Full wwPDB X-ray Structure Validation Report (i)

Feb 1, 2016 – 04:31 PM GMT

PDB ID	:	4FA8
Title	:	Multi-pronged modulation of cytokine signaling
Authors	:	He, X.; Shim, A.H.
Deposited on	:	2012-05-21
Resolution	:	2.20 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:

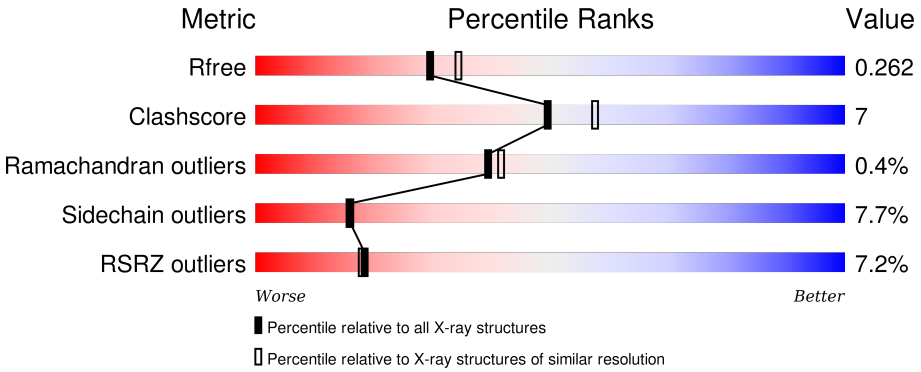
MolProbity	:	4.02b-467
Mogul	:	1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix)	:	1.9-1692
EDS	:	rb-20026688
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac	:	5.8.0135
CCP4	:	6.5.0
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	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 2.20 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	3774 (2.20-2.20)
Clashscore	102246	4477 (2.20-2.20)
Ramachandran outliers	100387	4404 (2.20-2.20)
Sidechain outliers	100360	4405 (2.20-2.20)
RSRZ outliers	91569	3781 (2.20-2.20)

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	203	3% 75% 16% • 7%
1	B	203	3% 81% 10% • 7%
1	D	203	7% 75% 14% • 7%
2	E	147	21% 75% 20% • •
2	F	147	6% 79% 14% 5% ••

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Mol	Chain	Length	Quality of chain
2	G	147	3% 71% 22% 6%

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
4	NAG	F	201	-	-	-	X
4	NAG	G	201	-	-	-	X

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 8676 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 Secreted protein BARF1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	188	Total	C	N	O	S	0	0	0
			1497	968	255	267	7			
1	B	189	Total	C	N	O	S	0	0	0
			1503	971	256	269	7			
1	D	188	Total	C	N	O	S	0	0	0
			1497	968	255	267	7			

- Molecule 2 is a protein called Macrophage colony-stimulating factor 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	E	145	Total	C	N	O	S	0	0	0
			1187	747	197	232	11			
2	F	146	Total	C	N	O	S	0	0	0
			1193	750	198	234	11			
2	G	147	Total	C	N	O	S	0	0	0
			1198	753	199	235	11			

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
E	2	ASP	-	EXPRESSION TAG	UNP P09603
E	3	PRO	-	EXPRESSION TAG	UNP P09603
F	2	ASP	-	EXPRESSION TAG	UNP P09603
F	3	PRO	-	EXPRESSION TAG	UNP P09603
G	2	ASP	-	EXPRESSION TAG	UNP P09603
G	3	PRO	-	EXPRESSION TAG	UNP P09603

- Molecule 3 is a polymer of unknown type called SUGAR (3-MER).

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	3	Total	C	N	O	0	0
			39	22	2	15		

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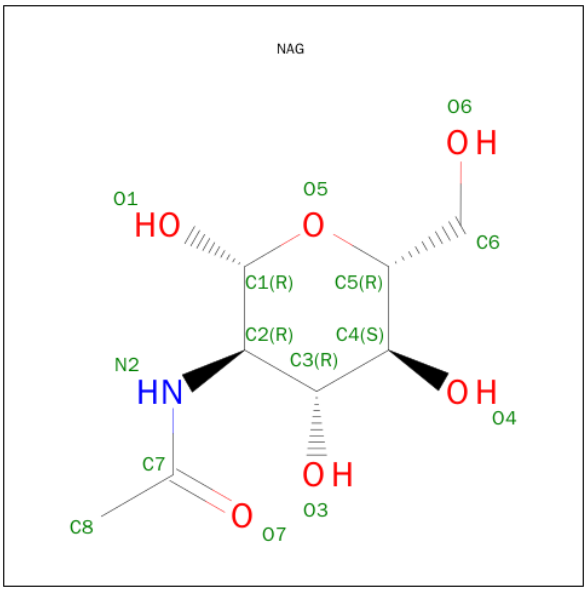
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	B	3	Total C N O 39 22 2 15	0	0
3	D	3	Total C N O 39 22 2 15	0	0

