Full wwPDB X-ray Structure Validation Report (i)

Feb 1, 2016 – 01:21 PM GMT

PDB ID	:	3TNN
Title	:	Crystal structure of N5-i5 Fab, an ADCC mediating and non-neutralizing CD4i anti-HIV- 1 antibody.
Authors	:	Wu, X.; Pazgier, M.
Deposited on	:	2011-09-01
Resolution	:	1.95 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 (i) symbol.

The following versions of software and data (see references (1)) were used in the production of this report:

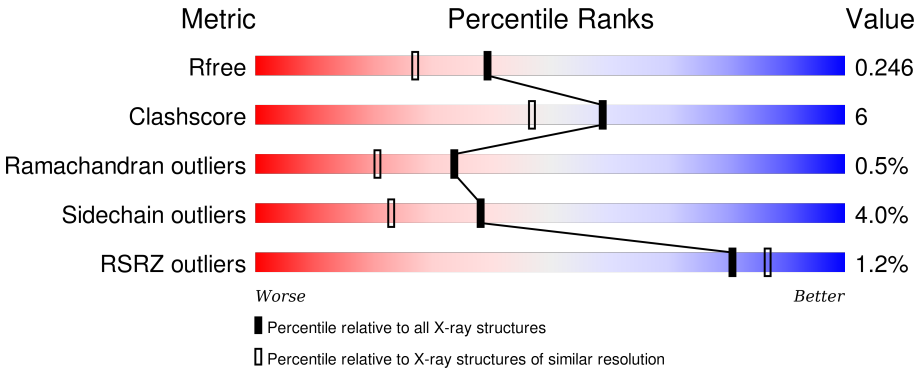
MolProbity	:	4.02b-467
Mogul	:	1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix)	:	1.9-1692
EDS	:	rb-20026688
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac	:	5.8.0135
CCP4	:	6.5.0
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)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

1 Overall quality at a glance (i)

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

The reported resolution of this entry is 1.95 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.



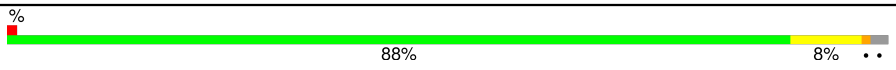
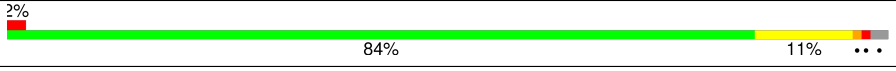
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	91344	1833 (1.96-1.96)
Clashscore	102246	1953 (1.96-1.96)
Ramachandran outliers	100387	1936 (1.96-1.96)
Sidechain outliers	100360	1936 (1.96-1.96)
RSRZ outliers	91569	1835 (1.96-1.96)

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 <=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	226	74% 18% • 6%
1	C	226	3% 77% 16% • 6%
1	E	226	% 76% 15% • 7%
1	H	226	% 79% 12% • 7%
2	B	217	88% 9% • •

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
2	D	217	
2	F	217	
2	L	217	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	SO4	H	222	-	-	-	X
4	GOL	H	223	-	-	-	X
5	CL	H	224	-	-	-	X

2 Entry composition (i)

There are 6 unique types of molecules in this entry. The entry contains 13429 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.

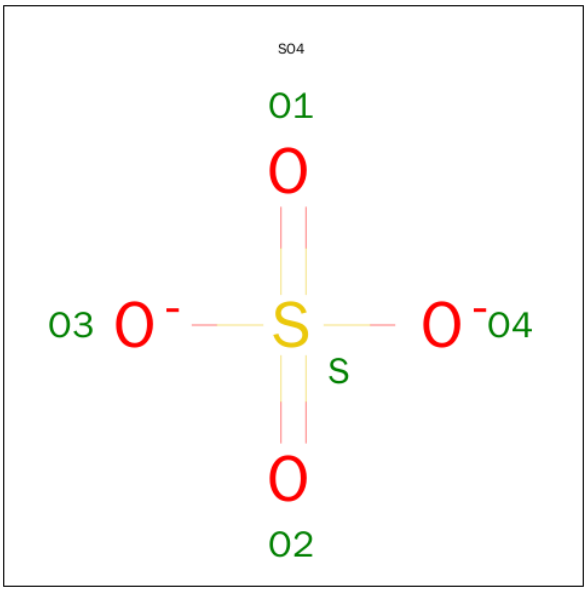
- Molecule 1 is a protein called Fab heavy chain of ADCC and non-neutralizing anti-HIV-1 antibody N5-i5.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	H	211	Total	C	N	O	S	0	0	0
			1564	982	268	308	6			
1	A	212	Total	C	N	O	S	0	0	0
			1571	987	269	309	6			
1	C	212	Total	C	N	O	S	0	0	0
			1571	987	269	309	6			
1	E	210	Total	C	N	O	S	0	0	0
			1555	977	267	305	6			

- Molecule 2 is a protein called Fab light chain of ADCC and non-neutralizing anti-HIV-1 antibody N5-i5.

