	26	LEU	3.6
1	I	136	LEU	3.5
1	G	5	ALA	3.5
1	G	144	ARG	3.5
1	D	82	VAL	3.5
1	C	112	TRP	3.5
1	D	3	ASP	3.4
1	G	168	GLY	3.4
1	H	154	LEU	3.4
1	G	93	SER	3.4
1	H	173	GLU	3.4
1	I	58	ASP	3.4
1	G	83	ALA	3.4
1	I	178	LYS	3.4

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	G	90	ILE	3.4
1	G	89	VAL	3.4
1	H	176	VAL	3.4
1	I	104	PHE	3.4
1	I	80	GLY	3.4
1	H	8	VAL	3.3
1	G	100	LEU	3.3
1	H	135	GLU	3.3
1	H	83	ALA	3.3
1	I	122	TYR	3.3
1	I	141	SER	3.3
1	E	120	ARG	3.3
1	I	131	ARG	3.3
1	G	17	ASP	3.3
1	G	164	MET	3.3
1	I	76	GLN	3.3
1	G	170	ALA	3.3
1	G	65	VAL	3.3
1	G	59	ILE	3.2
1	H	56	THR	3.2
1	G	160	SER	3.2
1	H	171	ILE	3.2
1	G	23	LEU	3.2
1	I	81	PRO	3.2
1	H	160	SER	3.2
1	I	33	ILE	3.2
1	I	147	ASN	3.2
1	H	167	SER	3.2
1	I	114	SER	3.2
1	I	56	THR	3.2
1	I	21	THR	3.2
1	A	81	PRO	3.2
1	G	78	ASN	3.2
1	I	45	TRP	3.2
1	H	27	GLY	3.1
1	H	136	LEU	3.1
1	I	19	LEU	3.1
1	G	8	VAL	3.1
1	I	149	TRP	3.1
1	G	6	GLY	3.1
1	H	37	ILE	3.1
1	I	35	VAL	3.1

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	I	108	TYR	3.1
1	E	28	ASN	3.1
1	H	13	GLY	3.1
1	B	82	VAL	3.1
1	H	123	LYS	3.0
1	I	68	GLY	3.0
1	I	14	LEU	3.0
1	H	142	PRO	3.0
1	G	130	GLN	3.0
1	H	66	ALA	3.0
1	G	33	ILE	3.0
1	H	4	VAL	3.0
1	I	121	VAL	3.0
1	I	37	ILE	3.0
1	H	105	SER	3.0
1	I	103	LEU	3.0
1	H	30	LYS	3.0
1	H	16	PHE	3.0
1	B	79	ARG	3.0
1	H	115	ASN	2.9
1	H	28	ASN	2.9
1	I	28	ASN	2.9
1	I	86	VAL	2.9
1	H	33	ILE	2.9
1	I	72	LEU	2.9
1	G	140	ARG	2.9
1	I	39	ASN	2.9
1	I	90	ILE	2.9
1	H	61	LEU	2.9
1	H	17	ASP	2.9
1	H	159	LYS	2.9
1	B	131	ARG	2.8
1	B	29	VAL	2.8
1	G	56	THR	2.8
1	G	16	PHE	2.8
1	A	82	VAL	2.8
1	H	161	ARG	2.8
1	H	163	PHE	2.8
1	I	159	LYS	2.8
1	E	79	ARG	2.8
1	H	71	LEU	2.8
1	I	30	LYS	2.8

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	I	73	TYR	2.8
1	G	117	TRP	2.8
1	H	50	THR	2.8
1	I	59	ILE	2.8
1	G	151	SER	2.7
1	G	81	PRO	2.7
1	D	112	TRP	2.7
1	G	11	GLY	2.7
1	H	125	GLN	2.7
1	H	151	SER	2.7
1	C	78	ASN	2.7
1	F	78	ASN	2.7
1	I	175	HIS	2.7
1	H	100	LEU	2.7
1	H	77	LYS	2.7
1	I	142	PRO	2.7
1	I	15	GLY	2.7
1	F	140	ARG	2.6
1	G	127	ARG	2.6
1	H	59	ILE	2.6
1	H	97	GLY	2.6
1	G	123	LYS	2.6
1	C	28	ASN	2.6
1	I	24	GLU	2.6
1	C	82	VAL	2.6
1	I	172	LEU	2.6
1	I	160	SER	2.6
1	G	86	VAL	2.6
1	H	22	VAL	2.6
1	G	67	HIS	2.6
1	H	68	GLY	2.6
1	I	70	ALA	2.6
1	I	106	VAL	2.6
1	I	63	HIS	2.6
1	G	103	LEU	2.6
1	G	178	LYS	2.6
1	H	29	VAL	2.6
1	H	48	MET	2.6
1	G	171	ILE	2.6
1	I	135	GLU	2.5
1	G	150	HIS	2.5
1	G	155	GLY	2.5

