



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 08:14 AM GMT

PDB ID : 3DUH
Title : Structure of Interleukin-23
Authors : Lupardus, P.J.; Garcia, K.C.
Deposited on : 2008-07-17
Resolution : 2.30 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.
We welcome your comments at validation@mail.wwpdb.org
A user guide is available at
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

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

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

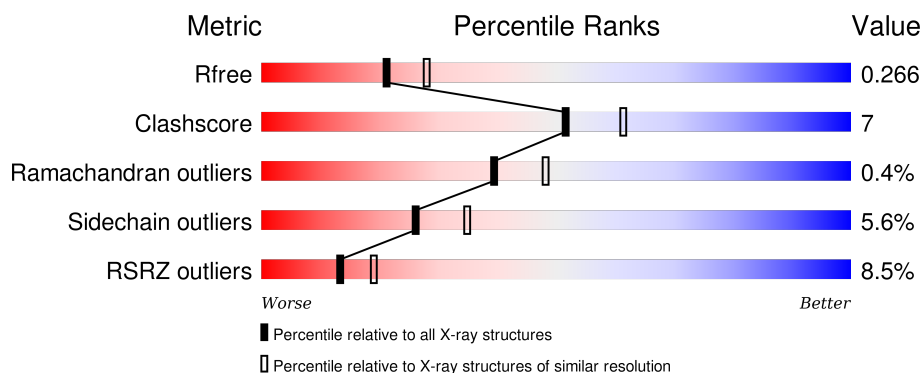
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.30 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	3852 (2.30-2.30)
Clashscore	102246	4452 (2.30-2.30)
Ramachandran outliers	100387	4410 (2.30-2.30)
Sidechain outliers	100360	4409 (2.30-2.30)
RSRZ outliers	91569	3857 (2.30-2.30)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	314	<div> <div>6%</div> <div>81% 13% . .</div> </div>
1	B	314	<div> <div>7%</div> <div>76% 16% . 6%</div> </div>
2	C	177	<div> <div>8%</div> <div>65% 11% . 23%</div> </div>
2	D	177	<div> <div>10%</div> <div>60% 15% . 23%</div> </div>

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	NAG	A	313	X	-	-	-

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 7010 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 Interleukin-12 subunit beta.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	300	Total	C	N	O	S	9	0	0
			2355	1488	385	470	12			
1	B	294	Total	C	N	O	S	6	0	0
			2314	1467	373	462	12			

There are 16 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-1	LEU	-	EXPRESSION TAG	UNP P29460
A	0	GLU	-	EXPRESSION TAG	UNP P29460
A	307	HIS	-	EXPRESSION TAG	UNP P29460
A	308	HIS	-	EXPRESSION TAG	UNP P29460
A	309	HIS	-	EXPRESSION TAG	UNP P29460
A	310	HIS	-	EXPRESSION TAG	UNP P29460
A	311	HIS	-	EXPRESSION TAG	UNP P29460
A	312	HIS	-	EXPRESSION TAG	UNP P29460
B	-1	LEU	-	EXPRESSION TAG	UNP P29460
B	0	GLU	-	EXPRESSION TAG	UNP P29460
B	307	HIS	-	EXPRESSION TAG	UNP P29460
B	308	HIS	-	EXPRESSION TAG	UNP P29460
B	309	HIS	-	EXPRESSION TAG	UNP P29460
B	310	HIS	-	EXPRESSION TAG	UNP P29460
B	311	HIS	-	EXPRESSION TAG	UNP P29460
B	312	HIS	-	EXPRESSION TAG	UNP P29460