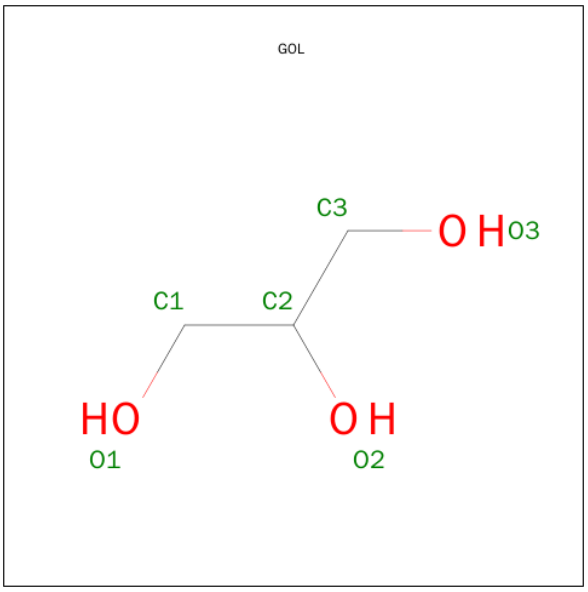
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	L	212	Total	C	N	O	S	0	0	0
			1575	982	264	324	5			
2	B	212	Total	C	N	O	S	0	0	0
			1575	982	264	324	5			
2	D	212	Total	C	N	O	S	0	0	0
			1575	982	264	324	5			
2	F	212	Total	C	N	O	S	0	0	0
			1575	982	264	324	5			

- Molecule 3 is SULFATE ION (three-letter code: SO4) (formula: O_4S).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	H	1	Total O S 5 4 1	0	0
3	H	1	Total O S 5 4 1	0	0
3	L	1	Total O S 5 4 1	0	0
3	B	1	Total O S 5 4 1	0	0
3	D	1	Total O S 5 4 1	0	0
3	D	1	Total O S 5 4 1	0	0
3	F	1	Total O S 5 4 1	0	0
3	F	1	Total O S 5 4 1	0	0

- Molecule 4 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	H	1	Total C O 6 3 3	0	0
4	L	1	Total C O 6 3 3	0	0

- Molecule 5 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	D	2	Total Cl 2 2	0	0
5	E	3	Total Cl 3 3	0	0
5	H	2	Total Cl 2 2	0	0
5	B	2	Total Cl 2 2	0	0
5	A	1	Total Cl 1 1	0	0
5	L	2	Total Cl 2 2	0	0
5	F	2	Total Cl 2 2	0	0

- Molecule 6 is water.

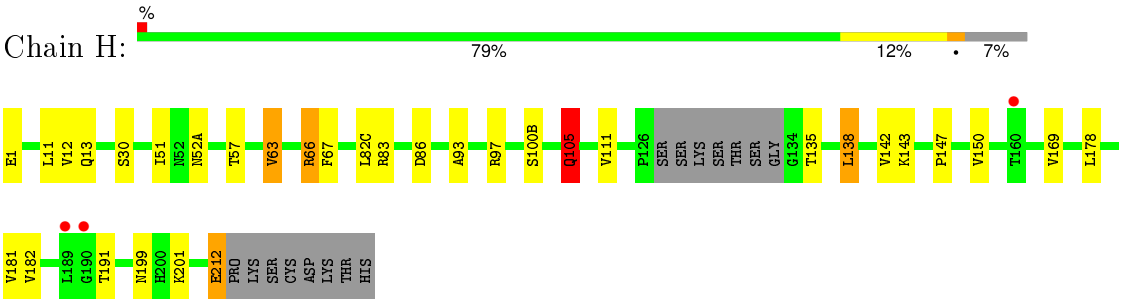
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	H	105	Total O 105 105	0	0
6	L	116	Total O 116 116	0	0
6	A	76	Total O 76 76	0	0
6	B	91	Total O 91 91	0	0
6	C	59	Total O 59 59	0	0
6	D	97	Total O 97 97	0	0
6	E	124	Total O 124 124	0	0
6	F	134	Total O 134 134	0	0

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.

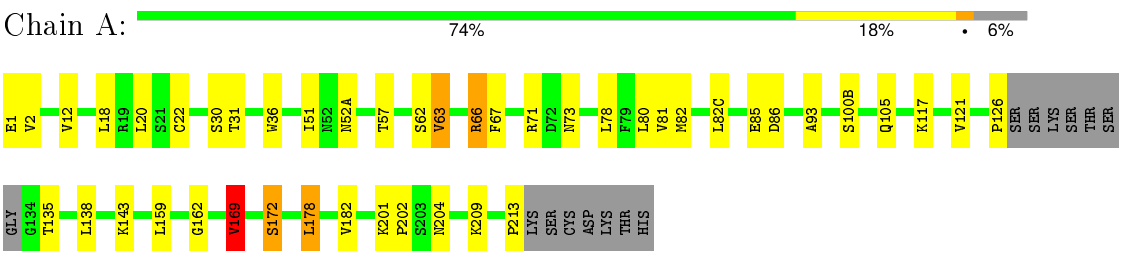
- Molecule 1: Fab heavy chain of ADCC and non-neutralizing anti-HIV-1 antibody N5-i5

Chain H:



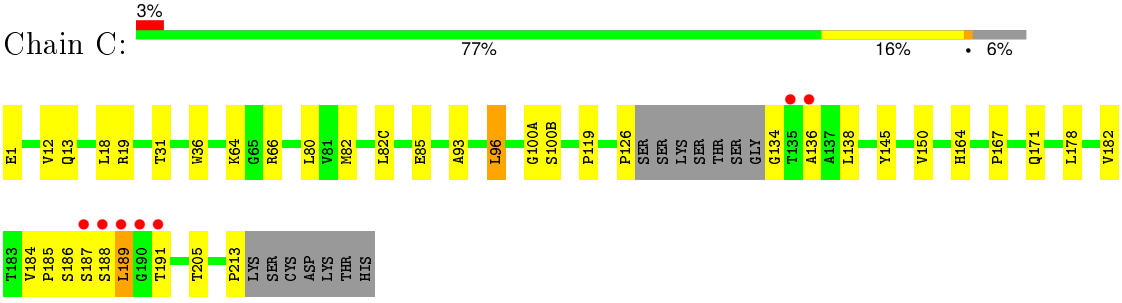
- Molecule 1: Fab heavy chain of ADCC and non-neutralizing anti-HIV-1 antibody N5-i5

Chain A:



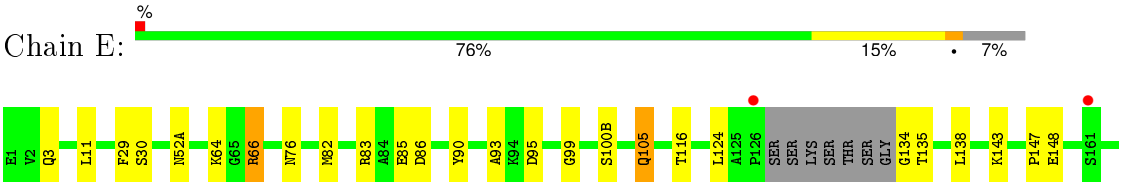
- Molecule 1: Fab heavy chain of ADCC and non-neutralizing anti-HIV-1 antibody N5-i5

Chain C:



- Molecule 1: Fab heavy chain of ADCC and non-neutralizing anti-HIV-1 antibody N5-i5

Chain E:

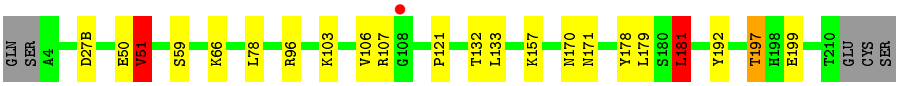


• Molecule 2: Fab light chain of ADCC and non-neutralizing anti-HIV-1 antibody N5-i5

Chain L:

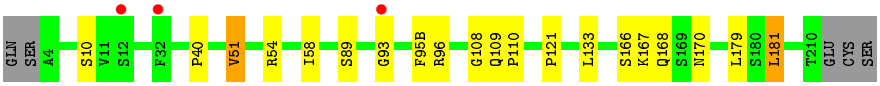
• Molecule 2: Fab light chain of ADCC and non-neutralizing anti-HIV-1 antibody N5-i5

Chain B:



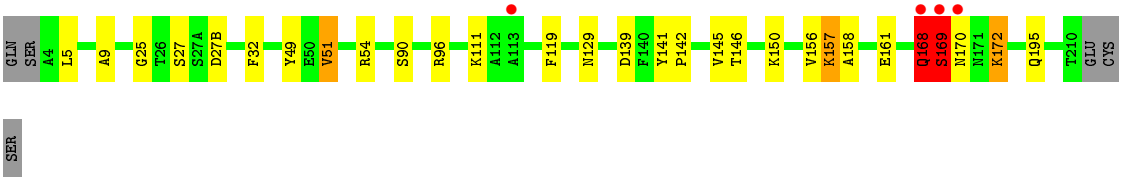
• Molecule 2: Fab light chain of ADCC and non-neutralizing anti-HIV-1 antibody N5-i5

Chain D:



• Molecule 2: Fab light chain of ADCC and non-neutralizing anti-HIV-1 antibody N5-i5

Chain F:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	73.44Å 84.50Å 143.12Å 90.00° 101.08° 90.00°	Depositor
Resolution (Å)	20.00 – 1.95 40.45 – 1.94	Depositor EDS
% Data completeness (in resolution range)	97.9 (20.00-1.95) 97.9 (40.45-1.94)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	0.08	Depositor
$< I/\sigma(I) >$ [1]	2.22 (at 1.95Å)	Xtriage
Refinement program	REFMAC 5.5.0109	Depositor
R, R_{free}	0.198 , 0.245 0.199 , 0.246	Depositor DCC
R_{free} test set	6186 reflections (5.29%)	DCC
Wilson B-factor (Å^2)	29.8	Xtriage
Anisotropy	0.555	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.39 , 51.5	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning[2]	$< \|L\| > = 0.48$, $< L^2 > = 0.31$	Xtriage
Outliers	8 of 123791 reflections (0.006%)	Xtriage
F_o,F_c correlation	0.96	EDS
Total number of atoms	13429	wwPDB-VP
Average B, all atoms (Å^2)	39.0	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 44.29 % of the origin peak, indicating pseudo translational symmetry.The chance of finding a peak of this or larger height randomly in a structure without pseudo translational symmetry is equal to 1.5582e-04.The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ for acentric reflections are 0.5, 0.375 respectively for untwinned datasets, and 0.333, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: GOL, SO4, CL

