



Full wwPDB X-ray Structure Validation Report ⓘ

May 15, 2020 – 04:34 am BST

PDB ID : 5GMI
Title : Crystal Structure of GRASP55 GRASP domain in complex with JAM-C C-terminus
Authors : Shi, N.; Shi, X.; Morelli, X.; Betzi, S.; Huang, X.
Deposited on : 2016-07-14
Resolution : 2.71 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 following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.11
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)	:	2.11

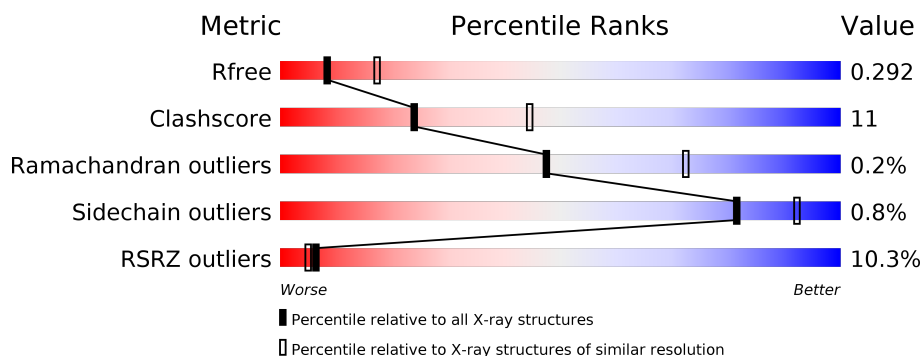
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.71 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	3359 (2.74-2.70)
Clashscore	141614	3686 (2.74-2.70)
Ramachandran outliers	138981	3622 (2.74-2.70)
Sidechain outliers	138945	3623 (2.74-2.70)
RSRZ outliers	127900	3276 (2.74-2.70)

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 on 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	235	<div> <div>9%</div> <div>72%</div> <div>20%</div> <div>• 5%</div> </div>
1	B	235	<div> <div>8%</div> <div>80%</div> <div>15%</div> <div>5%</div> </div>
2	C	19	<div> <div>26%</div> <div>11%</div> <div>16%</div> <div>74%</div> </div>
2	D	19	<div> <div>5%</div> <div>26%</div> <div>74%</div> </div>

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 3611 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 Golgi reassembly-stacking protein 2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	223	Total	C	N	O	S	0	2	0
			1727	1089	298	335	5			
1	B	223	Total	C	N	O	S	0	0	0
			1713	1080	294	334	5			

There are 56 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-26	MET	-	expression tag	UNP Q99JX3
A	-25	SER	-	expression tag	UNP Q99JX3
A	-24	TYR	-	expression tag	UNP Q99JX3
A	-23	TYR	-	expression tag	UNP Q99JX3
A	-22	HIS	-	expression tag	UNP Q99JX3
A	-21	HIS	-	expression tag	UNP Q99JX3
A	-20	HIS	-	expression tag	UNP Q99JX3
A	-19	HIS	-	expression tag	UNP Q99JX3
A	-18	HIS	-	expression tag	UNP Q99JX3
A	-17	HIS	-	expression tag	UNP Q99JX3
A	-16	LEU	-	expression tag	UNP Q99JX3
A	-15	GLU	-	expression tag	UNP Q99JX3
A	-14	SER	-	expression tag	UNP Q99JX3
A	-13	THR	-	expression tag	UNP Q99JX3
A	-12	SER	-	expression tag	UNP Q99JX3
A	-11	LEU	-	expression tag	UNP Q99JX3
A	-10	TYR	-	expression tag	UNP Q99JX3
A	-9	LYS	-	expression tag	UNP Q99JX3
A	-8	LYS	-	expression tag	UNP Q99JX3
A	-7	ALA	-	expression tag	UNP Q99JX3
A	-6	GLY	-	expression tag	UNP Q99JX3
A	-5	PHE	-	expression tag	UNP Q99JX3
A	-4	LEU	-	expression tag	UNP Q99JX3
A	-3	VAL	-	expression tag	UNP Q99JX3
A	-2	PRO	-	expression tag	UNP Q99JX3