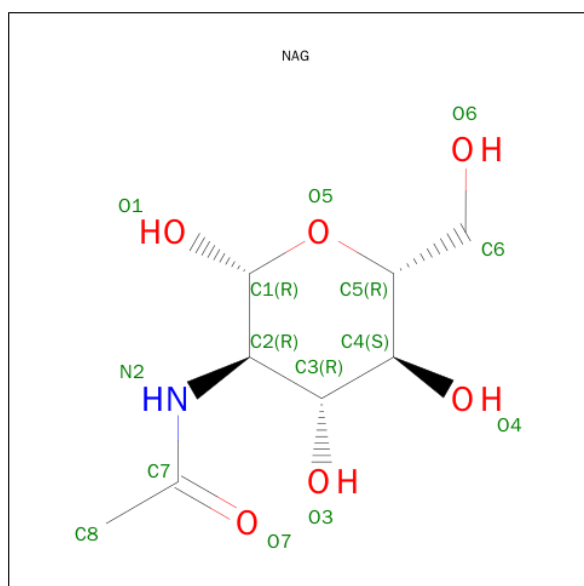
- Molecule 2 is a protein called Interleukin-23 subunit alpha.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	137	Total	C	N	O	S	0	0	0
			1049	669	192	183	5			
2	D	137	Total	C	N	O	S	0	0	0
			1064	676	198	185	5			

There are 14 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	0	LEU	-	EXPRESSION TAG	UNP Q9NPF7
C	171	HIS	-	EXPRESSION TAG	UNP Q9NPF7
C	172	HIS	-	EXPRESSION TAG	UNP Q9NPF7
C	173	HIS	-	EXPRESSION TAG	UNP Q9NPF7
C	174	HIS	-	EXPRESSION TAG	UNP Q9NPF7
C	175	HIS	-	EXPRESSION TAG	UNP Q9NPF7
C	176	HIS	-	EXPRESSION TAG	UNP Q9NPF7
D	0	LEU	-	EXPRESSION TAG	UNP Q9NPF7
D	171	HIS	-	EXPRESSION TAG	UNP Q9NPF7
D	172	HIS	-	EXPRESSION TAG	UNP Q9NPF7
D	173	HIS	-	EXPRESSION TAG	UNP Q9NPF7
D	174	HIS	-	EXPRESSION TAG	UNP Q9NPF7
D	175	HIS	-	EXPRESSION TAG	UNP Q9NPF7
D	176	HIS	-	EXPRESSION TAG	UNP Q9NPF7

- Molecule 3 is SUGAR (N-ACETYL-D-GLUCOSAMINE) (three-letter code: NAG) (formula: $C_8H_{15}NO_6$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	0	0
			14	8	1	5		
3	B	1	Total	C	N	O	0	0
			14	8	1	5		

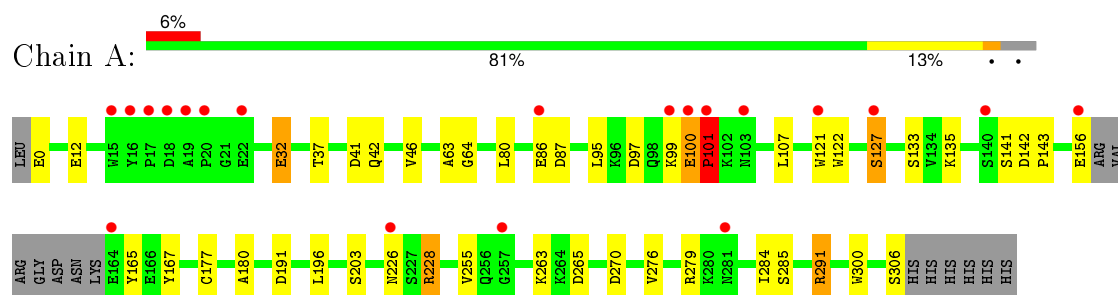
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	96	Total 96	O 96	0	0
4	B	77	Total 77	O 77	0	0
4	C	20	Total 20	O 20	0	0
4	D	7	Total 7	O 7	0	0

