Full wwPDB X-ray Structure Validation Report ⓘ

May 26, 2020 – 12:25 am BST

PDB ID	:	1E42
Title	:	Beta2-adaptin appendage domain, from clathrin adaptor AP2
Authors	:	Owen, D.J.; Evans, P.R.; McMahon, H.T.
Deposited on	:	2000-06-27
Resolution	:	1.70 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at *validation@mail.wwpdb.org*
A user guide is available at
https://www.wwpdb.org/validation/2017/XrayValidationReportHelp
with specific help available everywhere you see the ⓘ symbol.

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

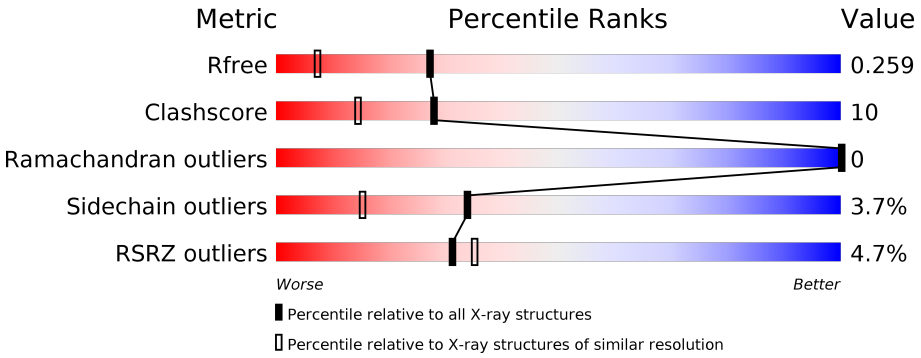
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.11
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.11

1 Overall quality at a glance (i)

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

The reported resolution of this entry is 1.70 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	4298 (1.70-1.70)
Clashscore	141614	4695 (1.70-1.70)
Ramachandran outliers	138981	4610 (1.70-1.70)
Sidechain outliers	138945	4610 (1.70-1.70)
RSRZ outliers	127900	4222 (1.70-1.70)

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 <=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	258	3% 73% 14% • 10%
1	B	258	5% 77% 11% • 10%

2 Entry composition (i)

There are 7 unique types of molecules in this entry. The entry contains 4555 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 AP-2 COMPLEX SUBUNIT BETA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	233	Total	C	N	O	S	0	0	0
			1844	1189	307	337	11			
1	B	233	Total	C	N	O	S	0	0	0
			1852	1193	311	337	11			

There are 42 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	680	MET	-	expression tag	UNP P63010
A	681	GLY	-	expression tag	UNP P63010
A	682	SER	-	expression tag	UNP P63010
A	683	SER	-	expression tag	UNP P63010
A	684	HIS	-	expression tag	UNP P63010
A	685	HIS	-	expression tag	UNP P63010
A	686	HIS	-	expression tag	UNP P63010
A	687	HIS	-	expression tag	UNP P63010
A	688	HIS	-	expression tag	UNP P63010
A	689	HIS	-	expression tag	UNP P63010
A	690	SER	-	expression tag	UNP P63010
A	691	SER	-	expression tag	UNP P63010
A	692	GLY	-	expression tag	UNP P63010
A	693	LEU	-	expression tag	UNP P63010
A	694	VAL	-	expression tag	UNP P63010
A	695	PRO	-	expression tag	UNP P63010
A	696	ARG	-	expression tag	UNP P63010
A	697	GLY	-	expression tag	UNP P63010
A	698	SER	-	expression tag	UNP P63010
A	699	HIS	-	expression tag	UNP P63010
A	700	MET	-	expression tag	UNP P63010
B	680	MET	-	expression tag	UNP P63010
B	681	GLY	-	expression tag	UNP P63010
B	682	SER	-	expression tag	UNP P63010
B	683	SER	-	expression tag	UNP P63010

