Full wwPDB X-ray Structure Validation Report (i)

Dec 12, 2023 – 08:24 pm GMT

PDB ID	:	4AGF
Title	:	MTSSL spin labeled L124C mutant of MscS in the open form
Authors	:	Pliotas, C.; Brannigan, E.; Naismith, J.H.
Deposited on	:	2012-01-26
Resolution	:	4.70 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 (i) 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 (1)) were used in the production of this report:

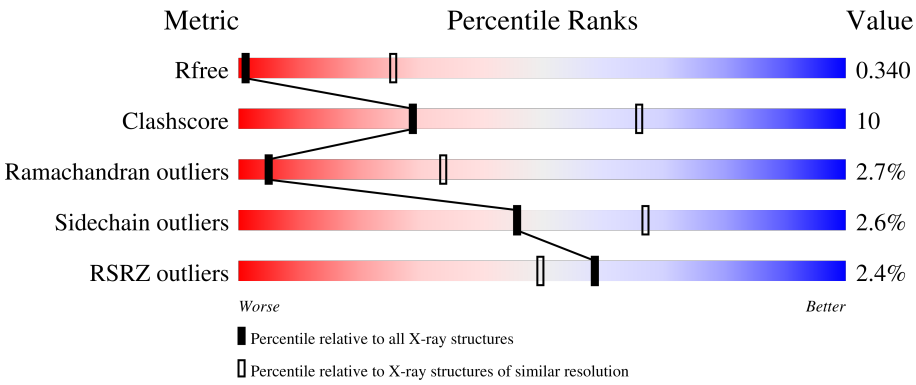
MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.36
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 4.70 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}	130704	1085 (5.58-3.80)
Clashscore	141614	1159 (5.60-3.80)
Ramachandran outliers	138981	1094 (5.58-3.80)
Sidechain outliers	138945	1074 (5.58-3.80)
RSRZ outliers	127900	1118 (5.70-3.70)

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 <=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	286	5%; 72%; 16%; • ; 10%
1	B	286	2%; 71%; 16%; • ; 10%
1	C	286	69%; 19%; • ; 10%
1	D	286	2%; 71%; 16%; • ; 10%
1	E	286	2%; 71%; 17%; • ; 10%

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
1	F	286	2% 71% 16% • 10%
1	G	286	2% 70% 18% • 10%

2 Entry composition (i)

There is only 1 type of molecule in this entry. The entry contains 13663 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 SMALL-CONDUCTANCE MECHANOSENSITIVE CHANNEL.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	257	1952	1251	342	352	7	0	0	1
1	B	257	1952	1251	342	352	7	0	0	1
1	C	257	1952	1251	342	352	7	0	0	1
1	D	257	1952	1251	342	352	7	0	0	1
1	E	256	1951	1251	341	352	7	0	0	0
1	F	257	1952	1251	342	352	7	0	0	1
1	G	257	1952	1251	342	352	7	0	0	1

There are 7 discrepancies between the modelled and reference sequences:

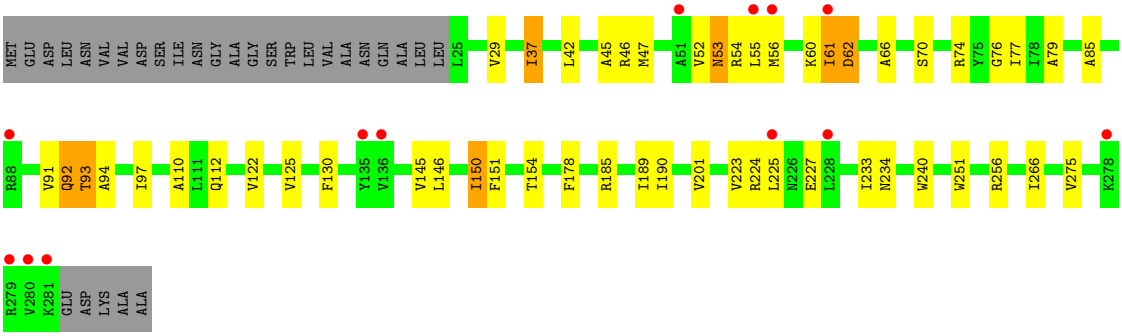
Chain	Residue	Modelled	Actual	Comment	Reference
A	124	CYS	LEU	engineered mutation	UNP P0C0S2
B	124	CYS	LEU	engineered mutation	UNP P0C0S2
C	124	CYS	LEU	engineered mutation	UNP P0C0S2
D	124	CYS	LEU	engineered mutation	UNP P0C0S2
E	124	CYS	LEU	engineered mutation	UNP P0C0S2
F	124	CYS	LEU	engineered mutation	UNP P0C0S2
G	124	CYS	LEU	engineered mutation	UNP P0C0S2