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	1/1605 (0.1%)	0.83	3/2184 (0.1%)
1	C	0.80	2/1605 (0.1%)	0.79	2/2184 (0.1%)
1	E	1.05	2/1588 (0.1%)	0.99	7/2160 (0.3%)
1	H	0.99	1/1597 (0.1%)	0.97	3/2172 (0.1%)
2	B	0.84	0/1613	0.78	1/2198 (0.0%)
2	D	0.82	1/1613 (0.1%)	0.80	0/2198
2	F	0.99	2/1613 (0.1%)	0.89	3/2198 (0.1%)
2	L	0.98	1/1613 (0.1%)	0.90	2/2198 (0.1%)
All	All	0.92	10/12847 (0.1%)	0.87	21/17492 (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
2	B	0	1
2	D	0	1
2	F	0	1
All	All	0	3

All (10) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	F	49	TYR	CD1-CE1	7.48	1.50	1.39
2	D	10	SER	C-N	6.73	1.49	1.34
1	E	90	TYR	CD2-CE2	6.38	1.49	1.39
1	E	148	GLU	CD-OE2	6.16	1.32	1.25
1	C	85	GLU	CG-CD	5.99	1.60	1.51
1	H	105	GLN	CG-CD	5.74	1.64	1.51
2	L	10	SER	C-N	5.33	1.46	1.34

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	F	9	ALA	CA-CB	5.20	1.63	1.52
1	C	85	GLU	CB-CG	5.04	1.61	1.52
1	A	85	GLU	CG-CD	5.02	1.59	1.51

All (21) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	E	66	ARG	NE-CZ-NH2	-15.18	112.71	120.30
1	H	66	ARG	NE-CZ-NH2	-12.03	114.29	120.30
1	E	66	ARG	NE-CZ-NH1	11.13	125.86	120.30
1	H	66	ARG	NE-CZ-NH1	9.94	125.27	120.30
1	C	66	ARG	NE-CZ-NH2	-8.85	115.88	120.30
2	L	54	ARG	NE-CZ-NH2	-8.55	116.02	120.30
2	L	54	ARG	NE-CZ-NH1	7.70	124.15	120.30
1	C	66	ARG	NE-CZ-NH1	7.58	124.09	120.30
2	F	169	SER	N-CA-C	-7.44	90.90	111.00
2	F	54	ARG	NE-CZ-NH1	6.95	123.78	120.30
1	E	169	VAL	CB-CA-C	-6.92	98.26	111.40
2	F	54	ARG	NE-CZ-NH2	-6.90	116.85	120.30
2	B	181	LEU	CA-CB-CG	6.17	129.50	115.30
1	A	66	ARG	NE-CZ-NH2	-5.95	117.33	120.30
1	A	169	VAL	CB-CA-C	-5.91	100.17	111.40
1	A	178	LEU	CA-CB-CG	5.90	128.88	115.30
1	E	95	ASP	CB-CG-OD2	5.49	123.24	118.30
1	E	82	MET	CG-SD-CE	-5.28	91.75	100.20
1	H	63	VAL	CG1-CB-CG2	5.15	119.14	110.90
1	E	66	ARG	CG-CD-NE	-5.15	100.99	111.80
1	E	66	ARG	CD-NE-CZ	5.13	130.78	123.60

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	B	106	VAL	Peptide
2	D	108	GLY	Peptide
2	F	156	VAL	Peptide

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	1571	0	1544	25	0
1	C	1571	0	1544	17	0
1	E	1555	0	1531	24	0
1	H	1564	0	1537	28	1
2	B	1575	0	1519	13	0
2	D	1575	0	1519	10	0
2	F	1575	0	1519	17	0
2	L	1575	0	1519	27	0
3	B	5	0	0	1	0
3	D	10	0	0	0	0
3	F	10	0	0	0	0
3	H	10	0	0	1	0
3	L	5	0	0	0	0
4	H	6	0	8	0	0
4	L	6	0	8	3	0
5	A	1	0	0	0	0
5	B	2	0	0	0	0
5	D	2	0	0	0	0
5	E	3	0	0	0	0
5	F	2	0	0	0	0
5	H	2	0	0	0	0
5	L	2	0	0	0	0
6	A	76	0	0	1	0
6	B	91	0	0	2	0
6	C	59	0	0	0	0
6	D	97	0	0	0	0
6	E	124	0	0	5	1
6	F	134	0	0	1	0
6	H	105	0	0	0	0
6	L	116	0	0	2	0
All	All	13429	0	12248	143	1

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 6.