- Molecule 4 is SUGAR (N-ACETYL-D-GLUCOSAMINE) (three-letter code: NAG) (formula: $C_8H_{15}NO_6$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	E	1	Total C N O 14 8 1 5	0	0
4	F	1	Total C N O 14 8 1 5	0	0
4	G	1	Total C N O 14 8 1 5	0	0

- Molecule 5 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	117	Total O 117 117	0	0
5	B	101	Total O 101 101	0	0
5	D	72	Total O 72 72	0	0
5	E	23	Total O 23 23	0	0

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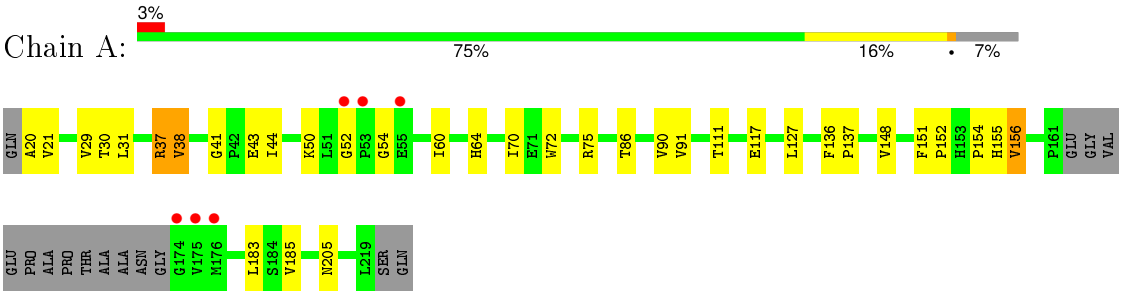
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	F	63	Total O 63 63	0	0
5	G	66	Total O 66 66	0	0

3 Residue-property plots

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.

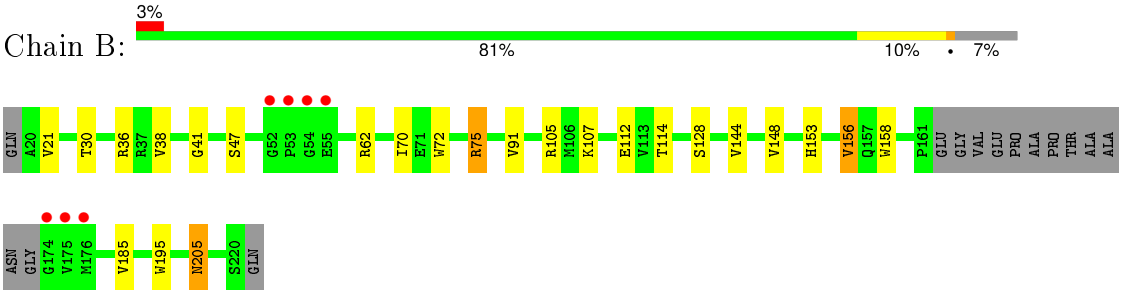
- Molecule 1: Secreted protein BARF1

Chain A:



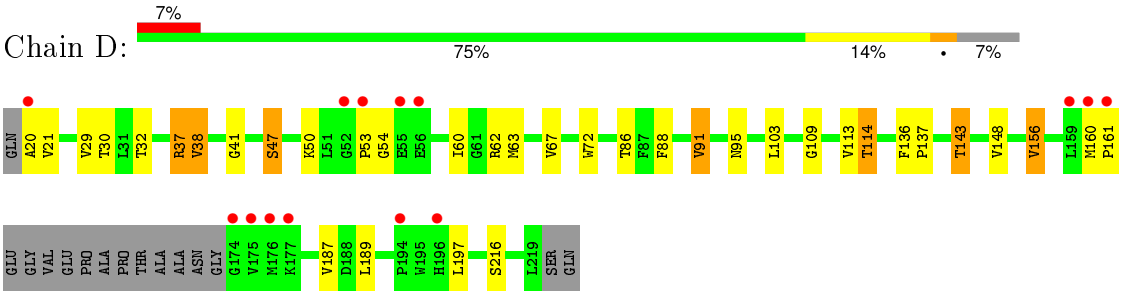
- Molecule 1: Secreted protein BARF1

Chain B:



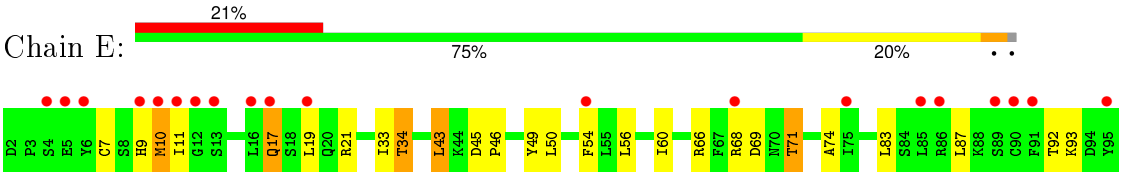
- Molecule 1: Secreted protein BARF1

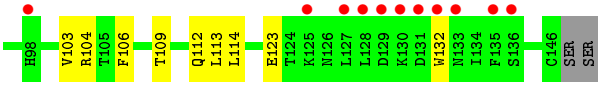
Chain D:



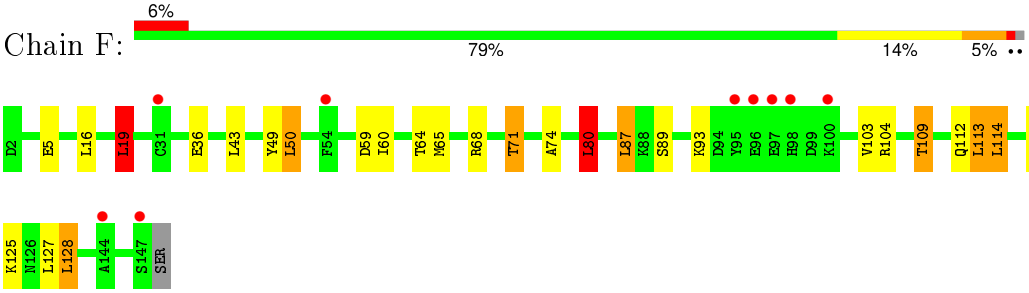
- Molecule 2: Macrophage colony-stimulating factor 1

Chain E:

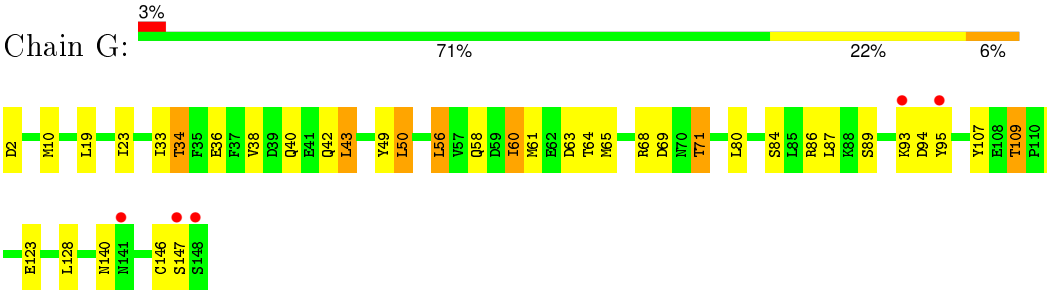




• Molecule 2: Macrophage colony-stimulating factor 1



• Molecule 2: Macrophage colony-stimulating factor 1



4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α, β, γ	199.55Å 162.70Å 57.34Å 90.00° 95.87° 90.00°	Depositor
Resolution (Å)	20.00 – 2.20 46.70 – 2.20	Depositor EDS
% Data completeness (in resolution range)	97.6 (20.00-2.20) 97.6 (46.70-2.20)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	3.07 (at 2.20Å)	Xtriage
Refinement program	REFMAC 5.7.0029	Depositor
R, R_{free}	0.222 , 0.260 0.222 , 0.262	Depositor DCC
R_{free} test set	4494 reflections (5.27%)	DCC
Wilson B-factor (Å^2)	31.5	Xtriage
Anisotropy	0.539	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.36 , 42.6	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning[2]	$< \|L\| > = 0.49$, $< L^2 > = 0.32$	Xtriage
Outliers	0 of 89831 reflections	Xtriage
F_o,F_c correlation	0.94	EDS
Total number of atoms	8676	wwPDB-VP
Average B, all atoms (Å^2)	45.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.11% 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, 0.375 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: BMA, NAG

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	1/1541 (0.1%)	0.66	0/2097
1	B	0.60	2/1547 (0.1%)	0.67	0/2105
1	D	0.60	1/1541 (0.1%)	0.62	0/2097
2	E	0.45	1/1208 (0.1%)	0.58	0/1628
2	F	0.57	0/1214	0.77	3/1636 (0.2%)
2	G	0.49	0/1219	0.65	0/1643
All	All	0.57	5/8270 (0.1%)	0.66	3/11206 (0.0%)