3 Residue-property plots (i)

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

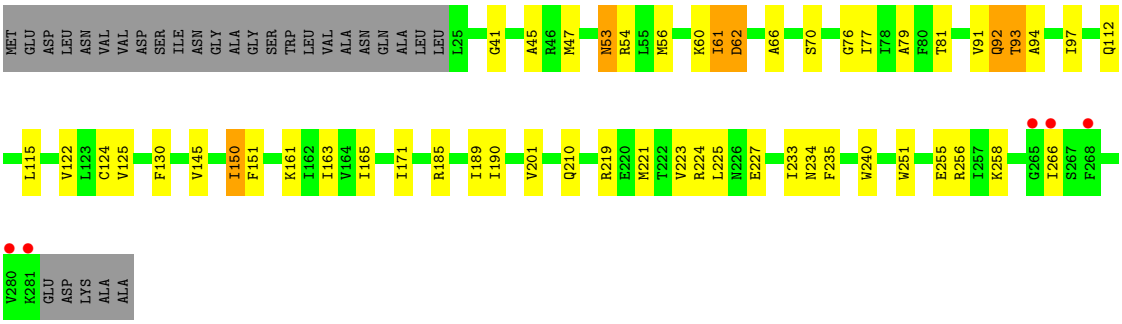
• Molecule 1: SMALL-CONDUCTANCE MECHANOSENSITIVE CHANNEL

Chain A: 5% 72% 16% • 10%



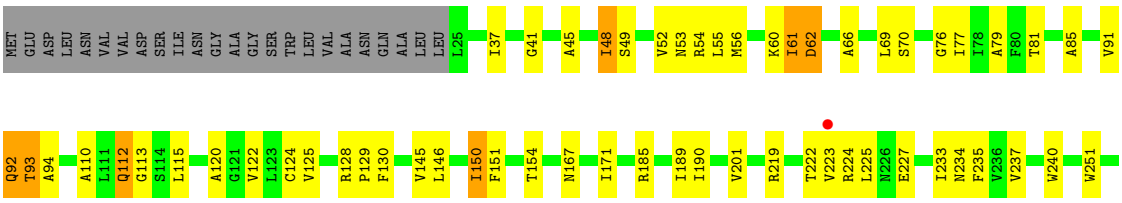
• Molecule 1: SMALL-CONDUCTANCE MECHANOSENSITIVE CHANNEL

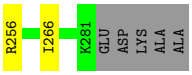
Chain B: 2% 71% 16% • 10%



• Molecule 1: SMALL-CONDUCTANCE MECHANOSENSITIVE CHANNEL

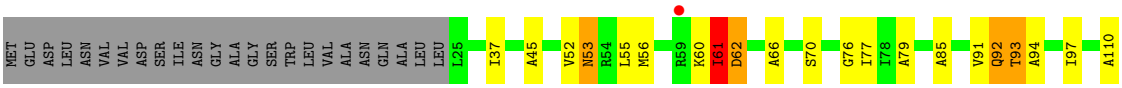
Chain C: 69% 19% • 10%

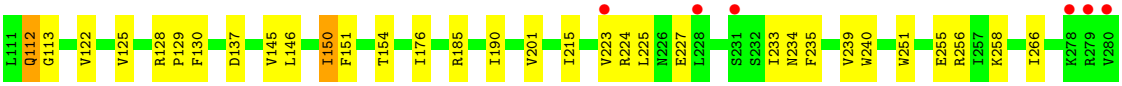




• Molecule 1: SMALL-CONDUCTANCE MECHANOSENSITIVE CHANNEL

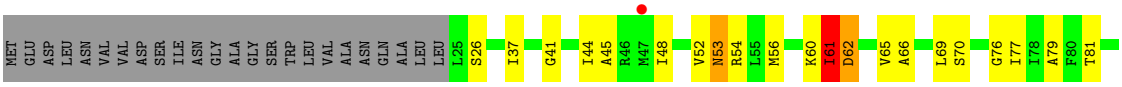
Chain D:

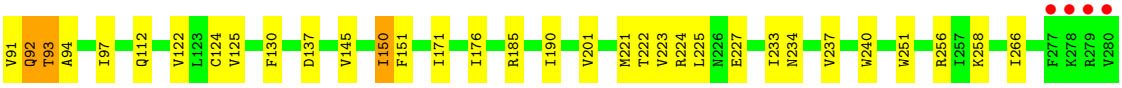




• Molecule 1: SMALL-CONDUCTANCE MECHANOSENSITIVE CHANNEL

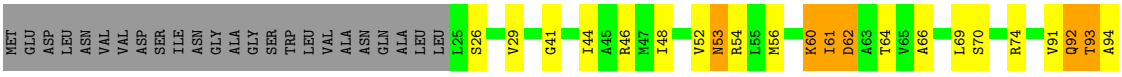
Chain E:

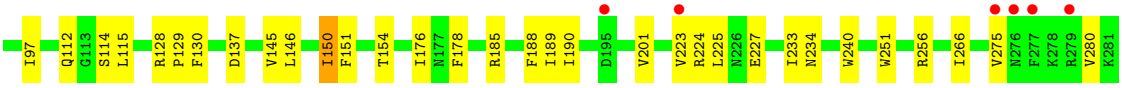




• Molecule 1: SMALL-CONDUCTANCE MECHANOSENSITIVE CHANNEL

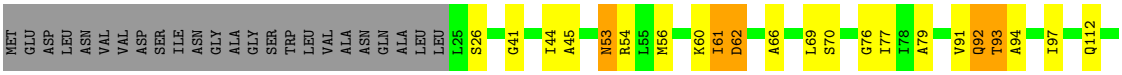
Chain F:

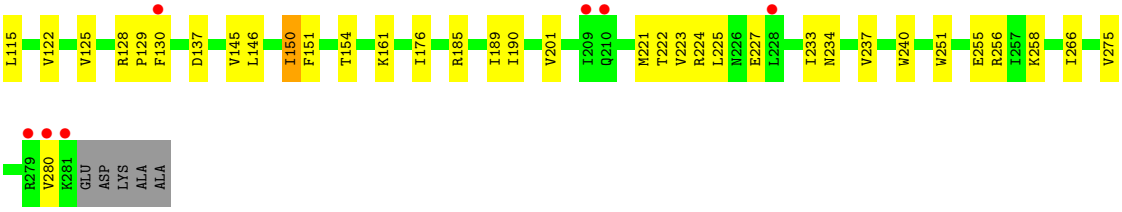




• Molecule 1: SMALL-CONDUCTANCE MECHANOSENSITIVE CHANNEL

Chain G:




L115
V122
V125
R128
P129
F130
D137
V145
L146
I150
F151
T154
K161
I176
R185
I189
I190
V201
I209
Q210
M221
T222
V223
R224
L225
N226
E227
L228
I233
N234
V237
W240
W251
E255
R256
I257
K258
I266
V275
R279
V280
K281
GLU
ASP
LYS
ALA
ALA

4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	128.84Å 150.22Å 175.81Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	114.21 – 4.70 97.80 – 4.70	Depositor EDS
% Data completeness (in resolution range)	94.7 (114.21-4.70) 94.7 (97.80-4.70)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.79 (at 4.66Å)	Xtriage
Refinement program	REFMAC 5.6.0119	Depositor
R, R_{free}	0.334 , 0.339 0.337 , 0.340	Depositor DCC
R_{free} test set	885 reflections (5.09%)	wwPDB-VP
Wilson B-factor (Å^2)	202.2	Xtriage
Anisotropy	0.369	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.23 , 16.2	EDS
L-test for twinning[2]	$< \|L\| > = 0.36$, $< L^2 > = 0.19$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.85	EDS
Total number of atoms	13663	wwPDB-VP
Average B, all atoms (Å^2)	113.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.08% of the height of the origin peak. No significant pseudotranslation is detected.*

[1]Intensities estimated from amplitudes.

[2]Theoretical values of $< |L| >$, $< L^2 >$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 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	0.63	0/1977	0.73	0/2681
1	B	0.65	0/1977	0.74	0/2681
1	C	0.64	0/1977	0.74	0/2681
1	D	0.63	0/1977	0.73	0/2681
1	E	0.60	0/1976	0.71	0/2679
1	F	0.62	0/1977	0.71	0/2681
1	G	0.63	0/1977	0.72	0/2681
All	All	0.63	0/13838	0.73	0/18765

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	1952	0	2042	40	0
1	B	1952	0	2042	44	0
1	C	1952	0	2042	50	0
1	D	1952	0	2042	41	0
1	E	1951	0	2042	38	0
1	F	1952	0	2042	40	0
1	G	1952	0	2042	48	0
All	All	13663	0	14294	272	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 (272) 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:B:61:ILE:HD12	1:B:62:ASP:N	1.72	1.04
1:F:61:ILE:HD11	1:F:66:ALA:HB2	1.40	1.00
1:E:61:ILE:HD11	1:E:66:ALA:HB2	1.43	0.98
1:B:61:ILE:HD11	1:B:66:ALA:HB2	1.45	0.96
1:D:56:MET:HE2	1:D:61:ILE:HD13	1.47	0.96
1:C:61:ILE:HD11	1:C:66:ALA:HB2	1.47	0.94
1:B:61:ILE:HD12	1:B:62:ASP:H	1.30	0.93
1:A:61:ILE:HD11	1:A:66:ALA:HB2	1.48	0.91
1:D:61:ILE:HD11	1:D:66:ALA:HB2	1.64	0.80
1:G:56:MET:HB3	1:G:61:ILE:HD11	1.65	0.78
1:G:56:MET:HE2	1:G:61:ILE:HD13	1.65	0.77
1:G:61:ILE:HD11	1:G:66:ALA:HB2	1.66	0.76
1:E:61:ILE:CD1	1:E:66:ALA:HB2	2.15	0.74
1:B:53:ASN:HB3	1:B:70:SER:HB2	1.69	0.73
1:G:56:MET:HE1	1:G:69:LEU:HD12	1.71	0.72
1:C:53:ASN:HB3	1:C:70:SER:HB2	1.72	0.72
1:C:56:MET:CE	1:C:66:ALA:HA	2.21	0.71
1:E:62:ASP:OD2	1:E:65:VAL:HG23	1.91	0.69
1:D:53:ASN:HB3	1:D:70:SER:HB2	1.76	0.67
1:D:201:VAL:HG22	1:D:266:ILE:HD13	1.76	0.67
1:E:201:VAL:HG22	1:E:266:ILE:HD13	1.79	0.64
1:B:61:ILE:CD1	1:B:62:ASP:H	2.08	0.64
1:A:61:ILE:HD12	1:A:62:ASP:N	2.14	0.63
1:B:201:VAL:HG22	1:B:266:ILE:HD13	1.80	0.63
1:F:61:ILE:CD1	1:F:66:ALA:HB2	2.25	0.63
1:G:56:MET:HB3	1:G:61:ILE:CD1	2.28	0.63
1:B:185:ARG:HB2	1:B:240:TRP:CD2	2.35	0.62
1:C:201:VAL:HG22	1:C:266:ILE:HD13	1.81	0.62
1:D:56:MET:HB3	1:D:61:ILE:CD1	2.30	0.62
1:G:201:VAL:HG22	1:G:266:ILE:HD13	1.82	0.61
1:C:225:LEU:CD1	1:C:233:ILE:HG23	2.31	0.61
1:G:56:MET:CE	1:G:61:ILE:HD13	2.30	0.61
1:D:225:LEU:CD1	1:D:233:ILE:HG23	2.30	0.61
1:A:150:ILE:HG23	1:A:151:PHE:N	2.16	0.61
1:B:45:ALA:HB2	1:B:77:ILE:HG22	1.82	0.61
1:D:61:ILE:CD1	1:D:66:ALA:HB2	2.30	0.61
1:F:201:VAL:HG22	1:F:266:ILE:HD13	1.83	0.60