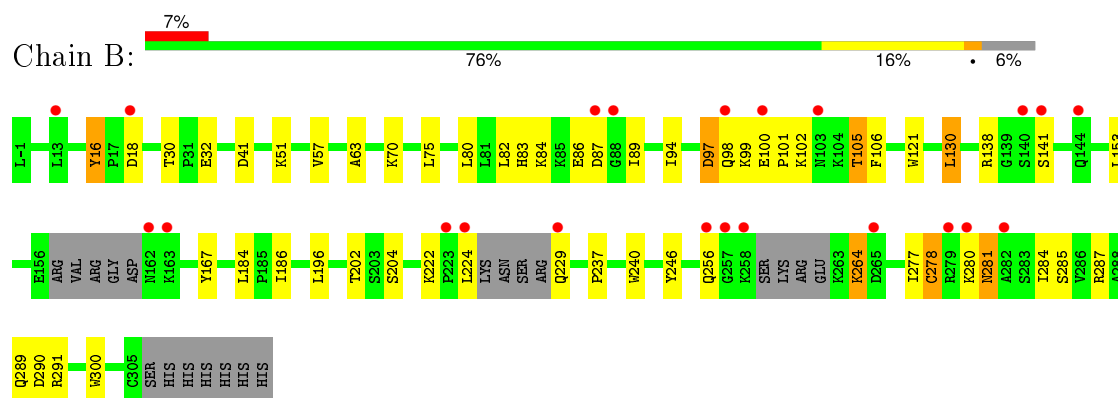
3 Residue-property plots

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.

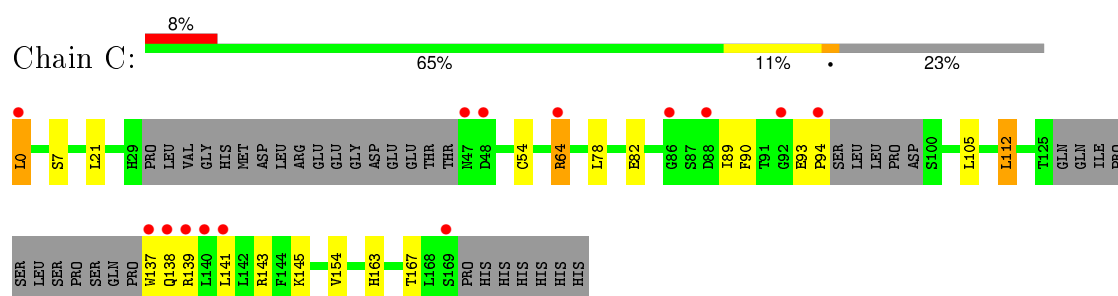
• Molecule 1: Interleukin-12 subunit beta