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	72	TRP	CD2-CE2	5.50	1.48	1.41
1	D	72	TRP	CD2-CE2	5.43	1.47	1.41
1	B	195	TRP	CD2-CE2	5.32	1.47	1.41
2	E	132	TRP	CD2-CE2	5.10	1.47	1.41
1	B	72	TRP	CD2-CE2	5.04	1.47	1.41

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	F	19	LEU	CA-CB-CG	5.95	128.98	115.30
2	F	80	LEU	CA-CB-CG	5.52	127.99	115.30
2	F	87	LEU	CA-CB-CG	5.24	127.35	115.30

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	1497	0	1471	24	0
1	B	1503	0	1476	13	0
1	D	1497	0	1471	26	0
2	E	1187	0	1150	16	0
2	F	1193	0	1154	20	0
2	G	1198	0	1156	28	0
3	A	39	0	34	0	0
3	B	39	0	34	0	0
3	D	39	0	34	0	0
4	E	14	0	13	0	0
4	F	14	0	13	0	0
4	G	14	0	13	0	0
5	A	117	0	0	1	0
5	B	101	0	0	0	0
5	D	72	0	0	3	0
5	E	23	0	0	2	0
5	F	63	0	0	2	0
5	G	66	0	0	2	0
All	All	8676	0	8019	115	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 7.

All (115) 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:D:20:ALA:CB	1:D:21:VAL:HA	1.76	1.13
1:A:20:ALA:HB1	1:A:21:VAL:HA	1.31	1.07
1:D:20:ALA:HB1	1:D:21:VAL:CA	1.90	1.01
1:D:20:ALA:HB1	1:D:21:VAL:HA	1.03	0.99
2:F:65:MET:CE	2:F:117:VAL:HG21	2.03	0.89
1:A:156:VAL:HG22	1:A:185:VAL:HG13	1.55	0.87
1:B:156:VAL:HG22	1:B:185:VAL:HG13	1.59	0.85
2:F:65:MET:HE3	2:F:117:VAL:HG21	1.58	0.84
2:G:95:TYR:H	2:G:140:ASN:HD21	1.27	0.82