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:48:ILE:O	1:E:52:VAL:HG23	2.01	0.60
1:E:150:ILE:HG23	1:E:151:PHE:N	2.17	0.60
1:C:56:MET:HE2	1:C:66:ALA:HA	1.82	0.60
1:E:53:ASN:HB3	1:E:70:SER:HB2	1.84	0.59
1:A:201:VAL:HG22	1:A:266:ILE:HD13	1.84	0.59
1:B:150:ILE:HG23	1:B:151:PHE:N	2.18	0.59
1:C:45:ALA:HB2	1:C:77:ILE:HG22	1.85	0.58
1:C:48:ILE:O	1:C:52:VAL:HG23	2.03	0.58
1:E:56:MET:HE2	1:E:61:ILE:HD13	1.84	0.58
1:F:56:MET:HB3	1:F:61:ILE:HG12	1.86	0.58
1:F:185:ARG:HB2	1:F:240:TRP:CD2	2.38	0.58
1:F:53:ASN:HB3	1:F:70:SER:HB2	1.86	0.58
1:G:56:MET:CE	1:G:69:LEU:HD12	2.35	0.57
1:D:56:MET:HB3	1:D:61:ILE:HD11	1.85	0.57
1:C:56:MET:HE1	1:C:66:ALA:HA	1.86	0.57
1:D:130:PHE:CD1	1:D:145:VAL:HG21	2.39	0.57
1:A:185:ARG:HB2	1:A:240:TRP:CD2	2.40	0.57
1:G:61:ILE:CD1	1:G:66:ALA:HB2	2.34	0.56
1:A:150:ILE:HG23	1:A:151:PHE:CD2	2.40	0.56
1:A:251:TRP:CE3	1:G:224:ARG:HD3	2.40	0.56
1:G:130:PHE:CD1	1:G:145:VAL:HG21	2.41	0.56
1:B:130:PHE:CD1	1:B:145:VAL:HG21	2.41	0.56
1:C:185:ARG:HB2	1:C:240:TRP:CD2	2.40	0.56
1:C:61:ILE:HD12	1:C:62:ASP:N	2.21	0.56
1:C:56:MET:HE3	1:C:69:LEU:HD12	1.87	0.55
1:A:275:VAL:HG23	1:G:275:VAL:HG13	1.89	0.55
1:G:185:ARG:HB2	1:G:240:TRP:CD2	2.42	0.55
1:A:91:VAL:O	1:A:93:THR:N	2.40	0.55
1:E:225:LEU:CD1	1:E:233:ILE:HG23	2.36	0.55
1:F:150:ILE:HG23	1:F:151:PHE:N	2.22	0.55
1:A:225:LEU:CD1	1:A:233:ILE:HG23	2.37	0.55
1:D:150:ILE:HG23	1:D:151:PHE:N	2.22	0.55
1:G:190:ILE:N	1:G:190:ILE:HD12	2.23	0.54
1:B:91:VAL:O	1:B:93:THR:N	2.41	0.54
1:D:45:ALA:HB2	1:D:77:ILE:HG22	1.88	0.54
1:G:91:VAL:O	1:G:93:THR:N	2.40	0.54
1:C:150:ILE:HG23	1:C:151:PHE:N	2.23	0.54
1:G:225:LEU:CD1	1:G:233:ILE:HG23	2.38	0.54
1:E:91:VAL:O	1:E:93:THR:N	2.41	0.54
1:E:130:PHE:CD1	1:E:145:VAL:HG21	2.42	0.54
1:B:225:LEU:CD1	1:B:233:ILE:HG23	2.38	0.53