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
A	-1	ARG	-	expression tag	UNP Q99JX3
A	0	GLY	-	expression tag	UNP Q99JX3
A	1	SER	-	expression tag	UNP Q99JX3
B	-26	MET	-	expression tag	UNP Q99JX3
B	-25	SER	-	expression tag	UNP Q99JX3
B	-24	TYR	-	expression tag	UNP Q99JX3
B	-23	TYR	-	expression tag	UNP Q99JX3
B	-22	HIS	-	expression tag	UNP Q99JX3
B	-21	HIS	-	expression tag	UNP Q99JX3
B	-20	HIS	-	expression tag	UNP Q99JX3
B	-19	HIS	-	expression tag	UNP Q99JX3
B	-18	HIS	-	expression tag	UNP Q99JX3
B	-17	HIS	-	expression tag	UNP Q99JX3
B	-16	LEU	-	expression tag	UNP Q99JX3
B	-15	GLU	-	expression tag	UNP Q99JX3
B	-14	SER	-	expression tag	UNP Q99JX3
B	-13	THR	-	expression tag	UNP Q99JX3
B	-12	SER	-	expression tag	UNP Q99JX3
B	-11	LEU	-	expression tag	UNP Q99JX3
B	-10	TYR	-	expression tag	UNP Q99JX3
B	-9	LYS	-	expression tag	UNP Q99JX3
B	-8	LYS	-	expression tag	UNP Q99JX3
B	-7	ALA	-	expression tag	UNP Q99JX3
B	-6	GLY	-	expression tag	UNP Q99JX3
B	-5	PHE	-	expression tag	UNP Q99JX3
B	-4	LEU	-	expression tag	UNP Q99JX3
B	-3	VAL	-	expression tag	UNP Q99JX3
B	-2	PRO	-	expression tag	UNP Q99JX3
B	-1	ARG	-	expression tag	UNP Q99JX3
B	0	GLY	-	expression tag	UNP Q99JX3
B	1	SER	-	expression tag	UNP Q99JX3

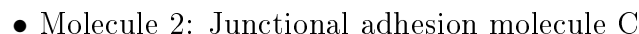
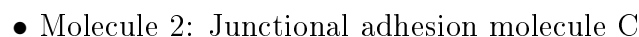
- Molecule 2 is a protein called Junctional adhesion molecule C.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	C	5	Total	C	N	O	0	1	0
			43	30	5	8			
2	D	5	Total	C	N	O	0	0	0
			39	26	5	8			

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	45	Total 45	O 45	0	0
3	B	44	Total 44	O 44	0	0

- Molecule 1: Golgi reassembly-stacking protein 2



4 Data and refinement statistics

Property	Value	Source
Space group	I 41 2 2	Depositor
Cell constants a, b, c, α , β , γ	132.49 Å 132.49 Å 220.71 Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	71.42 – 2.71 113.60 – 2.71	Depositor EDS
% Data completeness (in resolution range)	99.5 (71.42-2.71) 92.9 (113.60-2.71)	Depositor EDS
R_{merge}	0.14	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.36 (at 2.73 Å)	Xtriage
Refinement program	PHENIX 1.9_1692	Depositor
R, R_{free}	0.256 , 0.291 0.258 , 0.292	Depositor DCC
R_{free} test set	1990 reflections (7.42%)	wwPDB-VP
Wilson B-factor (Å ²)	46.5	Xtriage
Anisotropy	0.160	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 58.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.90	EDS
Total number of atoms	3611	wwPDB-VP
Average B, all atoms (Å ²)	72.0	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 41.86 % 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 2.2182e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

¹ Intensities estimated from amplitudes.

² Theoretical 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	0.29	0/1772	0.56	0/2403
1	B	0.28	0/1752	0.51	0/2377
2	C	0.27	0/51	0.36	0/66
2	D	0.23	0/39	0.32	0/50
All	All	0.28	0/3614	0.53	0/4896

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1
1	B	0	1
All	All	0	2

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	49	ASN	Peptide
1	B	90	TRP	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	1727	0	1694	49	0
1	B	1713	0	1673	28	0
2	C	43	0	39	5	0
2	D	39	0	38	0	0
3	A	45	0	0	4	0
3	B	44	0	0	7	0
All	All	3611	0	3444	77	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 11.