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:109:THR:HG22	2:F:112:GLN:H	1.44	0.81
1:B:148:VAL:HG23	1:B:156:VAL:HG13	1.63	0.78
1:B:144:VAL:HG23	1:B:158:TRP:CZ2	2.21	0.76
1:D:143:THR:HG22	5:D:448:HOH:O	1.85	0.76
2:G:34:THR:HG22	2:G:107:TYR:HD1	1.50	0.75
2:G:58:GLN:HE21	2:G:84:SER:HB2	1.52	0.73
2:G:43:LEU:HD13	2:G:49:TYR:HA	1.71	0.72
2:E:109:THR:HG21	5:E:314:HOH:O	1.93	0.68
1:B:148:VAL:CG2	1:B:156:VAL:HG13	2.23	0.68
2:G:34:THR:HG22	2:G:107:TYR:CD1	2.29	0.68
1:D:37:ARG:HD3	2:G:63:ASP:OD1	1.94	0.67
1:A:50:LYS:HB2	1:A:60:ILE:HD11	1.77	0.67
1:A:20:ALA:CB	1:A:21:VAL:HA	2.09	0.66
2:F:71:THR:HG22	2:F:74:ALA:H	1.61	0.66
1:A:20:ALA:HB1	1:A:21:VAL:CA	2.19	0.65
2:F:65:MET:HE1	2:F:117:VAL:HG21	1.76	0.65
1:A:148:VAL:HG23	1:A:156:VAL:HG13	1.79	0.65
2:E:7:CYS:HA	2:E:10:MET:HG3	1.78	0.65
1:A:156:VAL:CG2	1:A:185:VAL:HG13	2.27	0.65
1:D:86:THR:OG1	2:G:34:THR:HG23	1.99	0.63
2:G:58:GLN:NE2	2:G:84:SER:HB2	2.13	0.62
1:B:148:VAL:HG23	1:B:156:VAL:CG1	2.28	0.62
1:D:103:LEU:HD11	1:D:114:THR:HG23	1.82	0.61
2:F:43:LEU:HD13	2:F:49:TYR:HA	1.83	0.61
2:G:71:THR:HG23	5:G:306:HOH:O	1.99	0.61
1:A:29:VAL:HG12	1:A:91:VAL:HG22	1.83	0.60
2:G:109:THR:HG22	2:G:112:GLN:H	1.66	0.60
1:A:155:HIS:HD2	5:A:461:HOH:O	1.85	0.59
1:B:36:ARG:NH2	2:F:59:ASP:HB3	2.18	0.59
2:G:36:GLU:HB2	2:G:60:ILE:HD11	1.86	0.58
2:F:68:ARG:O	2:F:71:THR:HB	2.03	0.58
1:D:47:SER:HB3	1:D:62:ARG:HG2	1.89	0.55
1:B:47:SER:HB3	1:B:62:ARG:HG2	1.87	0.54
2:E:71:THR:HG22	2:E:74:ALA:H	1.70	0.54
2:E:109:THR:HG23	5:E:311:HOH:O	2.07	0.54
1:D:143:THR:CG2	5:D:448:HOH:O	2.51	0.53
2:G:109:THR:HB	2:G:112:GLN:OE1	2.08	0.53
1:A:151:PHE:CD1	1:A:152:PRO:HA	2.43	0.53
2:F:119:ASN:HB3	5:F:359:HOH:O	2.09	0.53
2:E:43:LEU:HD13	2:E:49:TYR:HA	1.91	0.52
1:A:127:LEU:O	1:B:128:SER:HA	2.10	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:148:VAL:CG2	1:A:156:VAL:HG13	2.40	0.52
2:E:34:THR:HA	2:E:106:PHE:O	2.09	0.52
1:A:86:THR:OG1	2:E:34:THR:HG22	2.10	0.52
1:A:30:THR:HG22	1:A:90:VAL:HG22	1.93	0.51
2:F:50:LEU:HD23	2:F:127:LEU:HD12	1.91	0.51
1:B:107:LYS:HG2	1:B:112:GLU:HG3	1.92	0.50
2:G:2:ASP:OD1	2:G:89:SER:HB2	2.10	0.50
2:G:68:ARG:O	2:G:71:THR:HB	2.11	0.50
1:A:86:THR:OG1	2:E:34:THR:CG2	2.60	0.50
2:G:10:MET:HE3	2:G:86:ARG:HB3	1.94	0.50
2:F:49:TYR:HD1	2:F:50:LEU:HD13	1.77	0.50
2:G:50:LEU:HD21	2:G:123:GLU:HB3	1.94	0.49
2:G:94:ASP:HB3	2:G:140:ASN:ND2	2.27	0.49
2:E:109:THR:HG22	2:E:112:GLN:H	1.77	0.49
2:E:17:GLN:HB3	2:E:21:ARG:NH2	2.28	0.49
2:G:58:GLN:NE2	5:G:329:HOH:O	2.46	0.48
1:A:31:LEU:HD22	1:A:117:GLU:HG2	1.94	0.48
1:A:52:GLY:O	1:A:54:GLY:HA2	2.13	0.48
1:A:37:ARG:HD2	2:E:66:ARG:NE	2.29	0.48
1:D:53:PRO:HA	1:D:54:GLY:HA2	1.58	0.48
1:D:156:VAL:HB	1:D:187:VAL:HG23	1.96	0.48
1:D:29:VAL:HG13	1:D:91:VAL:HG13	1.96	0.47
2:F:109:THR:HB	2:F:112:GLN:OE1	2.13	0.47
1:D:32:THR:HG22	1:D:88:PHE:CD1	2.49	0.47
1:D:86:THR:HG1	2:G:34:THR:HG23	1.79	0.47
2:E:56:LEU:HD11	2:E:103:VAL:CG2	2.45	0.47
1:D:136:PHE:CG	1:D:137:PRO:HA	2.51	0.46
2:F:109:THR:HG23	5:F:325:HOH:O	2.14	0.46
1:B:105:ARG:HG2	1:B:114:THR:HG22	1.98	0.46
1:A:38:VAL:HG21	2:E:33:ILE:HD12	1.99	0.45
1:D:20:ALA:CB	1:D:21:VAL:CA	2.60	0.45
2:F:19:LEU:HD13	2:F:80:LEU:HD21	1.99	0.45
1:A:136:PHE:CG	1:A:137:PRO:HA	2.52	0.45
2:G:94:ASP:HB3	2:G:140:ASN:HD21	1.80	0.45
2:F:64:THR:HB	2:F:113:LEU:HD11	1.99	0.44
2:E:68:ARG:O	2:E:71:THR:HB	2.18	0.44
1:D:95:ASN:HB2	5:D:425:HOH:O	2.18	0.44
2:F:124:THR:O	2:F:128:LEU:HB2	2.17	0.44
2:G:64:THR:HB	2:G:113:LEU:HD11	2.00	0.43
1:D:143:THR:HA	1:D:189:LEU:O	2.17	0.43
1:D:63:MET:HA	1:D:67:VAL:O	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:G:56:LEU:HD22	2:G:60:ILE:HD12	1.99	0.43
1:D:29:VAL:CG1	1:D:91:VAL:HG13	2.49	0.43
1:D:50:LYS:HB2	1:D:60:ILE:HD11	2.00	0.43
1:B:36:ARG:HH22	2:F:59:ASP:HB3	1.82	0.43
1:D:38:VAL:HG21	2:G:33:ILE:HD12	2.00	0.43
2:G:61:MET:HA	2:G:65:MET:HE2	2.00	0.43
2:G:109:THR:HG22	2:G:111:LEU:N	2.33	0.42
1:A:43:GLU:O	1:A:64:HIS:HE1	2.02	0.42
2:E:45:ASP:HA	2:E:46:PRO:HD3	1.93	0.42
2:F:16:LEU:HD11	2:F:125:LYS:HD3	2.01	0.42
1:A:154:PRO:HG3	1:A:183:LEU:HB2	2.02	0.42
2:G:42:GLN:HE21	2:G:146:CYS:HB3	1.83	0.42
1:D:197:LEU:HD13	1:D:216:SER:HA	2.02	0.41
1:D:160:MET:HA	1:D:161:PRO:HD2	1.94	0.41
1:B:153:HIS:H	1:B:205:ASN:ND2	2.17	0.41
1:D:148:VAL:HG23	1:D:156:VAL:HG13	2.03	0.41
2:F:36:GLU:HG2	2:F:103:VAL:CG1	2.51	0.41
2:E:11:ILE:HG12	2:E:83:LEU:HD21	2.03	0.41
1:B:70:ILE:O	1:B:75:ARG:NH1	2.51	0.40
1:A:70:ILE:HB	1:A:75:ARG:HD2	2.04	0.40
2:F:114:LEU:HA	2:F:114:LEU:HD12	1.95	0.40
1:D:86:THR:OG1	2:G:34:THR:CG2	2.66	0.40
2:G:23:ILE:HG12	2:G:114:LEU:HB3	2.04	0.40
1:A:44:ILE:CD1	1:A:44:ILE:N	2.85	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	184/203 (91%)	178 (97%)	5 (3%)	1 (0%)	34 35