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:91:VAL:O	1:F:93:THR:N	2.41	0.53
1:C:91:VAL:O	1:C:93:THR:N	2.42	0.53
1:A:53:ASN:HB3	1:A:70:SER:HB2	1.90	0.53
1:A:130:PHE:CD1	1:A:145:VAL:HG21	2.43	0.53
1:F:225:LEU:CD1	1:F:233:ILE:HG23	2.39	0.53
1:G:150:ILE:HG23	1:G:151:PHE:CD2	2.44	0.53
1:D:91:VAL:O	1:D:93:THR:N	2.41	0.52
1:E:150:ILE:HG23	1:E:151:PHE:CD2	2.44	0.52
1:B:61:ILE:CD1	1:B:62:ASP:N	2.61	0.52
1:D:150:ILE:HG23	1:D:151:PHE:CD2	2.45	0.52
1:F:224:ARG:HD3	1:G:251:TRP:CE3	2.45	0.52
1:B:150:ILE:HG23	1:B:151:PHE:CD2	2.44	0.51
1:F:150:ILE:HG23	1:F:151:PHE:CD2	2.45	0.51
1:E:92:GLN:O	1:E:94:ALA:N	2.44	0.51
1:F:130:PHE:CD1	1:F:145:VAL:HG21	2.45	0.51
1:A:251:TRP:CD2	1:G:224:ARG:HD3	2.45	0.51
1:G:56:MET:HE2	1:G:61:ILE:CD1	2.38	0.51
1:A:92:GLN:O	1:A:94:ALA:N	2.44	0.51
1:F:48:ILE:O	1:F:52:VAL:HG23	2.12	0.50
1:C:150:ILE:HG23	1:C:151:PHE:CD2	2.45	0.50
1:C:130:PHE:CD1	1:C:145:VAL:HG21	2.46	0.50
1:A:224:ARG:HD3	1:B:251:TRP:CE3	2.46	0.50
1:A:275:VAL:CG2	1:G:275:VAL:HG13	2.41	0.50
1:B:92:GLN:O	1:B:94:ALA:N	2.44	0.50
1:E:224:ARG:HD3	1:F:251:TRP:CE3	2.47	0.50
1:E:185:ARG:HB2	1:E:240:TRP:CD2	2.46	0.50
1:C:92:GLN:O	1:C:94:ALA:N	2.45	0.49
1:G:150:ILE:HG23	1:G:151:PHE:N	2.27	0.49
1:D:185:ARG:HB2	1:D:240:TRP:CD2	2.46	0.49
1:F:190:ILE:N	1:F:190:ILE:HD12	2.28	0.49
1:F:53:ASN:HB2	1:F:66:ALA:HB1	1.95	0.49
1:B:190:ILE:N	1:B:190:ILE:HD12	2.26	0.48
1:E:41:GLY:HA2	1:E:44:ILE:HG22	1.95	0.48
1:F:189:ILE:C	1:F:190:ILE:HD12	2.34	0.48
1:B:56:MET:HB3	1:B:61:ILE:HG12	1.95	0.48
1:A:146:LEU:HD12	1:A:154:THR:HG22	1.95	0.48
1:C:115:LEU:HD21	1:D:110:ALA:HB2	1.96	0.48
1:B:115:LEU:HD21	1:C:110:ALA:HB2	1.94	0.48
1:C:61:ILE:O	1:C:62:ASP:HB2	2.12	0.48
1:F:92:GLN:O	1:F:94:ALA:N	2.46	0.48
1:G:189:ILE:C	1:G:190:ILE:HD12	2.33	0.48