All (77) 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:A:-9:LYS:NZ	3:A:301:HOH:O	2.05	0.89
1:A:4:SER:HA	1:A:5:GLN:HB3	1.63	0.81
1:A:142:VAL:HG12	1:A:143:MET:HA	1.65	0.78
1:A:17:TYR:OH	1:A:50:LYS:NZ	2.22	0.73
1:A:140:ASP:OD1	2:C:306:SER:OG	2.06	0.71
1:A:4:SER:HA	1:A:5:GLN:CB	2.22	0.68
1:B:171:ASP:OD1	3:B:301:HOH:O	2.12	0.67
1:B:63:VAL:HG13	1:B:64:GLU:HG2	1.77	0.67
1:B:4:SER:HA	1:B:5:GLN:CG	2.27	0.65
1:A:63:VAL:HG13	1:A:64:GLU:HG2	1.78	0.65
1:B:168:THR:O	3:B:301:HOH:O	2.14	0.65
1:A:168:THR:O	3:B:301:HOH:O	2.14	0.65
1:A:107:GLY:O	1:A:111:ASN:ND2	2.32	0.62
1:A:7:VAL:HG13	1:A:8:GLU:HG2	1.79	0.62
1:A:101:ARG:NH1	1:A:139:ALA:O	2.33	0.62
1:A:156:HIS:HB3	1:A:159:LYS:O	2.00	0.61
1:B:0:GLY:O	1:B:201:ARG:NH2	2.33	0.60
1:B:26:SER:HA	1:B:90:TRP:NE1	2.17	0.60
1:A:50:LYS:HE3	1:A:55:LEU:H	1.67	0.59
1:A:100:ILE:HD13	2:C:310:ILE:HG12	1.84	0.59
1:A:50:LYS:CE	1:A:55:LEU:H	2.16	0.58
1:B:202:ILE:O	3:B:302:HOH:O	2.18	0.56
1:A:171:ASP:OD1	3:B:301:HOH:O	2.17	0.55
1:B:1:SER:N	1:B:3:SER:H	2.06	0.54
1:A:50:LYS:NZ	1:A:52:ASN:O	2.40	0.53
1:A:58:LEU:O	1:A:62:ASN:ND2	2.35	0.53
1:B:184:TRP:O	3:B:303:HOH:O	2.19	0.52
1:B:24:GLU:CD	1:B:24:GLU:H	2.13	0.52

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:90:TRP:O	1:B:90:TRP:CD1	2.64	0.51
1:A:3:SER:O	1:A:5:GLN:HB2	2.10	0.51
1:A:96:LEU:HD12	2:C:310:ILE:HD13	1.93	0.51
1:A:50:LYS:HG2	1:A:51:ASP:N	2.26	0.50
1:A:90:TRP:CZ3	1:A:92:GLY:HA3	2.47	0.49
1:B:146:SER:C	1:B:148:ASP:H	2.16	0.48
1:B:91:GLY:HA2	3:B:341:HOH:O	2.12	0.48
1:A:21:ARG:NH1	1:A:173:CYS:O	2.39	0.48
1:B:9:ILE:HG13	1:B:105:PHE:HZ	1.78	0.48
1:A:50:LYS:HE2	1:A:54:THR:HB	1.96	0.47
1:A:96:LEU:N	2:C:310:ILE:OXT	2.45	0.47
1:B:149:LEU:O	1:B:153:ILE:HG13	2.15	0.47
1:A:37:PHE:CD2	1:A:75:LYS:HB2	2.49	0.47
1:B:159:LYS:HA	1:B:159:LYS:HE3	1.96	0.47
1:B:109:ASN:HB3	1:B:201:ARG:NH2	2.30	0.47
1:A:50:LYS:HG3	1:A:52:ASN:OD1	2.15	0.46
1:A:17:TYR:HE2	1:A:50:LYS:HD3	1.80	0.46
1:A:51:ASP:HB2	1:A:102:PHE:CD2	2.50	0.46
1:B:90:TRP:O	1:B:90:TRP:CG	2.68	0.46
1:B:4:SER:HA	1:B:5:GLN:HG3	1.97	0.45
1:B:59:LEU:HD22	1:B:86:PRO:HG3	1.98	0.45
1:B:156:HIS:HB3	1:B:159:LYS:O	2.17	0.45
1:B:42:SER:HB3	1:B:70:LEU:HB3	1.99	0.44
1:A:110:GLU:HG2	1:A:201[A]:ARG:HH22	1.82	0.44
1:B:58:LEU:O	1:B:62:ASN:ND2	2.40	0.44
1:A:101:ARG:HG3	2:C:307:SER:HA	2.00	0.44
1:A:49:ASN:O	3:A:302:HOH:O	2.21	0.44
1:B:4:SER:HA	1:B:5:GLN:HG2	1.98	0.43
1:A:145:GLU:HG2	1:A:146:SER:N	2.33	0.43
1:A:50:LYS:HG2	1:A:52:ASN:H	1.82	0.43
1:A:0:GLY:O	1:A:201[B]:ARG:NH2	2.45	0.43
1:A:156:HIS:ND1	1:A:161:LEU:HB2	2.32	0.43
1:A:6:SER:O	1:A:8:GLU:HA	2.17	0.43
1:A:143:MET:CG	1:A:144:ASN:H	2.32	0.43
1:A:2:GLY:N	3:A:304:HOH:O	2.52	0.43
1:A:17:TYR:CD1	1:A:100:ILE:HD12	2.53	0.43
1:A:90:TRP:CH2	1:A:92:GLY:HA3	2.55	0.42
1:B:7:VAL:O	1:B:8:GLU:HG2	2.19	0.42
1:A:197:GLY:O	1:A:201[B]:ARG:HG3	2.20	0.42
1:B:1:SER:HA	1:B:2:GLY:HA2	1.71	0.42
1:A:143:MET:CG	1:A:144:ASN:N	2.83	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:156:HIS:CE1	1:A:161:LEU:HD13	2.55	0.42
1:A:154:GLU:N	1:A:154:GLU:OE1	2.52	0.41
1:A:184:TRP:CZ2	1:A:186:GLY:HA3	2.54	0.41
1:A:74:SER:O	1:A:109:ASN:ND2	2.53	0.41
1:A:91:GLY:N	3:A:315:HOH:O	2.46	0.41
1:A:50:LYS:HG3	1:A:52:ASN:CG	2.42	0.40
1:B:60:LYS:HE3	1:B:60:LYS:HB2	1.81	0.40
1:B:90:TRP:CH2	1:B:97:GLY:HA3	2.56	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	223/235 (95%)	203 (91%)	19 (8%)	1 (0%)	34	58
1	B	221/235 (94%)	204 (92%)	17 (8%)	0	100	100
2	C	4/19 (21%)	4 (100%)	0	0	100	100
2	D	3/19 (16%)	3 (100%)	0	0	100	100
All	All	451/508 (89%)	414 (92%)	36 (8%)	1 (0%)	47	72