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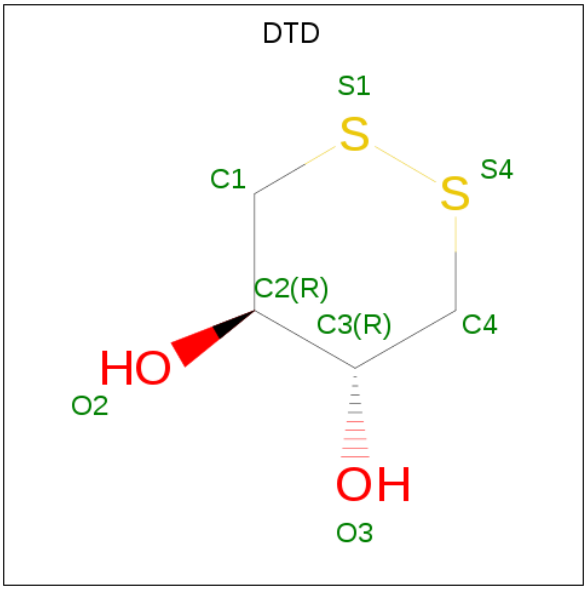
Chain	Residue	Modelled	Actual	Comment	Reference
B	684	HIS	-	expression tag	UNP P63010
B	685	HIS	-	expression tag	UNP P63010
B	686	HIS	-	expression tag	UNP P63010
B	687	HIS	-	expression tag	UNP P63010
B	688	HIS	-	expression tag	UNP P63010
B	689	HIS	-	expression tag	UNP P63010
B	690	SER	-	expression tag	UNP P63010
B	691	SER	-	expression tag	UNP P63010
B	692	GLY	-	expression tag	UNP P63010
B	693	LEU	-	expression tag	UNP P63010
B	694	VAL	-	expression tag	UNP P63010
B	695	PRO	-	expression tag	UNP P63010
B	696	ARG	-	expression tag	UNP P63010
B	697	GLY	-	expression tag	UNP P63010
B	698	SER	-	expression tag	UNP P63010
B	699	HIS	-	expression tag	UNP P63010
B	700	MET	-	expression tag	UNP P63010

- Molecule 2 is DITHIANE DIOL (three-letter code: DTD) (formula: $C_4H_8O_2S_2$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total C O S 8 4 2 2	0	0
2	B	1	Total C O S 8 4 2 2	0	0

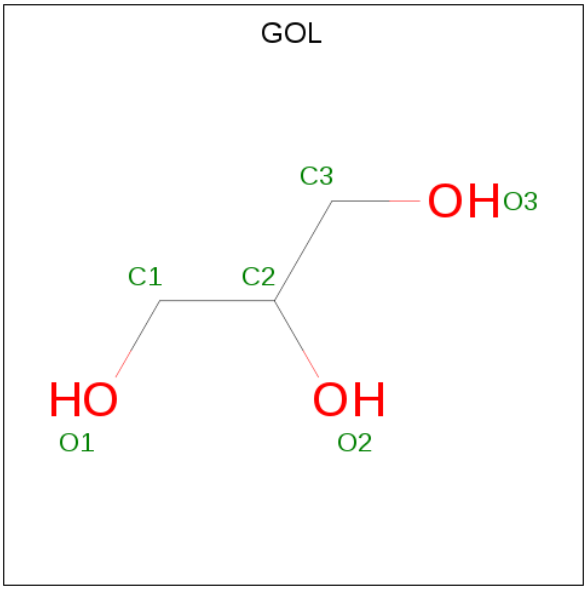
- Molecule 3 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	B	3	Total Mg 3 3	0	0
3	A	1	Total Mg 1 1	0	0

- Molecule 4 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	B	2	Total Cl 2 2	0	0
4	A	2	Total Cl 2 2	0	0

- Molecule 5 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	1	Total C O 6 3 3	0	0
5	B	1	Total C O 6 3 3	0	0

- Molecule 6 is NICKEL (II) ION (three-letter code: NI) (formula: Ni).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	B	1	Total Ni 1 1	0	0

- Molecule 7 is water.