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:37:ILE:CG2	1:D:85:ALA:HB2	2.43	0.48
1:C:56:MET:HB3	1:C:61:ILE:HG12	1.94	0.48
1:C:61:ILE:HD11	1:C:66:ALA:CB	2.33	0.48
1:D:92:GLN:O	1:D:94:ALA:N	2.46	0.48
1:A:190:ILE:N	1:A:190:ILE:HD12	2.28	0.47
1:G:92:GLN:O	1:G:94:ALA:N	2.47	0.47
1:B:124:CYS:SG	1:B:171:ILE:HD13	2.54	0.47
1:G:45:ALA:HB2	1:G:77:ILE:HG22	1.95	0.47
1:A:46:ARG:HE	1:A:74:ARG:HH21	1.61	0.47
1:A:56:MET:HB3	1:A:61:ILE:HG12	1.97	0.47
1:B:41:GLY:HA3	1:B:81:THR:HG21	1.96	0.47
1:C:190:ILE:HD12	1:C:190:ILE:N	2.29	0.47
1:D:56:MET:HE2	1:D:61:ILE:CD1	2.32	0.47
1:E:150:ILE:HG23	1:E:151:PHE:H	1.80	0.47
1:A:233:ILE:HD11	1:B:258:LYS:HE2	1.96	0.46
1:A:150:ILE:HG23	1:A:151:PHE:H	1.80	0.46
1:B:150:ILE:HG23	1:B:151:PHE:H	1.80	0.46
1:D:122:VAL:O	1:D:125:VAL:HG22	2.16	0.46
1:B:185:ARG:HB2	1:B:240:TRP:CE2	2.50	0.46
1:B:227:GLU:HB3	1:B:234:ASN:HB2	1.97	0.46
1:A:37:ILE:HG22	1:A:85:ALA:HB2	1.98	0.45
1:A:227:GLU:HB3	1:A:234:ASN:HB2	1.97	0.45
1:G:56:MET:HE2	1:G:66:ALA:HA	1.98	0.45
1:C:224:ARG:HD3	1:D:251:TRP:CE3	2.51	0.45
1:D:190:ILE:N	1:D:190:ILE:HD12	2.32	0.45
1:C:227:GLU:HB3	1:C:234:ASN:HB2	1.99	0.45
1:C:61:ILE:HD12	1:C:62:ASP:O	2.17	0.45
1:D:52:VAL:O	1:D:55:LEU:HB3	2.17	0.45
1:F:61:ILE:O	1:F:62:ASP:HB2	2.16	0.45
1:A:61:ILE:HD12	1:A:62:ASP:H	1.82	0.45
1:D:61:ILE:O	1:D:62:ASP:HB2	2.17	0.45
1:D:227:GLU:HB3	1:D:234:ASN:HB2	1.99	0.45
1:G:61:ILE:O	1:G:62:ASP:HB2	2.16	0.45
1:F:275:VAL:HG13	1:G:275:VAL:HG23	1.98	0.45
1:G:128:ARG:N	1:G:129:PRO:CD	2.79	0.45
1:E:45:ALA:HB2	1:E:77:ILE:HG22	1.99	0.45
1:F:46:ARG:HE	1:F:74:ARG:HH21	1.64	0.45
1:A:189:ILE:C	1:A:190:ILE:HD12	2.37	0.44
1:A:37:ILE:CG2	1:A:85:ALA:HB2	2.47	0.44
1:B:189:ILE:C	1:B:190:ILE:HD12	2.37	0.44
1:C:93:THR:HG21	1:D:92:GLN:HE21	1.82	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:53:ASN:HB3	1:G:70:SER:HB2	1.98	0.44
1:A:150:ILE:CG2	1:A:151:PHE:N	2.81	0.44
1:C:122:VAL:O	1:C:125:VAL:HG22	2.18	0.44
1:E:227:GLU:HB3	1:E:234:ASN:HB2	1.99	0.44
1:C:201:VAL:HG11	1:C:235:PHE:CD1	2.52	0.44
1:F:185:ARG:HB2	1:F:240:TRP:CE2	2.53	0.44
1:F:227:GLU:HB3	1:F:234:ASN:HB2	2.00	0.44
1:B:93:THR:HG21	1:C:92:GLN:HE21	1.83	0.44
1:A:251:TRP:HB3	1:G:224:ARG:HH11	1.83	0.44
1:C:53:ASN:HB2	1:C:66:ALA:HB1	1.99	0.44
1:C:225:LEU:HD23	1:D:255:GLU:HA	1.99	0.44
1:F:137:ASP:HB3	1:F:176:ILE:HB	2.00	0.44
1:C:189:ILE:C	1:C:190:ILE:HD12	2.38	0.43
1:F:94:ALA:HA	1:F:97:ILE:HG12	2.00	0.43
1:C:124:CYS:SG	1:C:171:ILE:HD13	2.58	0.43
1:C:233:ILE:HD11	1:D:258:LYS:HE2	2.01	0.43
1:E:56:MET:HB3	1:E:61:ILE:CD1	2.47	0.43
1:G:94:ALA:HA	1:G:97:ILE:HG12	2.00	0.43
1:C:37:ILE:CG2	1:C:85:ALA:HB2	2.49	0.43
1:C:223:VAL:O	1:C:224:ARG:HG3	2.19	0.43
1:D:37:ILE:HG22	1:D:85:ALA:HB2	2.00	0.43
1:D:45:ALA:HB2	1:D:77:ILE:CG2	2.48	0.43
1:G:227:GLU:HB3	1:G:234:ASN:HB2	2.00	0.43
1:G:56:MET:HE1	1:G:69:LEU:HB2	2.00	0.43
1:G:122:VAL:O	1:G:125:VAL:HG22	2.18	0.43
1:G:146:LEU:HD12	1:G:154:THR:HG22	2.00	0.43
1:B:45:ALA:HB2	1:B:77:ILE:CG2	2.46	0.43
1:E:150:ILE:CG2	1:E:151:PHE:N	2.81	0.43
1:C:146:LEU:HD12	1:C:154:THR:HG22	2.01	0.43
1:E:190:ILE:HD12	1:E:190:ILE:N	2.34	0.43
1:B:201:VAL:HG11	1:B:235:PHE:CD1	2.53	0.43
1:D:146:LEU:HD12	1:D:154:THR:HG22	2.00	0.43
1:A:122:VAL:O	1:A:125:VAL:HG22	2.19	0.42
1:A:178:PHE:CE2	1:B:161:LYS:HD3	2.54	0.42
1:B:150:ILE:CG2	1:B:151:PHE:N	2.82	0.42
1:D:223:VAL:O	1:D:224:ARG:HG3	2.19	0.42
1:E:56:MET:HB3	1:E:61:ILE:HG12	2.01	0.42
1:A:45:ALA:HB2	1:A:77:ILE:HG22	2.01	0.42
1:C:41:GLY:HA3	1:C:81:THR:HG21	2.01	0.42
1:D:94:ALA:HA	1:D:97:ILE:HG12	2.01	0.42