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
1	B	185/203 (91%)	177 (96%)	7 (4%)	1 (0%)	34 35
1	D	184/203 (91%)	176 (96%)	6 (3%)	2 (1%)	17 14
2	E	143/147 (97%)	138 (96%)	5 (4%)	0	100 100
2	F	144/147 (98%)	140 (97%)	4 (3%)	0	100 100
2	G	145/147 (99%)	139 (96%)	6 (4%)	0	100 100
All	All	985/1050 (94%)	948 (96%)	33 (3%)	4 (0%)	39 42

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	41	GLY
1	A	41	GLY
1	B	41	GLY
1	D	109	GLY

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	167/177 (94%)	162 (97%)	5 (3%)	48 60
1	B	168/177 (95%)	161 (96%)	7 (4%)	36 44
1	D	167/177 (94%)	158 (95%)	9 (5%)	27 31
2	E	138/140 (99%)	120 (87%)	18 (13%)	5 4
2	F	139/140 (99%)	125 (90%)	14 (10%)	9 8
2	G	139/140 (99%)	121 (87%)	18 (13%)	5 4
All	All	918/951 (96%)	847 (92%)	71 (8%)	16 16

All (71) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	37	ARG
1	A	38	VAL

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Mol	Chain	Res	Type
1	A	111	THR
1	A	156	VAL
1	A	205	ASN
1	B	21	VAL
1	B	30	THR
1	B	38	VAL
1	B	75	ARG
1	B	91	VAL
1	B	156	VAL
1	B	205	ASN
1	D	30	THR
1	D	37	ARG
1	D	38	VAL
1	D	47	SER
1	D	91	VAL
1	D	113	VAL
1	D	114	THR
1	D	143	THR
1	D	156	VAL
2	E	9	HIS
2	E	10	MET
2	E	17	GLN
2	E	19	LEU
2	E	34	THR
2	E	43	LEU
2	E	50	LEU
2	E	54	PHE
2	E	60	ILE
2	E	69	ASP
2	E	71	THR
2	E	87	LEU
2	E	92	THR
2	E	93	LYS
2	E	104	ARG
2	E	113	LEU
2	E	114	LEU
2	E	123	GLU
2	F	5	GLU
2	F	19	LEU
2	F	50	LEU
2	F	60	ILE
2	F	71	THR