• Molecule 1: Interleukin-12 subunit beta

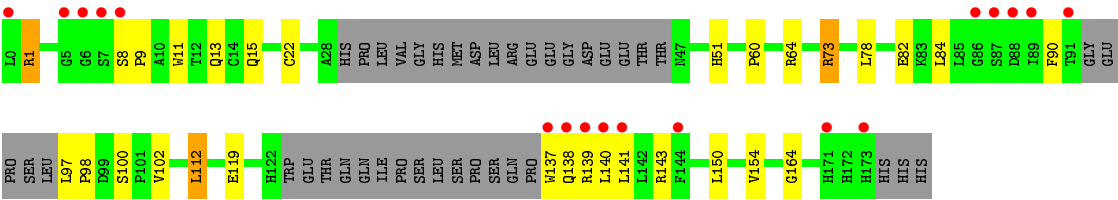


• Molecule 2: Interleukin-23 subunit alpha



• Molecule 2: Interleukin-23 subunit alpha





4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	116.09Å 59.97Å 160.37Å 90.00° 90.46° 90.00°	Depositor
Resolution (Å)	30.00 – 2.30 29.99 – 2.30	Depositor EDS
% Data completeness (in resolution range)	100.0 (30.00-2.30) 100.0 (29.99-2.30)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.50 (at 2.31Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.228 , 0.268 0.227 , 0.266	Depositor DCC
R_{free} test set	2502 reflections (5.33%)	DCC
Wilson B-factor (Å ²)	41.8	Xtriage
Anisotropy	0.336	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 47.9	EDS
Estimated twinning fraction	0.013 for -h,-k,l	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	1 of 49424 reflections (0.002%)	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	7010	wwPDB-VP
Average B, all atoms (Å ²)	46.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.11% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: 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	0.62	1/2413 (0.0%)	0.69	1/3285 (0.0%)
1	B	0.55	0/2370	0.64	1/3225 (0.0%)
2	C	0.59	0/1073	0.66	0/1454
2	D	0.51	0/1090	0.69	0/1477
All	All	0.57	1/6946 (0.0%)	0.67	2/9441 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	101	PRO	N-CD	6.60	1.57	1.47

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	100	GLU	N-CA-C	5.32	125.36	111.00
1	B	130	LEU	CA-CB-CG	5.05	126.91	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	2355	0	2224	26	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	B	2314	0	2190	34	0
2	C	1049	0	1031	14	0
2	D	1064	0	1050	17	0
3	A	14	0	13	0	0
3	B	14	0	13	1	0
4	A	96	0	0	1	0
4	B	77	0	0	2	0
4	C	20	0	0	0	0
4	D	7	0	0	1	0
All	All	7010	0	6521	90	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 (90) 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:102:LYS:O	1:B:105:THR:HG22	1.51	1.10
2:D:51:HIS:O	2:D:73:ARG:NH1	1.89	1.06
1:B:100:GLU:CB	1:B:101:PRO:HD3	1.95	0.96
1:A:32:GLU:HB2	4:A:410:HOH:O	1.71	0.90
1:B:102:LYS:O	1:B:105:THR:CG2	2.21	0.87
1:A:0:GLU:HB3	1:A:12:GLU:HB2	1.59	0.82
2:D:138:GLN:HG3	2:D:139:ARG:H	1.51	0.74
1:B:100:GLU:CB	1:B:101:PRO:CD	2.66	0.73
1:B:97:ASP:C	1:B:97:ASP:OD1	2.30	0.69
2:D:8:SER:HB2	2:D:9:PRO:HD2	1.74	0.67
2:C:93:GLU:CB	2:C:94:PRO:HD2	2.27	0.65
2:C:89:ILE:O	2:C:143:ARG:HD2	1.97	0.64
2:C:141:LEU:O	2:C:145:LYS:HG2	1.98	0.63
2:C:21:LEU:HB3	2:C:154:VAL:HG21	1.81	0.61
2:C:0:LEU:HD12	2:C:0:LEU:N	2.14	0.61
1:A:263:LYS:O	1:A:279:ARG:NH2	2.34	0.60
1:A:133:SER:HB3	1:A:191:ASP:HB2	1.85	0.59
1:A:255:VAL:HB	1:A:265:ASP:HB2	1.85	0.58
2:C:137:TRP:HB3	2:C:139:ARG:HG3	1.86	0.58
1:A:177:CYS:SG	1:A:180:ALA:HB2	2.45	0.56
1:A:270:ASP:OD1	1:A:291:ARG:HD2	2.06	0.56
1:B:30:THR:O	1:B:51:LYS:HE3	2.05	0.56
2:C:89:ILE:HG22	2:C:143:ARG:HG3	1.89	0.55
2:D:138:GLN:HG3	2:D:139:ARG:N	2.21	0.55