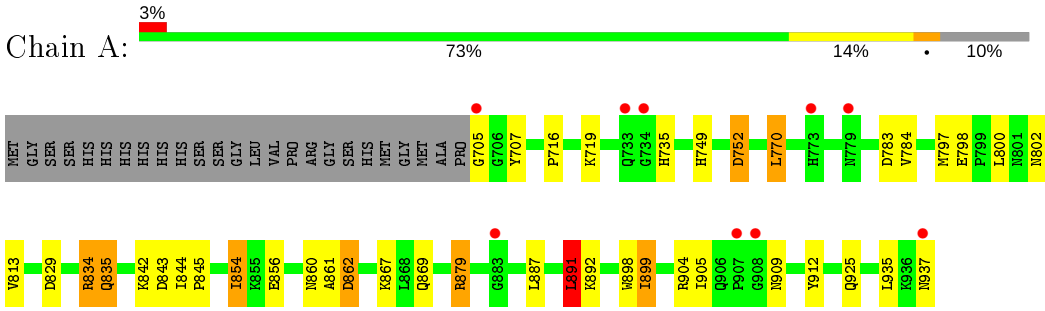
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	A	403	Total O 403 403	0	0
7	B	419	Total O 419 419	0	0

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

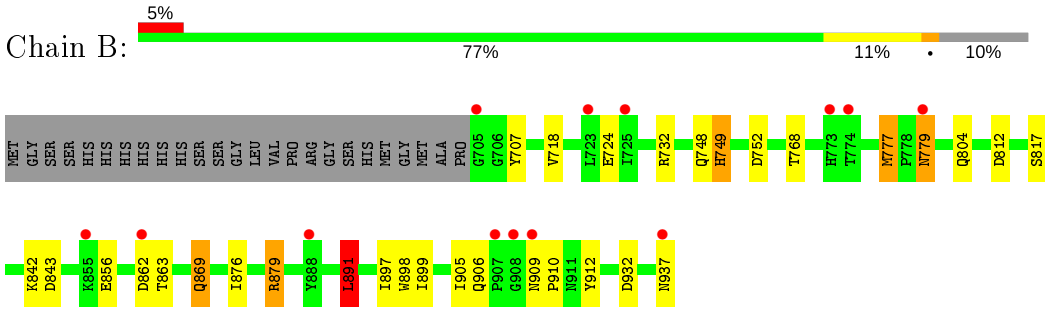
- Molecule 1: AP-2 COMPLEX SUBUNIT BETA

Chain A:



- Molecule 1: AP-2 COMPLEX SUBUNIT BETA

Chain B:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α, β, γ	97.04Å 124.59Å 67.64Å 90.00° 124.18° 90.00°	Depositor
Resolution (Å)	67.42 – 1.70 19.95 – 1.70	Depositor EDS
% Data completeness (in resolution range)	98.3 (67.42-1.70) 98.3 (19.95-1.70)	Depositor EDS
R_{merge}	0.16	Depositor
R_{sym}	0.16	Depositor
$< I/\sigma(I) >$ [1]	1.69 (at 1.70Å)	Xtriage
Refinement program	REFMAC 5	Depositor
R, R_{free}	0.196 , 0.246 0.206 , 0.259	Depositor DCC
R_{free} test set	7151 reflections (5.06%)	wwPDB-VP
Wilson B-factor (Å^2)	22.8	Xtriage
Anisotropy	0.615	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.36 , 46.3	EDS
L-test for twinning[2]	$< \|L\| > = 0.51$, $< L^2 > = 0.35$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.96	EDS
Total number of atoms	4555	wwPDB-VP
Average B, all atoms (Å^2)	31.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.11% 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, 0.333 respectively for untwinned datasets, and 0.375, 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, MG, CL, DTD, NI

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	0.81	0/1886	0.99	7/2562 (0.3%)
1	B	0.87	1/1895 (0.1%)	0.97	4/2574 (0.2%)
All	All	0.84	1/3781 (0.0%)	0.98	11/5136 (0.2%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	898	TRP	CB-CG	-6.01	1.39	1.50

All (11) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	752	ASP	CB-CG-OD2	7.33	124.89	118.30
1	A	783	ASP	CB-CG-OD2	7.26	124.83	118.30
1	B	752	ASP	CB-CG-OD2	6.70	124.33	118.30
1	A	862	ASP	CB-CG-OD1	6.69	124.32	118.30
1	A	891	LEU	CA-CB-CG	6.23	129.64	115.30
1	B	891	LEU	CA-CB-CG	6.16	129.46	115.30
1	B	812	ASP	CB-CG-OD1	5.61	123.35	118.30
1	A	770	LEU	CB-CG-CD2	-5.29	102.01	111.00
1	B	932	ASP	CB-CG-OD2	5.25	123.02	118.30
1	A	812	ASP	CB-CG-OD1	5.13	122.92	118.30
1	A	829	ASP	CB-CG-OD2	5.05	122.84	118.30

