



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 09:56 AM GMT

PDB ID : 3K90
Title : The Absciscic acid receptor PYR1 in complex with Absciscic Acid
Authors : Dupeux, F.D.; Santiago, J.; Rodriguez, P.L.; Marquez, J.A.
Deposited on : 2009-10-15
Resolution : 2.00 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

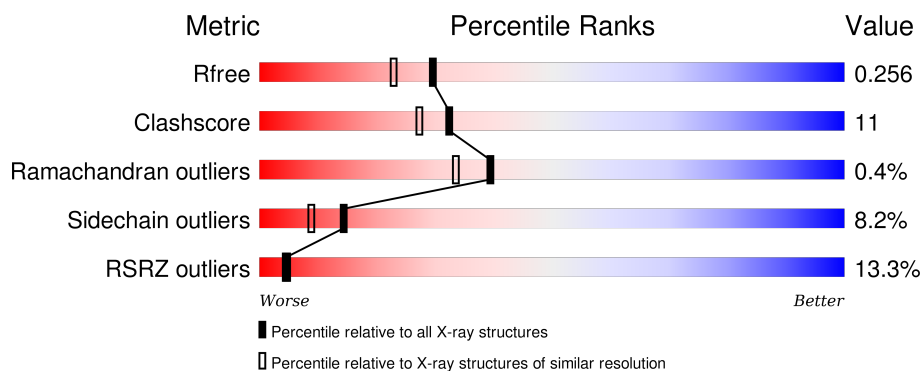
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.00 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	6249 (2.00-2.00)
Clashscore	102246	7340 (2.00-2.00)
Ramachandran outliers	100387	7248 (2.00-2.00)
Sidechain outliers	100360	7247 (2.00-2.00)
RSRZ outliers	91569	6262 (2.00-2.00)

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	193	<div> <div>13%</div> <div> <div></div> <div>75%</div> <div>13%</div> <div>•</div> <div>9%</div> </div> </div>
1	B	193	<div> <div>10%</div> <div> <div></div> <div>68%</div> <div>17%</div> <div>6%</div> <div>9%</div> </div> </div>
1	C	193	<div> <div>12%</div> <div> <div></div> <div>77%</div> <div>10%</div> <div>•</div> <div>10%</div> </div> </div>
1	D	193	<div> <div>13%</div> <div> <div></div> <div>78%</div> <div>13%</div> <div>•</div> <div>7%</div> </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 crite-

ria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	A8S	A	192	-	-	-	X
2	A8S	D	192	-	-	-	X
3	GOL	B	3968	-	-	-	X
3	GOL	C	3968	-	-	-	X
4	ACY	B	192	-	-	X	X

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 6244 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.

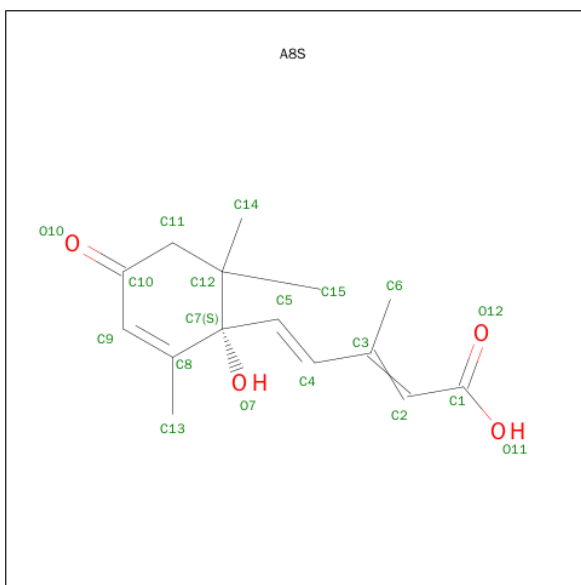
- Molecule 1 is a protein called Putative uncharacterized protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	176	Total	C	N	O	S	0	2	0
			1403	879	246	270	8			
1	B	175	Total	C	N	O	S	0	3	0
			1425	892	252	272	9			
1	C	174	Total	C	N	O	S	0	1	0
			1385	868	245	265	7			
1	D	180	Total	C	N	O	S	0	0	0
			1421	890	250	273	8			