1:F:150:ILE:HG23	1:F:151:PHE:H	1.84	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:224:ARG:HD3	1:B:251:TRP:CD2	2.54	0.42
1:D:53:ASN:HB2	1:D:66:ALA:HB1	2.00	0.42
1:E:56:MET:HE1	1:E:69:LEU:HB2	2.02	0.42
1:E:61:ILE:O	1:E:62:ASP:HB2	2.20	0.42
1:C:45:ALA:HB2	1:C:77:ILE:CG2	2.48	0.42
1:C:201:VAL:HG11	1:C:235:PHE:CE1	2.54	0.42
1:F:225:LEU:HD23	1:G:255:GLU:HA	2.01	0.42
1:A:110:ALA:HB2	1:G:115:LEU:HD21	2.01	0.42
1:F:41:GLY:HA2	1:F:44:ILE:HG22	2.01	0.42
1:A:94:ALA:HA	1:A:97:ILE:HG12	2.02	0.42
1:C:128:ARG:N	1:C:129:PRO:CD	2.82	0.42
1:E:94:ALA:HA	1:E:97:ILE:HG12	2.02	0.42
1:D:233:ILE:HD11	1:E:258:LYS:HE2	2.02	0.42
1:E:221:MET:HB3	1:E:221:MET:HE2	1.79	0.42
1:G:223:VAL:O	1:G:224:ARG:HG3	2.19	0.42
1:A:223:VAL:O	1:A:224:ARG:HG3	2.20	0.42
1:B:201:VAL:HG11	1:B:235:PHE:CE1	2.55	0.42
1:C:112:GLN:O	1:C:113:GLY:C	2.59	0.41
1:C:185:ARG:HB2	1:C:240:TRP:CE2	2.55	0.41
1:E:124:CYS:SG	1:E:171:ILE:HD13	2.60	0.41
1:G:41:GLY:HA2	1:G:44:ILE:HG22	2.02	0.41
1:D:128:ARG:N	1:D:129:PRO:CD	2.82	0.41
1:E:93:THR:HG21	1:F:92:GLN:HE21	1.85	0.41
1:E:137:ASP:HB3	1:E:176:ILE:HB	2.01	0.41
1:B:223:VAL:O	1:B:224:ARG:HG3	2.21	0.41
1:C:76:GLY:O	1:C:79:ALA:HB3	2.20	0.41
1:B:224:ARG:HD3	1:C:251:TRP:CE3	2.55	0.41
1:D:215:ILE:HD11	1:D:239:VAL:HG21	2.03	0.41
1:E:223:VAL:O	1:E:224:ARG:HG3	2.20	0.41
1:F:233:ILE:HD11	1:G:258:LYS:HE2	2.02	0.41
1:B:61:ILE:HD12	1:B:62:ASP:O	2.20	0.41
1:C:120:ALA:HB3	1:C:167:ASN:HB3	2.03	0.41
1:E:76:GLY:O	1:E:79:ALA:HB3	2.21	0.41
1:F:128:ARG:N	1:F:129:PRO:CD	2.83	0.41
1:F:223:VAL:O	1:F:224:ARG:HG3	2.21	0.41
1:B:61:ILE:O	1:B:62:ASP:HB2	2.19	0.41
1:D:224:ARG:HD3	1:E:251:TRP:CE3	2.56	0.41
1:E:122:VAL:O	1:E:125:VAL:HG22	2.20	0.41
1:F:61:ILE:HD12	1:F:62:ASP:N	2.36	0.41
1:G:222:THR:O	1:G:237:VAL:HA	2.21	0.41
1:A:92:GLN:O	1:A:92:GLN:HG3	2.21	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:122:VAL:O	1:B:125:VAL:HG22	2.21	0.41
1:B:163:ILE:HG22	1:B:165:ILE:HG13	2.03	0.41
1:C:52:VAL:O	1:C:55:LEU:HB3	2.21	0.41
1:D:76:GLY:O	1:D:79:ALA:HB3	2.21	0.41
1:D:112:GLN:O	1:D:113:GLY:C	2.58	0.41
1:E:37:ILE:HG22	1:E:81:THR:HG23	2.03	0.41
1:E:92:GLN:O	1:E:92:GLN:HG3	2.21	0.41
1:F:92:GLN:O	1:F:92:GLN:HG3	2.21	0.41
1:F:178:PHE:CE2	1:G:161:LYS:HD3	2.56	0.41
1:G:221:MET:HB3	1:G:221:MET:HE2	1.84	0.41
1:B:76:GLY:O	1:B:79:ALA:HB3	2.21	0.41
1:B:210:GLN:OE1	1:B:221:MET:HE1	2.21	0.41
1:C:92:GLN:O	1:C:92:GLN:HG3	2.21	0.41
1:C:222:THR:O	1:C:237:VAL:HA	2.22	0.41
1:D:201:VAL:HG11	1:D:235:PHE:CD1	2.56	0.41
1:G:92:GLN:O	1:G:92:GLN:HG3	2.21	0.41
1:F:188:PHE:HB3	1:F:190:ILE:CD1	2.51	0.40
1:A:225:LEU:HD23	1:B:255:GLU:HA	2.03	0.40
1:F:146:LEU:HD12	1:F:154:THR:HG22	2.03	0.40
1:A:52:VAL:O	1:A:55:LEU:HB3	2.22	0.40
1:A:76:GLY:O	1:A:79:ALA:HB3	2.21	0.40
1:D:137:ASP:HB3	1:D:176:ILE:HB	2.04	0.40
1:F:56:MET:HE3	1:F:69:LEU:HD12	2.03	0.40
1:F:114:SER:O	1:F:115:LEU:C	2.58	0.40
1:G:76:GLY:O	1:G:79:ALA:HB3	2.21	0.40
1:B:94:ALA:HA	1:B:97:ILE:HG12	2.02	0.40
1:E:222:THR:O	1:E:237:VAL:HA	2.21	0.40
1:B:92:GLN:O	1:B:92:GLN:HG3	2.21	0.40
1:F:224:ARG:HD3	1:G:251:TRP:CD2	2.56	0.40
1:G:137:ASP:HB3	1:G:176:ILE:HB	2.04	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	255/286 (89%)	231 (91%)	17 (7%)	7 (3%)	5	34
1	B	255/286 (89%)	229 (90%)	19 (8%)	7 (3%)	5	34
1	C	255/286 (89%)	230 (90%)	18 (7%)	7 (3%)	5	34
1	D	255/286 (89%)	231 (91%)	17 (7%)	7 (3%)	5	34
1	E	254/286 (89%)	230 (91%)	17 (7%)	7 (3%)	5	33
1	F	255/286 (89%)	229 (90%)	19 (8%)	7 (3%)	5	34
1	G	255/286 (89%)	230 (90%)	18 (7%)	7 (3%)	5	34
All	All	1784/2002 (89%)	1610 (90%)	125 (7%)	49 (3%)	5	34