All (143) 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)
2:F:157:LYS:HD2	2:F:158:ALA:H	1.24	1.03

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:L:61:ARG:HE	4:L:215:GOL:H31	1.25	1.00
2:F:157:LYS:HD2	2:F:158:ALA:N	1.79	0.96
1:A:105:GLN:HG2	6:A:801:HOH:O	1.80	0.81
1:E:105:GLN:NE2	1:E:105:GLN:H	1.79	0.81
1:H:105:GLN:NE2	1:H:105:GLN:H	1.76	0.81
2:F:27:SER:HB3	6:F:658:HOH:O	1.82	0.78
2:B:133:LEU:HD12	2:B:179:LEU:HD23	1.68	0.75
2:L:170:ASN:O	2:L:171:ASN:HB2	1.88	0.74
1:E:66:ARG:HD3	6:E:794:HOH:O	1.86	0.73
2:F:168:GLN:HA	2:F:168:GLN:OE1	1.85	0.71
1:C:126:PRO:HD3	1:C:138:LEU:HB3	1.72	0.71
2:B:197:THR:HG23	6:B:395:HOH:O	1.91	0.70
2:L:61:ARG:HH21	4:L:215:GOL:H11	1.57	0.69
1:A:51:ILE:HG13	1:A:57:THR:HG22	1.76	0.68
2:F:168:GLN:C	2:F:169:SER:O	2.30	0.68
2:L:61:ARG:NE	4:L:215:GOL:H31	2.06	0.68
2:F:141:TYR:CD1	2:F:142:PRO:HA	2.30	0.67
2:D:40:PRO:HG3	2:D:167:LYS:HB3	1.78	0.66
1:A:12:VAL:HG11	1:A:82(C):LEU:HD13	1.78	0.65
1:C:82:MET:HE2	1:C:82(C):LEU:HD21	1.78	0.65
1:A:63:VAL:HG13	1:A:67:PHE:HB2	1.78	0.65
1:H:66:ARG:HD2	1:H:83:ARG:HH21	1.62	0.64
1:H:169:VAL:HG21	2:L:178:TYR:CD2	2.34	0.62
1:E:99:GLY:O	2:F:96:ARG:NH1	2.32	0.61
1:E:30:SER:O	1:E:52(A):ASN:HB2	2.00	0.61
1:E:134:GLY:HA2	1:E:186:SER:H	1.65	0.61
2:F:111:LYS:HD2	2:F:142:PRO:HD3	1.83	0.60
1:C:119:PRO:HB3	1:C:145:TYR:HB3	1.84	0.59
2:B:59:SER:HB2	3:B:214:SO4:O4	2.02	0.59
1:C:126:PRO:HD3	1:C:138:LEU:CB	2.32	0.58
2:L:121:PRO:HD3	2:L:133:LEU:HD21	1.84	0.58
1:H:11:LEU:HB2	1:H:147:PRO:HG3	1.85	0.58
1:A:30:SER:O	1:A:52(A):ASN:HB2	2.03	0.57
1:H:97:ARG:NH2	2:L:32:PHE:HE1	2.03	0.57
2:B:103:LYS:HE3	6:B:613:HOH:O	2.03	0.57
1:A:126:PRO:HG2	1:A:213:PRO:HA	1.87	0.57
1:H:105:GLN:HE21	1:H:105:GLN:H	1.51	0.56
1:C:119:PRO:HD2	1:C:205:THR:HG21	1.88	0.55
2:L:141:TYR:CD1	2:L:142:PRO:HA	2.41	0.55
1:E:210:ARG:NH1	6:E:251:HOH:O	2.26	0.55
1:H:169:VAL:HG21	2:L:178:TYR:CE2	2.43	0.54