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-1	GLY	-	EXPRESSION TAG	UNP O49686
A	0	ALA	-	EXPRESSION TAG	UNP O49686
A	2	ALA	PRO	ENGINEERED	UNP O49686
B	-1	GLY	-	EXPRESSION TAG	UNP O49686
B	0	ALA	-	EXPRESSION TAG	UNP O49686
B	2	ALA	PRO	ENGINEERED	UNP O49686
C	-1	GLY	-	EXPRESSION TAG	UNP O49686
C	0	ALA	-	EXPRESSION TAG	UNP O49686
C	2	ALA	PRO	ENGINEERED	UNP O49686
D	-1	GLY	-	EXPRESSION TAG	UNP O49686
D	0	ALA	-	EXPRESSION TAG	UNP O49686
D	2	ALA	PRO	ENGINEERED	UNP O49686

- Molecule 2 is (2Z,4E)-5-[(1S)-1-HYDROXY-2,6,6-TRIMETHYL-4-OXOCYCLOHEX-2-EN-1-YL]-3-METHYLPENTA-2,4-DIENOIC ACID (three-letter code: A8S) (formula: C₁₅H₂₀O₄).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	C	O	0	0
			19	15	4		
2	D	1	Total	C	O	0	0
			19	15	4		

- Molecule 3 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$).



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

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

- Molecule 4 is ACETIC ACID (three-letter code: ACY) (formula: C₂H₄O₂).



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

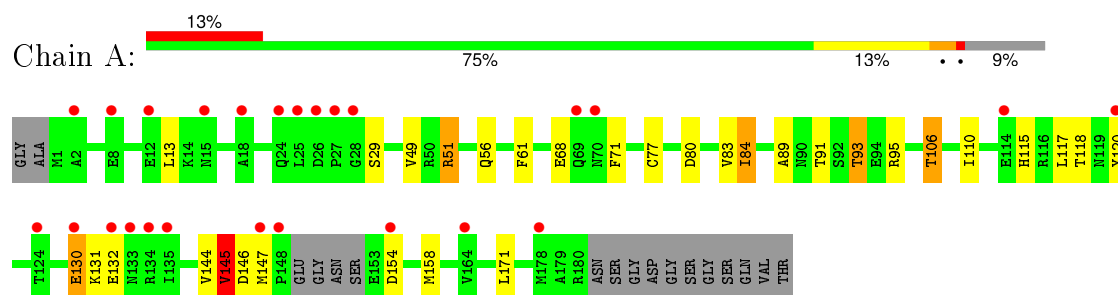
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	132	Total	O	0	0
			132	132		
5	B	141	Total	O	0	0
			141	141		
5	C	129	Total	O	0	0
			129	129		
5	D	148	Total	O	0	0
			148	148		

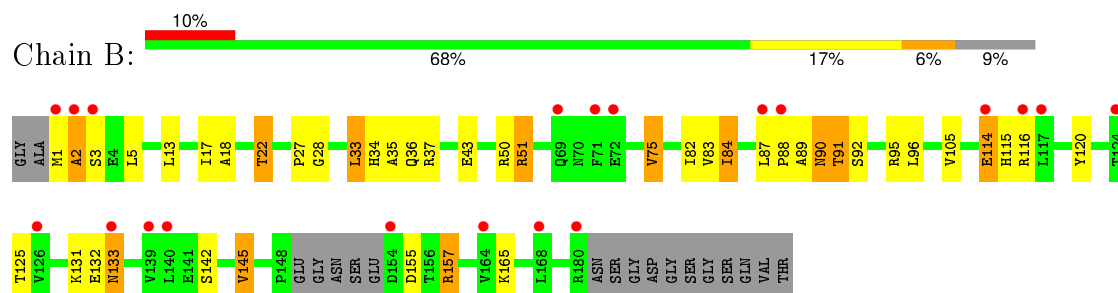
3 Residue-property plots [i](#)

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.