All (49) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	60	LYS
1	A	61	ILE
1	A	62	ASP
1	A	92	GLN
1	A	93	THR
1	A	112	GLN
1	A	150	ILE
1	B	60	LYS
1	B	61	ILE
1	B	62	ASP
1	B	92	GLN
1	B	112	GLN
1	B	150	ILE
1	C	60	LYS
1	C	61	ILE
1	C	62	ASP
1	C	92	GLN
1	C	112	GLN
1	C	150	ILE
1	D	60	LYS
1	D	61	ILE
1	D	62	ASP
1	D	92	GLN
1	D	112	GLN
1	D	150	ILE
1	E	60	LYS

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	E	61	ILE
1	E	62	ASP
1	E	92	GLN
1	E	93	THR
1	E	112	GLN
1	E	150	ILE
1	F	60	LYS
1	F	61	ILE
1	F	62	ASP
1	F	92	GLN
1	F	112	GLN
1	F	150	ILE
1	G	60	LYS
1	G	61	ILE
1	G	62	ASP
1	G	92	GLN
1	G	112	GLN
1	G	150	ILE
1	B	93	THR
1	C	93	THR
1	D	93	THR
1	F	93	THR
1	G	93	THR

5.3.2 Protein sidechains (i)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all 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	208/231 (90%)	201 (97%)	7 (3%)	37	61
1	B	208/231 (90%)	203 (98%)	5 (2%)	49	69
1	C	208/231 (90%)	203 (98%)	5 (2%)	49	69
1	D	208/231 (90%)	205 (99%)	3 (1%)	67	81
1	E	208/231 (90%)	203 (98%)	5 (2%)	49	69
1	F	208/231 (90%)	200 (96%)	8 (4%)	33	58

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	G	208/231 (90%)	203 (98%)	5 (2%)	49	69
All	All	1456/1617 (90%)	1418 (97%)	38 (3%)	46	67

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

Mol	Chain	Res	Type
1	A	29	VAL
1	A	37	ILE
1	A	42	LEU
1	A	47	MET
1	A	53	ASN
1	A	54	ARG
1	A	256	ARG
1	B	47	MET
1	B	53	ASN
1	B	54	ARG
1	B	219	ARG
1	B	256	ARG
1	C	48	ILE
1	C	49	SER
1	C	54	ARG
1	C	219	ARG
1	C	256	ARG
1	D	53	ASN
1	D	61	ILE
1	D	256	ARG
1	E	26	SER
1	E	53	ASN
1	E	54	ARG
1	E	61	ILE
1	E	256	ARG
1	F	26	SER
1	F	29	VAL
1	F	53	ASN
1	F	54	ARG
1	F	60	LYS
1	F	64	THR
1	F	256	ARG
1	F	280	VAL
1	G	26	SER
1	G	53	ASN
1	G	54	ARG

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	G	256	ARG
1	G	280	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	C	53	ASN

5.3.3 RNA (i)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates (i)

There are no monosaccharides 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 (i)

6.1 Protein, DNA and RNA chains (i)

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	257/286 (89%)	0.04	13 (5%)	28	25	110, 113, 118, 134	0
1	B	257/286 (89%)	-0.12	5 (1%)	66	58	110, 113, 118, 135	0
1	C	257/286 (89%)	-0.17	1 (0%)	92	87	110, 113, 118, 135	0
1	D	257/286 (89%)	-0.05	7 (2%)	54	45	110, 113, 118, 134	0
1	E	256/286 (89%)	-0.09	5 (1%)	65	56	110, 113, 117, 134	0
1	F	257/286 (89%)	-0.09	6 (2%)	60	52	110, 113, 118, 134	0
1	G	257/286 (89%)	-0.07	7 (2%)	54	45	110, 113, 118, 135	0
All	All	1798/2002 (89%)	-0.08	44 (2%)	59	50	110, 113, 118, 135	0

All (44) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	G	281	LYS	6.7
1	G	280	VAL	5.1
1	A	280	VAL	3.6
1	E	279	ARG	3.6
1	E	278	LYS	3.5
1	F	277	PHE	3.5
1	F	275	VAL	3.4
1	A	279	ARG	3.4
1	D	280	VAL	3.3
1	A	281	LYS	3.3
1	G	279	ARG	3.1
1	E	277	PHE	3.0
1	D	231	SER	3.0
1	A	55	LEU	3.0
1	G	130	PHE	2.9
1	A	88	ARG	2.8
1	C	223	VAL	2.7

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	D	59	ARG	2.7
1	D	278	LYS	2.7
1	B	266	ILE	2.7
1	E	280	VAL	2.6
1	D	228	LEU	2.5
1	B	268	PHE	2.5
1	D	279	ARG	2.5
1	A	135	TYR	2.5
1	D	223	VAL	2.5
1	G	210	GLN	2.5
1	B	280	VAL	2.4
1	A	136	VAL	2.3
1	G	228	LEU	2.3
1	F	223	VAL	2.3
1	B	281	LYS	2.3
1	E	47	MET	2.3
1	F	195	ASP	2.2
1	A	225	LEU	2.2
1	A	278	LYS	2.2
1	B	265	GLY	2.1
1	F	279	ARG	2.1
1	A	228	LEU	2.1
1	G	209	ILE	2.1
1	A	61	ILE	2.1
1	A	56	MET	2.1
1	A	51	ALA	2.0
1	F	276	ASN	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 monosaccharides 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.