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:90:PHE:CE1	2:D:143:ARG:HB2	2.42	0.55
1:B:285:SER:HB3	1:B:300:TRP:CE3	2.43	0.54
1:A:100:GLU:CB	1:A:101:PRO:HD3	2.39	0.53
1:A:156:GLU:OE2	1:A:165:TYR:CE2	2.62	0.53
1:B:256:GLN:HG3	1:B:264:LYS:HB3	1.91	0.52
1:B:186:ILE:O	1:B:204:SER:HA	2.10	0.52
1:B:63:ALA:HB1	1:B:80:LEU:O	2.10	0.52
1:A:127:SER:HB3	1:A:165:TYR:CZ	2.45	0.51
2:C:0:LEU:H3	2:C:0:LEU:HD12	1.73	0.50
1:B:97:ASP:HB2	1:B:106:PHE:CE2	2.47	0.50
1:A:156:GLU:OE2	1:A:165:TYR:HE2	1.95	0.50
2:D:11:TRP:CZ3	2:D:164:GLY:HA3	2.46	0.50
1:A:107:LEU:HD12	1:A:203:SER:HB2	1.92	0.50
2:D:137:TRP:HA	2:D:140:LEU:HB2	1.94	0.50
1:B:63:ALA:HB3	1:B:196:LEU:HD13	1.94	0.50
1:A:228:ARG:H	1:A:228:ARG:HH11	1.57	0.49
1:A:255:VAL:HG22	1:A:284:ILE:HD12	1.93	0.49
2:D:8:SER:CB	2:D:9:PRO:HD2	2.41	0.49
1:B:229:GLN:HE21	1:B:277:ILE:HD11	1.78	0.49
2:C:21:LEU:CB	2:C:154:VAL:HG21	2.43	0.48
1:A:63:ALA:HB1	1:A:80:LEU:O	2.13	0.48
2:D:22:CYS:SG	2:D:154:VAL:HG12	2.54	0.47
1:B:280:LYS:HD3	1:B:280:LYS:HA	1.65	0.47
1:B:224:LEU:HD12	1:B:229:GLN:HB3	1.96	0.47
1:A:87:ASP:OD2	1:A:87:ASP:N	2.47	0.47
1:B:222:LYS:HG2	4:B:390:HOH:O	2.15	0.47
1:A:285:SER:HB3	1:A:300:TRP:CE3	2.50	0.47
2:D:100:SER:OG	2:D:102:VAL:HG22	2.15	0.46
2:D:11:TRP:CE3	2:D:164:GLY:HA3	2.51	0.46
1:B:289:GLN:HG2	1:B:290:ASP:N	2.32	0.45
2:C:78:LEU:HD11	2:C:112:LEU:HD13	1.98	0.44
1:B:138:ARG:NH1	1:B:184:LEU:O	2.49	0.44
1:B:94:ILE:HG23	1:B:130:LEU:HD11	2.00	0.44
1:B:278:CYS:SG	1:B:284:ILE:HD11	2.57	0.44
1:B:98:GLN:O	1:B:99:LYS:CB	2.64	0.44
1:B:229:GLN:HE21	1:B:277:ILE:CD1	2.30	0.44
2:D:8:SER:HB2	2:D:9:PRO:CD	2.47	0.44
1:B:86:GLU:O	1:B:89:ILE:HG22	2.19	0.43
1:A:37:THR:HB	1:A:46:VAL:HG13	2.00	0.43
1:A:142:ASP:HA	1:A:143:PRO:HD2	1.84	0.43
1:B:57:VAL:HG11	1:B:82:LEU:HD21	1.99	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:1:ARG:HH11	2:D:1:ARG:HB3	1.84	0.43
2:D:78:LEU:HD11	2:D:112:LEU:HD13	2.00	0.43
1:A:41:ASP:HB3	1:A:42:GLN:H	1.56	0.43
1:A:64:GLY:HA2	1:A:196:LEU:HD11	2.01	0.43
2:C:64:ARG:HH11	2:C:64:ARG:HB3	1.84	0.43
2:D:8:SER:CB	2:D:9:PRO:CD	2.97	0.42
1:A:97:ASP:OD2	1:A:99:LYS:N	2.51	0.42
1:A:100:GLU:CB	1:A:101:PRO:CD	2.96	0.42
1:B:141:SER:HB3	4:B:362:HOH:O	2.19	0.42
1:B:16:TYR:N	1:B:16:TYR:CD1	2.87	0.42
1:A:276:VAL:HG21	1:A:284:ILE:HD12	2.02	0.42
1:A:122:TRP:NE1	1:A:167:TYR:HB2	2.35	0.42
2:D:13:GLN:HG3	4:D:182:HOH:O	2.19	0.41
1:B:246:TYR:CG	2:D:60:PRO:HG3	2.55	0.41
2:C:90:PHE:CE1	2:C:143:ARG:HG2	2.54	0.41
1:B:237:PRO:HG2	1:B:240:TRP:HB2	2.02	0.41
1:B:281:ASN:HD22	1:B:281:ASN:HA	1.56	0.41
2:C:0:LEU:CD1	2:C:0:LEU:N	2.84	0.41
1:A:95:LEU:HD21	1:A:122:TRP:CD1	2.57	0.40
1:B:70:LYS:HB2	1:B:75:LEU:HD11	2.03	0.40
1:B:16:TYR:CD2	1:B:18:ASP:O	2.74	0.40
1:B:121:TRP:HA	1:B:167:TYR:O	2.21	0.40
2:C:163:HIS:CE1	2:C:167:THR:HG21	2.57	0.40
1:B:287:ARG:HB2	1:B:300:TRP:CE3	2.56	0.40
1:B:83:HIS:HD1	3:B:313:NAG:C6	2.33	0.40