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:93:ALA:HB1	1:C:100(B):SER:HB3	1.89	0.54
1:H:97:ARG:CZ	2:L:32:PHE:HE1	2.20	0.54
1:H:169:VAL:CG2	2:L:178:TYR:CE2	2.91	0.53
1:A:159:LEU:HD21	1:A:182:VAL:HG21	1.90	0.53
1:A:66:ARG:NH2	1:A:86:ASP:OD1	2.41	0.53
1:A:172:SER:HB3	1:E:193:THR:OG1	2.09	0.53
1:A:93:ALA:HB1	1:A:100(B):SER:HB3	1.92	0.52
1:H:12:VAL:HG11	1:H:82(C):LEU:HD13	1.92	0.51
1:E:83:ARG:HG3	1:E:85:GLU:HG2	1.92	0.51
2:F:168:GLN:O	2:F:169:SER:O	2.29	0.51
1:E:3:GLN:NE2	6:E:740:HOH:O	2.26	0.51
2:D:133:LEU:HD12	2:D:179:LEU:HD23	1.92	0.51
1:E:11:LEU:HB2	1:E:147:PRO:HG3	1.92	0.50
2:L:111:LYS:NZ	2:L:199:GLU:OE2	2.42	0.50
2:L:19:ILE:HD11	2:L:75:ILE:HD12	1.94	0.50
1:E:66:ARG:CD	6:E:794:HOH:O	2.52	0.50
1:C:12:VAL:HG11	1:C:82(C):LEU:HD13	1.93	0.50
1:H:178:LEU:HD12	1:H:178:LEU:C	2.32	0.50
2:F:141:TYR:CG	2:F:142:PRO:HA	2.47	0.49
1:H:181:VAL:HG11	2:L:136:LEU:HD12	1.94	0.49
1:A:20:LEU:HG	1:A:82:MET:CE	2.42	0.49
1:C:182:VAL:HG12	1:C:184:VAL:HG13	1.94	0.49
2:D:89:SER:OG	2:D:96:ARG:NH1	2.45	0.48
2:L:121:PRO:HD3	2:L:133:LEU:CD2	2.42	0.48
2:B:170:ASN:O	2:B:171:ASN:HB2	2.14	0.48
1:C:13:GLN:HG2	2:F:129:ASN:OD1	2.13	0.47
1:H:97:ARG:NH2	2:L:32:PHE:CE1	2.82	0.47
2:L:209:PRO:O	2:L:210:THR:C	2.53	0.47
1:A:1:GLU:CG	1:A:2:VAL:H	2.27	0.47
2:D:121:PRO:HD3	2:D:133:LEU:CD2	2.44	0.47
1:E:93:ALA:HB1	1:E:100(B):SER:HB3	1.96	0.47
1:H:169:VAL:HG22	2:L:163:THR:CG2	2.44	0.47
2:F:157:LYS:O	2:F:158:ALA:HB3	2.15	0.47
2:F:168:GLN:N	2:F:172:LYS:O	2.43	0.46
2:L:32:PHE:O	2:L:90:SER:HA	2.15	0.46
1:E:29:PHE:CD2	1:E:76:ASN:HA	2.50	0.46
1:H:143:LYS:HE2	3:H:222:SO4:O1	2.15	0.46
1:E:192:GLN:HG2	1:E:194:TYR:CZ	2.51	0.46
1:E:178:LEU:C	1:E:178:LEU:HD12	2.36	0.46
1:C:167:PRO:HG2	2:D:166:SER:OG	2.16	0.45
1:H:138:LEU:CD1	1:H:182:VAL:HG13	2.46	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:134:GLY:O	1:C:185:PRO:HA	2.17	0.45
1:E:143:LYS:CE	6:E:734:HOH:O	2.64	0.45
1:E:116:THR:HG21	1:E:202:PRO:O	2.17	0.45
2:L:105:THR:HG23	6:L:331:HOH:O	2.17	0.45
1:E:134:GLY:HA2	1:E:135:THR:HA	1.68	0.44
1:H:63:VAL:HG13	1:H:67:PHE:HB2	1.99	0.44
1:A:22:CYS:HB3	1:A:78:LEU:HB3	2.00	0.44
1:E:66:ARG:NH2	1:E:86:ASP:OD1	2.33	0.44
2:L:11:VAL:HG23	2:L:104:LEU:HD13	1.99	0.44
2:B:133:LEU:HG	2:B:181:LEU:HD11	1.99	0.44
1:H:142:VAL:HG11	1:H:150:VAL:HG11	1.99	0.44
2:L:50:GLU:O	2:L:51:VAL:HG13	2.17	0.44
1:E:105:GLN:CD	1:E:105:GLN:H	2.21	0.44
2:D:54:ARG:HG2	2:D:58:ILE:HB	1.99	0.44
2:B:51:VAL:HG21	2:B:66:LYS:HG2	2.00	0.44
1:C:96:LEU:HG	1:C:100(A):GLY:O	2.18	0.44
2:F:32:PHE:O	2:F:90:SER:HA	2.18	0.44
1:E:134:GLY:HA2	1:E:185:PRO:HA	2.00	0.43
1:A:169:VAL:HG21	2:B:178:TYR:CD2	2.53	0.43
1:C:136:ALA:CB	1:C:189:LEU:HD21	2.48	0.43
1:H:212:GLU:HA	1:H:212:GLU:OE2	2.18	0.43
1:A:162:GLY:O	1:A:182:VAL:HA	2.18	0.43
1:A:143:LYS:HE3	2:B:132:THR:OG1	2.18	0.43
2:D:168:GLN:HE21	2:D:170:ASN:HB2	1.82	0.43
2:B:121:PRO:HD3	2:B:133:LEU:CD2	2.48	0.43
1:A:51:ILE:HD13	1:A:71:ARG:HG2	2.01	0.43
2:L:96:ARG:NH1	6:L:617:HOH:O	2.50	0.43
1:A:36:TRP:NE1	1:A:80:LEU:HB2	2.34	0.43
1:H:169:VAL:CG2	2:L:178:TYR:HE2	2.31	0.43
1:H:30:SER:O	1:H:52(A):ASN:HB2	2.18	0.43
1:A:20:LEU:HG	1:A:82:MET:HE2	2.00	0.43
2:D:109:GLN:HA	2:D:110:PRO:HD2	1.90	0.43
2:D:93:GLY:O	2:D:95(B):PHE:HA	2.19	0.43
2:B:181:LEU:HD23	2:B:192:TYR:CZ	2.54	0.43
1:H:66:ARG:NH2	1:H:86:ASP:OD1	2.41	0.43
1:A:169:VAL:HG22	2:B:178:TYR:CE2	2.54	0.43
2:B:50:GLU:O	2:B:51:VAL:HG13	2.19	0.42
1:A:67:PHE:HA	1:A:81:VAL:O	2.19	0.42
1:E:124:LEU:HB3	2:F:119:PHE:CG	2.55	0.42
2:D:181:LEU:HD23	2:D:181:LEU:H	1.85	0.42
1:A:201:LYS:N	1:A:202:PRO:CD	2.82	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:199:ASN:OD1	1:H:201:LYS:HG3	2.19	0.41
1:H:105:GLN:CD	1:H:105:GLN:H	2.22	0.41
1:C:145:TYR:CE1	1:C:150:VAL:HG23	2.54	0.41
1:H:181:VAL:CG1	2:L:136:LEU:CD1	2.99	0.41
1:E:138:LEU:O	1:E:181:VAL:HG23	2.21	0.41
2:L:143:GLY:O	2:L:165:PRO:HG2	2.20	0.41
1:A:126:PRO:HD3	1:A:138:LEU:HB3	2.03	0.41
2:F:150:LYS:HE2	2:F:195:GLN:NE2	2.36	0.41
1:C:126:PRO:HG2	1:C:213:PRO:HA	2.02	0.41
2:F:5:LEU:HD22	2:F:25:GLY:CA	2.50	0.41
1:C:36:TRP:CE2	1:C:80:LEU:HB2	2.56	0.41
1:C:186:SER:O	1:C:188:SER:N	2.54	0.41
1:H:51:ILE:HD12	1:H:57:THR:HG22	2.02	0.41
1:A:71:ARG:HD2	1:A:73:ASN:OD1	2.20	0.40
1:H:12:VAL:O	1:H:111:VAL:HA	2.21	0.40
2:L:62:PHE:CE2	2:L:75:ILE:HG12	2.56	0.40
1:E:116:THR:HG21	1:E:202:PRO:C	2.42	0.40
1:A:121:VAL:O	1:A:209:LYS:HE3	2.21	0.40
1:H:93:ALA:HB1	1:H:100(B):SER:HB3	2.04	0.40