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	1844	0	1852	41	0
1	B	1852	0	1862	33	0
2	A	8	0	8	0	0
2	B	8	0	8	0	0
3	A	1	0	0	0	0
3	B	3	0	0	0	0
4	A	2	0	0	0	0
4	B	2	0	0	0	0
5	A	6	0	8	1	0
5	B	6	0	8	3	0
6	B	1	0	0	0	0
7	A	403	0	0	16	7
7	B	419	0	0	16	8
All	All	4555	0	3746	74	9

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 10.

All (74) 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:732:ARG:NH1	7:B:2041:HOH:O	2.07	0.86
1:B:724:GLU:OE1	7:B:2026:HOH:O	1.95	0.84
1:B:749:HIS:HB3	7:B:2094:HOH:O	1.76	0.83
1:B:856:GLU:O	7:B:2340:HOH:O	2.04	0.75
1:B:779:ASN:HB2	7:B:2191:HOH:O	1.85	0.75
1:B:748:GLN:OE1	7:B:2092:HOH:O	2.05	0.74
1:B:843:ASP:OD1	7:B:2324:HOH:O	2.05	0.74
1:B:777:MET:HE2	7:B:2094:HOH:O	1.88	0.73
1:A:898:TRP:C	1:A:899:ILE:HD12	2.08	0.73
1:A:735:HIS:ND1	7:A:2041:HOH:O	2.21	0.73
1:A:860:ASN:HB2	1:A:862:ASP:OD1	1.89	0.73
1:A:854:ILE:HG23	1:A:912:TYR:HB2	1.72	0.72
1:A:862:ASP:OD2	7:A:2324:HOH:O	2.08	0.71
1:B:937:ASN:OXT	7:B:2418:HOH:O	2.07	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:862:ASP:OD2	7:A:2327:HOH:O	2.11	0.69
1:B:897:ILE:CD1	5:B:980:GOL:O1	2.41	0.68
1:A:798:GLU:OE2	7:A:2216:HOH:O	2.10	0.68
1:A:843:ASP:OD1	7:A:2295:HOH:O	2.13	0.67
1:A:856:GLU:OE1	7:A:2316:HOH:O	2.11	0.66
1:B:897:ILE:HD12	5:B:980:GOL:O1	1.96	0.66
1:B:804:GLN:NE2	1:B:817:SER:OG	2.29	0.65
1:A:862:ASP:CB	7:A:2327:HOH:O	2.45	0.64
1:A:909:ASN:O	7:A:2377:HOH:O	2.16	0.62
1:B:869:GLN:NE2	7:B:2352:HOH:O	2.29	0.61
1:A:808:LYS:HG3	1:A:813:VAL:HG22	1.82	0.60
1:B:909:ASN:OD1	1:B:910:PRO:HD2	2.00	0.60
1:B:905:ILE:HG12	1:B:912:TYR:CZ	2.36	0.60
1:A:854:ILE:HD13	1:A:935:LEU:HD12	1.84	0.59
1:A:898:TRP:O	1:A:899:ILE:HD12	2.03	0.59
1:B:897:ILE:HD12	5:B:980:GOL:HO1	1.69	0.57
1:A:862:ASP:CG	7:A:2327:HOH:O	2.42	0.57
1:B:833:GLU:OE1	1:B:835:GLN:NE2	2.37	0.57