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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	296/314 (94%)	276 (93%)	18 (6%)	2 (1%)	26	31

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	286/314 (91%)	273 (96%)	13 (4%)	0	100	100
2	C	129/177 (73%)	124 (96%)	5 (4%)	0	100	100
2	D	129/177 (73%)	118 (92%)	10 (8%)	1 (1%)	24	27
All	All	840/982 (86%)	791 (94%)	46 (6%)	3 (0%)	39	48

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	D	98	PRO
1	A	141	SER
1	A	101	PRO

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	262/285 (92%)	252 (96%)	10 (4%)	40	54
1	B	259/285 (91%)	246 (95%)	13 (5%)	30	41
2	C	109/151 (72%)	101 (93%)	8 (7%)	17	22
2	D	114/151 (76%)	103 (90%)	11 (10%)	10	12
All	All	744/872 (85%)	702 (94%)	42 (6%)	26	35

All (42) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	32	GLU
1	A	86	GLU
1	A	101	PRO
1	A	121	TRP
1	A	127	SER
1	A	135	LYS
1	A	226	ASN
1	A	228	ARG

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	291	ARG
1	A	306	SER
1	B	16	TYR
1	B	32	GLU
1	B	41	ASP
1	B	84	LYS
1	B	87	ASP
1	B	97	ASP
1	B	105	THR
1	B	153	LEU
1	B	202	THR
1	B	264	LYS
1	B	278	CYS
1	B	281	ASN
1	B	291	ARG
2	C	0	LEU
2	C	7	SER
2	C	54	CYS
2	C	64	ARG
2	C	82	GLU
2	C	105	LEU
2	C	112	LEU
2	C	138	GLN
2	D	1	ARG
2	D	15	GLN
2	D	64	ARG
2	D	73	ARG
2	D	82	GLU
2	D	84	LEU
2	D	97	LEU
2	D	112	LEU
2	D	119	GLU
2	D	141	LEU
2	D	150	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (8) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	42	GLN
1	A	65	GLN
1	A	144	GLN
1	A	226	ASN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	B	172	GLN
1	B	220	GLN
1	B	229	GLN
1	B	281	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 carbohydrates in this entry.