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	5	GLN

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	190/200 (95%)	187 (98%)	3 (2%)	62	83
1	B	188/200 (94%)	188 (100%)	0	100	100
2	C	6/18 (33%)	6 (100%)	0	100	100
2	D	5/18 (28%)	5 (100%)	0	100	100
All	All	389/436 (89%)	386 (99%)	3 (1%)	81	92

All (3) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	6	SER
1	A	8	GLU
1	A	142	VAL

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

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry ⓘ

There are no ligands in this entry.

5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	223/235 (94%)	1.11	22 (9%) 7 6	41, 63, 144, 177	0
1	B	223/235 (94%)	1.03	19 (8%) 10 9	33, 58, 140, 191	0
2	C	5/19 (26%)	3.31	5 (100%) 0 0	134, 138, 170, 178	0
2	D	5/19 (26%)	1.59	1 (20%) 1 0	63, 68, 90, 108	0
All	All	456/508 (89%)	1.10	47 (10%) 6 5	33, 61, 146, 191	0

All (47) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	142	VAL	9.3
1	A	4	SER	6.6
1	A	153	ILE	6.2
1	B	143	MET	6.1
1	A	177	ILE	5.9
1	B	7	VAL	5.4
2	C	310	ILE	5.3
1	A	146	SER	5.3
1	A	159	LYS	5.3
1	B	3	SER	4.1
1	A	149	LEU	3.8
1	A	142	VAL	3.6
1	A	147	GLU	3.6
2	C	306	SER	3.6
1	B	147	GLU	3.3
1	B	5	GLN	3.3
1	B	139	ALA	3.2
1	B	153	ILE	3.2
1	A	152	LEU	3.2
1	A	162	LYS	3.2
1	A	145	GLU	3.1

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	B	185	GLY	3.0
2	C	309	VAL	2.9
1	A	148	ASP	2.8
1	A	3	SER	2.8
1	B	105	PHE	2.8
1	A	150	PHE	2.8
1	B	162	LYS	2.7
1	A	110	GLU	2.7
1	A	144	ASN	2.7
1	A	141	THR	2.7
1	B	90	TRP	2.6
1	B	1	SER	2.6
1	B	146	SER	2.5
2	C	308[A]	PHE	2.5
1	A	112	VAL	2.5
1	B	144	ASN	2.4
1	A	63	VAL	2.4
1	A	84	VAL	2.3
2	D	308	PHE	2.3
1	B	206	PRO	2.2
2	C	307	SER	2.2
1	A	161	LEU	2.2
1	B	164	TYR	2.2
1	B	2	GLY	2.2
1	B	157	GLU	2.1
1	A	113	TRP	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

There are no such residues in this entry.