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Mol	Chain	Res	Type
2	F	80	LEU
2	F	87	LEU
2	F	89	SER
2	F	93	LYS
2	F	104	ARG
2	F	109	THR
2	F	113	LEU
2	F	114	LEU
2	F	128	LEU
2	G	19	LEU
2	G	34	THR
2	G	38	VAL
2	G	40	GLN
2	G	43	LEU
2	G	50	LEU
2	G	56	LEU
2	G	60	ILE
2	G	69	ASP
2	G	71	THR
2	G	80	LEU
2	G	87	LEU
2	G	93	LYS
2	G	109	THR
2	G	113	LEU
2	G	114	LEU
2	G	128	LEU
2	G	147	SER

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (21) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	64	HIS
1	A	65	HIS
1	A	101	ASN
1	A	116	GLN
1	A	155	HIS
1	A	205	ASN
1	B	101	ASN
1	B	116	GLN
1	B	157	GLN
1	B	205	ASN
1	D	64	HIS

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Mol	Chain	Res	Type
2	E	119	ASN
2	E	126	ASN
2	E	141	ASN
2	F	141	ASN
2	G	42	GLN
2	G	58	GLN
2	G	98	HIS
2	G	119	ASN
2	G	140	ASN
2	G	141	ASN

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

9 carbohydrates are modelled in this entry.

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	NAG	A	301	1,3	14,14,15	0.60	0	15,19,21	1.19	2 (13%)
3	NAG	A	302	3	14,14,15	0.66	0	15,19,21	0.98	1 (6%)
3	BMA	A	303	3	11,11,12	0.38	0	14,15,17	1.54	3 (21%)
3	NAG	B	301	1,3	14,14,15	0.72	0	15,19,21	1.23	1 (6%)
3	NAG	B	302	3	14,14,15	0.72	0	15,19,21	1.18	2 (13%)
3	BMA	B	303	3	11,11,12	0.64	0	14,15,17	2.03	3 (21%)
3	NAG	D	301	1,3	14,14,15	0.75	0	15,19,21	1.17	1 (6%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\|>2$	Counts	RMSZ	$\#\|Z\|>2$
3	NAG	D	302	3	14,14,15	0.53	0	15,19,21	1.25	1 (6%)
3	BMA	D	303	3	11,11,12	0.31	0	14,15,17	0.90	2 (14%)

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	NAG	A	301	1,3	-	0/6/23/26	0/1/1/1
3	NAG	A	302	3	-	0/6/23/26	0/1/1/1
3	BMA	A	303	3	-	0/2/19/22	0/1/1/1
3	NAG	B	301	1,3	-	0/6/23/26	0/1/1/1
3	NAG	B	302	3	-	0/6/23/26	0/1/1/1
3	BMA	B	303	3	-	0/2/19/22	0/1/1/1
3	NAG	D	301	1,3	-	0/6/23/26	0/1/1/1
3	NAG	D	302	3	-	0/6/23/26	0/1/1/1
3	BMA	D	303	3	-	0/2/19/22	0/1/1/1

There are no bond length outliers.

All (16) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	D	301	NAG	C2-N2-C7	-3.98	117.92	123.04
3	A	301	NAG	C2-N2-C7	-2.73	119.53	123.04
3	A	303	BMA	C1-O5-C5	-2.51	109.06	112.25
3	B	302	NAG	C3-C4-C5	-2.49	105.85	110.20
3	B	303	BMA	C6-C5-C4	-2.37	107.18	113.02
3	B	302	NAG	C1-O5-C5	-2.33	109.29	112.25
3	A	302	NAG	C2-N2-C7	-2.19	120.22	123.04
3	D	303	BMA	O5-C5-C6	2.01	111.70	107.35
3	D	303	BMA	C1-C2-C3	2.36	112.33	109.54
3	A	301	NAG	C1-O5-C5	2.41	115.31	112.25
3	D	302	NAG	C2-N2-C7	2.68	126.48	123.04
3	A	303	BMA	O5-C5-C6	2.90	113.62	107.35
3	B	301	NAG	C1-O5-C5	3.25	116.37	112.25
3	A	303	BMA	C1-C2-C3	3.40	113.56	109.54
3	B	303	BMA	C1-C2-C3	3.90	114.16	109.54
3	B	303	BMA	C1-O5-C5	5.37	119.07	112.25

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.6 Ligand geometry (i)

3 ligands are modelled in this entry.