5.6 Ligand geometry [i](#)

2 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	$\# Z > 2$
3	NAG	A	313	1	14,14,15	0.54	0	15,19,21	1.87	2 (13%)
3	NAG	B	313	1	14,14,15	0.59	0	15,19,21	1.41	3 (20%)

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	313	1	1/1/5/7	0/6/23/26	0/1/1/1
3	NAG	B	313	1	-	0/6/23/26	0/1/1/1

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	313	NAG	C3-C4-C5	2.22	114.06	110.20
3	B	313	NAG	C2-N2-C7	2.28	125.97	123.04
3	A	313	NAG	C2-N2-C7	3.58	127.64	123.04
3	B	313	NAG	C1-O5-C5	3.63	116.86	112.25
3	A	313	NAG	C1-O5-C5	5.20	118.85	112.25

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
3	A	313	NAG	C1

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	313	NAG	1	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, 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	300/314 (95%)	0.39	20 (6%)	21 29	22, 43, 67, 80	3 (1%)
1	B	294/314 (93%)	0.31	22 (7%)	17 24	29, 44, 67, 76	2 (0%)
2	C	137/177 (77%)	0.56	14 (10%)	9 13	22, 41, 70, 83	0
2	D	137/177 (77%)	0.75	18 (13%)	5 7	31, 54, 76, 92	0
All	All	868/982 (88%)	0.45	74 (8%)	13 19	22, 45, 70, 92	5 (0%)

All (74) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	D	140	LEU	8.1
1	A	19	ALA	5.2
2	C	48	ASP	4.5
2	C	141	LEU	4.4
1	A	18	ASP	4.3
2	C	169	SER	4.0
1	A	16	TYR	4.0
2	D	0	LEU	4.0
1	B	88	GLY	3.9
2	D	173	HIS	3.9
2	C	92	GLY	3.8
1	B	100	GLU	3.7
2	C	137	TRP	3.7
2	C	94	PRO	3.7
2	D	89	ILE	3.6
2	D	7	SER	3.6
1	B	279	ARG	3.5
2	C	140	LEU	3.4
2	D	144	PHE	3.4
1	B	162	ASN	3.3
2	D	6	GLY	3.3

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
2	C	47	ASN	3.3
2	D	139	ARG	3.2
1	A	17	PRO	3.2
2	D	5	GLY	3.1
1	B	13	LEU	3.0
2	D	88	ASP	2.9
1	A	156	GLU	2.9
2	D	86	GLY	2.8
1	B	18	ASP	2.8
2	D	91	THR	2.8
1	A	100	GLU	2.8
1	B	223	PRO	2.7
1	A	164	GLU	2.7
1	B	257	GLY	2.7
1	A	15	TRP	2.7
2	C	88	ASP	2.7
1	B	141	SER	2.7
1	A	86	GLU	2.7
1	B	144	GLN	2.6
1	A	140	SER	2.5
1	A	226	ASN	2.5
1	A	281	ASN	2.5
1	B	282	ALA	2.5
2	D	141	LEU	2.5
1	A	257	GLY	2.5
1	B	140	SER	2.5
2	D	8	SER	2.5
1	B	98	GLN	2.4
2	C	138	GLN	2.4
1	A	20	PRO	2.4
2	C	139	ARG	2.4
1	A	103	ASN	2.3
2	D	87	SER	2.3
2	C	64	ARG	2.3
2	D	138	GLN	2.3
1	B	224	LEU	2.3
1	A	127	SER	2.3
1	B	258	LYS	2.3
2	C	0	LEU	2.3
1	B	265	ASP	2.2
1	A	99	LYS	2.2
2	D	171	HIS	2.2

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	B	280	LYS	2.2
1	A	101	PRO	2.2
1	A	22	GLU	2.1
2	D	137	TRP	2.1
1	B	256	GLN	2.1
1	B	163	LYS	2.1
1	B	103	ASN	2.1
1	A	121	TRP	2.1
1	B	87	ASP	2.1
1	B	229	GLN	2.0
2	C	86	GLY	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, 95th 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	B	313	14/15	0.88	0.14	0.27	54,57,60,61	0
3	NAG	A	313	14/15	0.90	0.14	-0.73	54,55,56,57	0

6.5 Other polymers [i](#)

There are no such residues in this entry.