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:1:GLU:OE1	6:E:471:HOH:O[2_655]	1.79	0.41

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	208/226 (92%)	204 (98%)	3 (1%)	1 (0%)	34 21

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
1	C	208/226 (92%)	203 (98%)	3 (1%)	2 (1%)	19 8
1	E	206/226 (91%)	203 (98%)	3 (2%)	0	100 100
1	H	207/226 (92%)	203 (98%)	4 (2%)	0	100 100
2	B	210/217 (97%)	202 (96%)	7 (3%)	1 (0%)	34 21
2	D	210/217 (97%)	201 (96%)	8 (4%)	1 (0%)	34 21
2	F	210/217 (97%)	200 (95%)	7 (3%)	3 (1%)	14 4
2	L	210/217 (97%)	200 (95%)	10 (5%)	0	100 100
All	All	1669/1772 (94%)	1616 (97%)	45 (3%)	8 (0%)	34 21

All (8) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	F	169	SER
1	C	189	LEU
1	A	62	SER
1	C	187	SER
2	F	168	GLN
2	B	51	VAL
2	D	51	VAL
2	F	51	VAL

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	176/189 (93%)	167 (95%)	9 (5%)	29 13
1	C	176/189 (93%)	166 (94%)	10 (6%)	25 11
1	E	174/189 (92%)	168 (97%)	6 (3%)	44 30
1	H	175/189 (93%)	169 (97%)	6 (3%)	44 30
2	B	177/182 (97%)	168 (95%)	9 (5%)	29 13
2	D	177/182 (97%)	175 (99%)	2 (1%)	80 77

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
2	F	177/182 (97%)	166 (94%)	11 (6%)	23 8
2	L	177/182 (97%)	174 (98%)	3 (2%)	68 63
All	All	1409/1484 (95%)	1353 (96%)	56 (4%)	38 23

All (56) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	H	13	GLN
1	H	105	GLN
1	H	135	THR
1	H	138	LEU
1	H	191	THR
1	H	212	GLU
2	L	51	VAL
2	L	115	SER
2	L	210	THR
1	A	18	LEU
1	A	31	THR
1	A	63	VAL
1	A	117	LYS
1	A	135	THR
1	A	169	VAL
1	A	172	SER
1	A	178	LEU
1	A	204	ASN
2	B	27(B)	ASP
2	B	51	VAL
2	B	78	LEU
2	B	96	ARG
2	B	107	ARG
2	B	157	LYS
2	B	181	LEU
2	B	197	THR
2	B	199	GLU
1	C	1	GLU
1	C	18	LEU
1	C	19	ARG
1	C	31	THR
1	C	64	LYS
1	C	96	LEU
1	C	164	HIS

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	C	171	GLN
1	C	178	LEU
1	C	191	THR
2	D	51	VAL
2	D	181	LEU
1	E	64	LYS
1	E	105	GLN
1	E	169	VAL
1	E	191	THR
1	E	192	GLN
1	E	201	LYS
2	F	27(B)	ASP
2	F	51	VAL
2	F	139	ASP
2	F	145	VAL
2	F	146	THR
2	F	157	LYS
2	F	161	GLU
2	F	168	GLN
2	F	169	SER
2	F	170	ASN
2	F	172	LYS

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

Mol	Chain	Res	Type
1	A	171	GLN

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 (i)