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	H	11	GLY	2.5
1	C	139	HIS	2.5
1	H	126	LYS	2.5
1	I	87	VAL	2.5
1	G	76	GLN	2.5
1	G	145	GLY	2.5
1	H	85	GLY	2.5
1	G	30	LYS	2.5
1	I	8	VAL	2.5
1	G	94	MET	2.5
1	A	79	ARG	2.5
1	G	62	PRO	2.4
1	G	24	GLU	2.4
1	H	18	VAL	2.4
1	I	91	ALA	2.4
1	H	81	PRO	2.4
1	I	100	LEU	2.4
1	E	82	VAL	2.4
1	G	50	THR	2.4
1	G	136	LEU	2.4
1	H	14	LEU	2.4
1	I	167	SER	2.4
1	F	131	ARG	2.4
1	H	45	TRP	2.4
1	E	123	LYS	2.4
1	F	114	SER	2.3
1	E	131	ARG	2.3
1	I	98	ASN	2.3
1	H	124	GLY	2.3
1	G	146	ASP	2.3
1	H	38	ASP	2.3
1	H	170	ALA	2.3
1	I	107	PRO	2.3
1	I	78	ASN	2.3
1	H	153	GLY	2.3
1	A	3	ASP	2.3
1	B	81	PRO	2.3
1	H	91	ALA	2.3
1	I	99	THR	2.3
1	G	106	VAL	2.3
1	I	6	GLY	2.3
1	G	159	LYS	2.3

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	I	69	LYS	2.3
1	I	89	VAL	2.3
1	B	3	ASP	2.3
1	I	3	ASP	2.3
1	A	22	VAL	2.2
1	H	108	TYR	2.2
1	F	28	ASN	2.2
1	H	145	GLY	2.2
1	I	85	GLY	2.2
1	G	45	TRP	2.2
1	E	83	ALA	2.2
1	H	96	ASP	2.2
1	G	114	SER	2.2
1	I	158	LEU	2.2
1	G	58	ASP	2.2
1	D	21	THR	2.2
1	E	56	THR	2.2
1	G	34	ALA	2.2
1	H	102	VAL	2.2
1	G	153	GLY	2.2
1	G	31	ARG	2.2
1	H	130	GLN	2.2
1	B	80	GLY	2.2
1	I	17	ASP	2.2
1	E	29	VAL	2.2
1	H	106	VAL	2.2
1	H	78	ASN	2.2
1	G	169	HIS	2.2
1	I	171	ILE	2.1
1	G	108	TYR	2.1
1	H	57	SER	2.1
1	I	71	LEU	2.1
1	I	46	THR	2.1
1	G	77	LYS	2.1
1	G	87	VAL	2.1
1	B	112	TRP	2.1
1	D	16	PHE	2.1
1	I	38	ASP	2.1
1	F	29	VAL	2.1
1	H	46	THR	2.1
1	H	150	HIS	2.1
1	H	104	PHE	2.1

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	F	5	ALA	2.1
1	H	24	GLU	2.1
1	I	134	GLU	2.1
1	I	13	GLY	2.0
1	I	48	MET	2.0
1	I	66	ALA	2.0
1	B	140	ARG	2.0
1	D	78	ASN	2.0
1	G	15	GLY	2.0
1	G	102	VAL	2.0
1	I	22	VAL	2.0
1	D	158	LEU	2.0
1	D	28	ASN	2.0
1	C	29	VAL	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 carbohydrates 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.