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	$\#\|Z\| > 2$
4	NAG	E	201	2	14,14,15	0.62	0	15,19,21	1.08	1 (6%)
4	NAG	F	201	2	14,14,15	0.42	0	15,19,21	0.84	1 (6%)
4	NAG	G	201	2	14,14,15	0.49	0	15,19,21	0.78	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
4	NAG	E	201	2	-	0/6/23/26	0/1/1/1
4	NAG	F	201	2	-	0/6/23/26	0/1/1/1
4	NAG	G	201	2	-	0/6/23/26	0/1/1/1

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
4	F	201	NAG	O5-C5-C6	2.14	111.97	107.35
4	E	201	NAG	C4-C3-C2	2.66	115.36	111.23

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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, 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	188/203 (92%)	0.05	6 (3%) 51 50	21, 33, 57, 71	0
1	B	189/203 (93%)	0.07	7 (3%) 45 44	26, 34, 57, 85	0
1	D	188/203 (92%)	0.24	14 (7%) 17 17	24, 42, 69, 85	0
2	E	145/147 (98%)	1.23	31 (21%) 1 1	34, 65, 104, 117	0
2	F	146/147 (99%)	0.16	9 (6%) 24 23	24, 37, 74, 95	0
2	G	147/147 (100%)	0.14	5 (3%) 49 47	28, 40, 71, 97	0
All	All	1003/1050 (95%)	0.29	72 (7%) 18 18	21, 39, 82, 117	0

All (72) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	E	6	TYR	7.3
1	D	53	PRO	6.6
2	E	86	ARG	6.1
2	G	148	SER	5.6
2	E	9	HIS	5.3
2	E	11	ILE	5.2
2	E	132	TRP	5.2
1	D	161	PRO	4.9
2	E	54	PHE	4.8
1	B	174	GLY	4.7
2	E	95	TYR	4.7
1	D	174	GLY	4.7
2	E	130	LYS	4.6
1	B	53	PRO	4.2
2	E	128	LEU	4.1
1	D	160	MET	3.9
2	E	12	GLY	3.9
1	B	55	GLU	3.8
1	D	55	GLU	3.7

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Mol	Chain	Res	Type	RSRZ
2	E	5	GLU	3.7
2	G	95	TYR	3.7
1	B	52	GLY	3.6
1	A	53	PRO	3.6
1	A	55	GLU	3.6
2	F	95	TYR	3.5
2	E	125	LYS	3.4
2	F	54	PHE	3.2
2	E	129	ASP	3.1
1	D	20	ALA	3.1
1	D	194	PRO	3.1
1	D	196	HIS	3.1
2	E	16	LEU	3.0
2	E	90	CYS	3.0
2	F	97	GLU	3.0
2	E	85	LEU	3.0
2	E	10	MET	2.9
2	E	136	SER	2.9
1	A	174	GLY	2.8
1	B	54	GLY	2.8
2	E	17	GLN	2.8
1	D	56	GLU	2.8
2	G	93	LYS	2.8
2	E	127	LEU	2.7
2	E	133	ASN	2.7
1	D	176	MET	2.7
2	E	4	SER	2.7
2	G	141	ASN	2.7
1	A	176	MET	2.7
2	F	96	GLU	2.6
2	E	75	ILE	2.6
2	E	131	ASP	2.6
2	F	147	SER	2.5
1	D	175	VAL	2.5
2	E	135	PHE	2.5
2	E	19	LEU	2.5
1	B	175	VAL	2.5
2	E	91	PHE	2.5
2	E	89	SER	2.4
2	E	98	HIS	2.4
2	E	68	ARG	2.3
1	D	177	LYS	2.3

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Mol	Chain	Res	Type	RSRZ
2	E	13	SER	2.3
1	A	175	VAL	2.2
2	F	31	CYS	2.2
2	F	98	HIS	2.2
2	F	144	ALA	2.2
1	A	52	GLY	2.1
1	D	159	LEU	2.1
1	D	52	GLY	2.1
2	G	147	SER	2.1
1	B	176	MET	2.1
2	F	100	LYS	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)

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
3	NAG	D	301	14/15	0.95	0.18	1.38	56,63,83,83	0
3	NAG	B	301	14/15	0.93	0.20	1.26	69,72,97,103	0
3	NAG	A	301	14/15	0.94	0.19	1.08	59,70,92,99	0
3	NAG	D	302	14/15	0.95	0.16	-	57,70,74,83	0
3	NAG	B	302	14/15	0.93	0.18	-	75,88,101,102	0
3	BMA	D	303	11/12	0.83	0.22	-	88,96,111,117	0
3	BMA	B	303	11/12	0.84	0.20	-	113,131,153,158	0
3	NAG	A	302	14/15	0.95	0.16	-	59,71,82,89	0
3	BMA	A	303	11/12	0.88	0.18	-	88,109,121,126	0

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
4	NAG	G	201	14/15	0.68	0.45	10.00	82,90,100,101	0
4	NAG	F	201	14/15	0.84	0.28	4.38	51,67,70,71	0
4	NAG	E	201	14/15	0.78	0.36	-	91,98,104,106	0

6.5 Other polymers

There are no such residues in this entry.