1:A:835:GLN:H	1:A:835:GLN:CD	2.08	0.57
1:A:867:LYS:NZ	1:A:937:ASN:O	2.37	0.56
1:A:707:TYR:OH	7:A:2004:HOH:O	2.17	0.56
1:B:732:ARG:HD3	7:B:2056:HOH:O	2.06	0.55
1:B:905:ILE:HG12	1:B:912:TYR:CE1	2.41	0.55
1:A:891:LEU:HD13	1:A:899:ILE:HB	1.90	0.54
1:A:842:LYS:NZ	7:A:2292:HOH:O	2.29	0.54
1:B:856:GLU:HB3	7:B:2340:HOH:O	2.07	0.54
1:A:925:GLN:HG2	7:A:2392:HOH:O	2.07	0.53
7:A:2130:HOH:O	1:B:768:THR:HG22	2.10	0.51
1:B:804:GLN:CD	1:B:817:SER:OG	2.50	0.50
1:A:904:ARG:NH1	7:A:2368:HOH:O	2.45	0.49
1:A:834:ARG:HB3	1:A:835:GLN:OE1	2.13	0.49
1:B:718:VAL:HG13	7:B:2020:HOH:O	2.11	0.49
1:A:899:ILE:HD12	1:A:899:ILE:N	2.28	0.48
1:A:752:ASP:O	1:A:808:LYS:HE2	2.14	0.47
1:B:891:LEU:HD13	1:B:899:ILE:O	2.13	0.47
1:A:860:ASN:CB	1:A:862:ASP:OD1	2.61	0.47
1:A:861:ALA:HB1	1:A:887:LEU:HD21	1.97	0.47
1:A:854:ILE:HD13	1:A:935:LEU:CD1	2.44	0.47
1:A:892:LYS:HE3	1:A:898:TRP:CZ2	2.50	0.46
1:A:770:LEU:HD11	1:A:784:VAL:HG11	1.98	0.45
1:A:705:GLY:N	7:A:2001:HOH:O	2.48	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:842:LYS:NZ	7:B:2318:HOH:O	2.43	0.45
1:A:891:LEU:CD1	1:A:899:ILE:HB	2.47	0.45
1:A:899:ILE:CD1	1:A:899:ILE:N	2.80	0.45
1:A:800:LEU:HD21	5:A:980:GOL:H12	1.99	0.44
1:A:716:PRO:HG2	1:A:719:LYS:HD2	1.99	0.44
1:A:797:MET:HE3	1:A:802:ASN:HB3	1.99	0.44
1:A:844:ILE:HA	1:A:845:PRO:HD3	1.90	0.44
1:B:707:TYR:HE2	7:B:2173:HOH:O	2.01	0.43
1:B:905:ILE:HG12	1:B:912:TYR:CE2	2.53	0.43
1:A:798:GLU:CD	7:A:2215:HOH:O	2.56	0.42
1:A:854:ILE:CG1	1:A:854:ILE:O	2.66	0.42
1:A:905:ILE:HG23	1:A:912:TYR:CE1	2.54	0.42
1:B:906:GLN:HB2	1:B:909:ASN:HB3	2.02	0.41
1:B:834:ARG:HD2	7:B:2231:HOH:O	2.20	0.41
1:B:876:ILE:HD13	1:B:876:ILE:N	2.34	0.41
1:B:862:ASP:OD1	1:B:863:THR:N	2.54	0.40
1:B:879:ARG:HD3	1:B:879:ARG:HA	1.82	0.40
1:B:869:GLN:HB3	1:B:869:GLN:HE21	1.74	0.40
1:A:879:ARG:HA	1:A:879:ARG:HD3	1.79	0.40