Of 24 ligands modelled in this entry, 14 are monoatomic - leaving 10 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
3	SO4	B	214	-	4,4,4	0.15	0	6,6,6	0.18	0
3	SO4	D	214	-	4,4,4	0.37	0	6,6,6	0.85	0
3	SO4	D	215	-	4,4,4	0.22	0	6,6,6	0.27	0
3	SO4	F	214	-	4,4,4	0.18	0	6,6,6	0.32	0
3	SO4	F	215	-	4,4,4	0.14	0	6,6,6	0.39	0
3	SO4	H	221	-	4,4,4	0.50	0	6,6,6	0.67	0
3	SO4	H	222	-	4,4,4	0.16	0	6,6,6	0.20	0
4	GOL	H	223	-	5,5,5	0.54	0	5,5,5	0.46	0
3	SO4	L	214	-	4,4,4	0.22	0	6,6,6	0.55	0
4	GOL	L	215	-	5,5,5	0.68	0	5,5,5	1.08	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the chemical component dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	SO4	B	214	-	-	0/0/0/0	0/0/0/0
3	SO4	D	214	-	-	0/0/0/0	0/0/0/0
3	SO4	D	215	-	-	0/0/0/0	0/0/0/0
3	SO4	F	214	-	-	0/0/0/0	0/0/0/0
3	SO4	F	215	-	-	0/0/0/0	0/0/0/0
3	SO4	H	221	-	-	0/0/0/0	0/0/0/0
3	SO4	H	222	-	-	0/0/0/0	0/0/0/0
4	GOL	H	223	-	-	0/4/4/4	0/0/0/0
3	SO4	L	214	-	-	0/0/0/0	0/0/0/0
4	GOL	L	215	-	-	0/4/4/4	0/0/0/0

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

3 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	214	SO4	1	0
3	H	222	SO4	1	0
4	L	215	GOL	3	0

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, 95^{th} 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	212/226 (93%)	-0.01	0 100 100	27, 42, 56, 66	0
1	C	212/226 (93%)	0.23	7 (3%) 50 61	31, 44, 65, 82	0
1	E	210/226 (92%)	-0.06	2 (0%) 84 89	21, 32, 53, 63	0
1	H	211/226 (93%)	-0.03	3 (1%) 78 85	21, 33, 54, 59	0
2	B	212/217 (97%)	-0.07	1 (0%) 91 95	24, 39, 50, 59	0
2	D	212/217 (97%)	0.06	3 (1%) 78 85	26, 42, 52, 58	0
2	F	212/217 (97%)	-0.00	4 (1%) 70 78	21, 34, 51, 69	0
2	L	212/217 (97%)	-0.05	0 100 100	22, 34, 53, 62	0
All	All	1693/1772 (95%)	0.01	20 (1%) 81 87	21, 38, 55, 82	0

All (20) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	F	170	ASN	5.2
1	C	189	LEU	4.9
1	C	188	SER	4.8
1	H	160	THR	4.8
2	F	169	SER	4.7
1	C	190	GLY	3.9
1	C	187	SER	3.5
1	C	135	THR	3.3
1	E	126	PRO	2.6
2	D	93	GLY	2.5
2	D	12	SER	2.4
2	D	32	PHE	2.4
2	F	168	GLN	2.4
1	H	189	LEU	2.4
2	F	113	ALA	2.3
1	H	190	GLY	2.3

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	C	191	THR	2.3
2	B	108	GLY	2.1
1	C	136	ALA	2.1
1	E	161	SER	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)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95^{th} percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(Å^2)	Q<0.9
5	CL	H	224	1/1	0.96	0.17	3.84	72,72,72,72	0
4	GOL	H	223	6/6	0.89	0.23	3.65	49,51,52,53	0
3	SO4	H	222	5/5	0.84	0.18	2.04	89,89,90,90	0
3	SO4	H	221	5/5	0.97	0.11	0.78	59,59,62,62	0
3	SO4	L	214	5/5	0.94	0.11	-0.19	67,68,69,70	0
5	CL	F	217	1/1	0.99	0.09	-0.67	33,33,33,33	0
3	SO4	F	214	5/5	0.93	0.09	-0.68	71,71,72,72	0
3	SO4	D	214	5/5	0.98	0.08	-0.71	42,45,49,50	0
5	CL	E	223	1/1	0.96	0.18	-	63,63,63,63	0
5	CL	D	1	1/1	0.95	0.21	-	59,59,59,59	0
3	SO4	D	215	5/5	0.92	0.11	-	86,87,87,89	0
5	CL	L	216	1/1	0.92	0.24	-	68,68,68,68	0
5	CL	E	222	1/1	0.65	0.19	-	68,68,68,68	0
5	CL	D	216	1/1	0.76	0.17	-	86,86,86,86	0
5	CL	B	215	1/1	0.91	0.23	-	63,63,63,63	0
4	GOL	L	215	6/6	0.82	0.18	-	51,52,53,57	0
5	CL	L	217	1/1	0.94	0.14	-	68,68,68,68	0

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(Å^2)	Q<0.9
5	CL	A	221	1/1	0.93	0.23	-	66,66,66,66	0
5	CL	H	225	1/1	0.91	0.10	-	75,75,75,75	0
5	CL	F	216	1/1	0.95	0.28	-	63,63,63,63	0
5	CL	E	221	1/1	0.96	0.24	-	60,60,60,60	0
3	SO4	B	214	5/5	0.86	0.10	-	93,94,95,95	0
3	SO4	F	215	5/5	0.87	0.18	-	78,79,81,82	0
5	CL	B	216	1/1	0.82	0.17	-	73,73,73,73	0

6.5 Other polymers (i)

There are no such residues in this entry.