All (9) 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)
7:B:2141:HOH:O	7:B:2228:HOH:O[2_555]	1.95	0.25
7:A:2327:HOH:O	7:B:2324:HOH:O[3_546]	2.02	0.18
7:A:2324:HOH:O	7:B:2324:HOH:O[3_546]	2.03	0.17
7:A:2205:HOH:O	7:A:2247:HOH:O[4_546]	2.07	0.13
7:B:2342:HOH:O	7:B:2342:HOH:O[2_455]	2.10	0.10
7:A:2139:HOH:O	7:B:2404:HOH:O[2_555]	2.12	0.08
7:A:2139:HOH:O	7:B:2402:HOH:O[2_555]	2.13	0.07
7:A:2064:HOH:O	7:B:2138:HOH:O[2_555]	2.13	0.07
7:A:2140:HOH:O	7:B:2404:HOH:O[2_555]	2.19	0.01

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	231/258 (90%)	228 (99%)	3 (1%)	0	100	100
1	B	231/258 (90%)	227 (98%)	4 (2%)	0	100	100
All	All	462/516 (90%)	455 (98%)	7 (2%)	0	100	100

There are no Ramachandran outliers to report.

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	204/229 (89%)	196 (96%)	8 (4%)	32	13
1	B	206/229 (90%)	199 (97%)	7 (3%)	37	18
All	All	410/458 (90%)	395 (96%)	15 (4%)	34	15

All (15) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	749	HIS
1	A	834	ARG
1	A	835	GLN
1	A	854	ILE
1	A	869	GLN
1	A	879	ARG
1	A	891	LEU
1	A	899	ILE
1	B	749	HIS
1	B	777	MET
1	B	779	ASN
1	B	835	GLN
1	B	869	GLN
1	B	879	ARG

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Mol	Chain	Res	Type
1	B	891	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	869	GLN
1	B	748	GLN
1	B	749	HIS
1	B	779	ASN
1	B	804	GLN
1	B	860	ASN
1	B	869	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

Of 13 ligands modelled in this entry, 9 are monoatomic - leaving 4 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	$\#\|Z\| > 2$
2	DTD	A	950	-	6,8,8	0.40	0	6,10,10	1.68	2 (33%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\|>2$	Counts	RMSZ	$\#\|Z\|>2$
5	GOL	B	980	-	5,5,5	0.44	0	5,5,5	0.27	0
2	DTD	B	950	-	6,8,8	0.58	0	6,10,10	1.44	2 (33%)
5	GOL	A	980	-	5,5,5	0.49	0	5,5,5	0.81	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
2	DTD	A	950	-	-	-	0/0/1/1
5	GOL	B	980	-	-	0/4/4/4	-
2	DTD	B	950	-	-	-	0/0/1/1
5	GOL	A	980	-	-	0/4/4/4	-

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	B	950	DTD	C1-C2-C3	2.47	117.33	112.45
2	A	950	DTD	C1-C2-C3	2.24	116.87	112.45
2	B	950	DTD	O3-C3-C4	-2.22	106.09	109.91
2	A	950	DTD	O3-C3-C4	-2.17	106.16	109.91

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	B	980	GOL	3	0
5	A	980	GOL	1	0

5.7 Other polymers (i)

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	233/258 (90%)	0.25	9 (3%)	39	44	15, 28, 45, 54	0
1	B	233/258 (90%)	0.35	13 (5%)	24	27	14, 28, 45, 55	0
All	All	466/516 (90%)	0.30	22 (4%)	31	35	14, 28, 45, 55	0

All (22) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	908	GLY	5.2
1	B	907	PRO	4.6
1	A	907	PRO	4.2
1	B	705	GLY	3.8
1	A	773	HIS	3.8
1	A	733	GLN	3.3
1	A	908	GLY	3.3
1	B	723	LEU	2.7
1	B	779	ASN	2.6
1	B	862	ASP	2.6
1	B	888	TYR	2.6
1	B	773	HIS	2.5
1	A	705	GLY	2.4
1	A	883	GLY	2.3
1	B	855	LYS	2.3
1	A	734	GLY	2.2
1	A	779	ASN	2.1
1	B	909	ASN	2.1
1	B	725	ILE	2.1
1	A	937	ASN	2.0
1	B	937	ASN	2.0
1	B	774	THR	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. 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	B-factors(Å^2)	Q<0.9
3	MG	B	961	1/1	0.55	0.18	44,44,44,44	0
3	MG	B	962	1/1	0.59	0.28	50,50,50,50	0
5	GOL	B	980	6/6	0.84	0.19	30,45,50,56	0
5	GOL	A	980	6/6	0.86	0.17	33,50,53,57	0
2	DTD	B	950	8/8	0.91	0.12	30,36,39,46	0
2	DTD	A	950	8/8	0.94	0.08	28,32,35,36	0
3	MG	A	960	1/1	0.94	0.15	42,42,42,42	0
6	NI	B	970	1/1	0.96	0.18	38,38,38,38	1
3	MG	B	960	1/1	0.97	0.15	35,35,35,35	0
4	CL	A	971	1/1	0.98	0.05	25,25,25,25	0
4	CL	B	971	1/1	0.99	0.04	22,22,22,22	0
4	CL	A	972	1/1	0.99	0.03	26,26,26,26	0
4	CL	B	972	1/1	1.00	0.03	24,24,24,24	0

6.5 Other polymers (i)

There are no such residues in this entry.