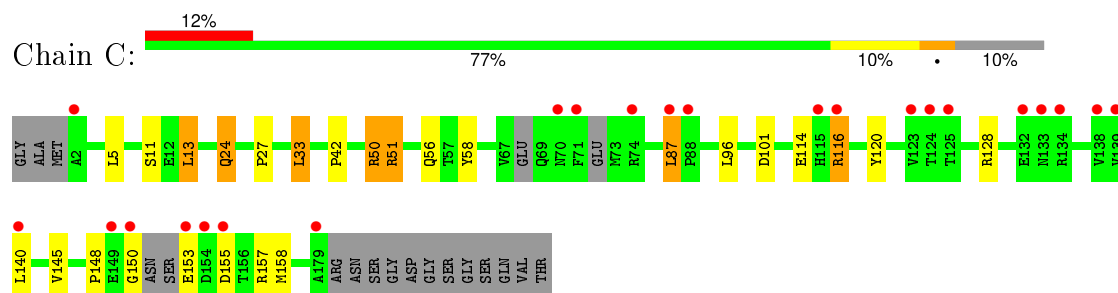
- Molecule 1: Putative uncharacterized protein



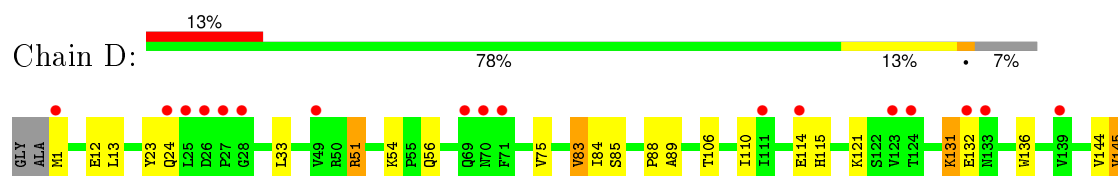
- Molecule 1: Putative uncharacterized protein

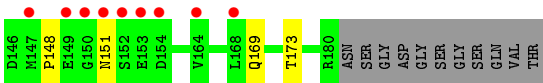


- Molecule 1: Putative uncharacterized protein



- Molecule 1: Putative uncharacterized protein





4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	49.81Å 61.28Å 72.55Å 105.65° 102.23° 89.91°	Depositor
Resolution (Å)	24.67 – 2.00 24.67 – 2.00	Depositor EDS
% Data completeness (in resolution range)	100.0 (24.67-2.00) 88.1 (24.67-2.00)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.92 (at 1.99Å)	Xtriage
Refinement program	REFMAC 5.5.0072	Depositor
R, R_{free}	0.200 , 0.234 0.226 , 0.256	Depositor DCC
R_{free} test set	2647 reflections (5.26%)	DCC
Wilson B-factor (Å ²)	31.4	Xtriage
Anisotropy	0.081	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.38 , 55.4	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	0 of 52935 reflections	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	6244	wwPDB-VP
Average B, all atoms (Å ²)	26.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.18% 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: GOL, ACY, A8S

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	0.65	3/1429 (0.2%)	0.70	2/1938 (0.1%)
1	B	0.62	1/1451 (0.1%)	0.74	0/1963
1	C	0.65	0/1409	0.70	0/1906
1	D	0.59	1/1448 (0.1%)	0.72	1/1962 (0.1%)
All	All	0.63	5/5737 (0.1%)	0.72	3/7769 (0.0%)

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	145	VAL	CB-CG1	-5.90	1.40	1.52
1	A	144	VAL	CB-CG2	-5.90	1.40	1.52
1	A	145	VAL	CA-CB	-5.59	1.43	1.54
1	D	83	VAL	CB-CG1	-5.48	1.41	1.52
1	B	2	ALA	C-O	5.23	1.33	1.23

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	145	VAL	N-CA-C	-5.58	95.94	111.00
1	D	145	VAL	CB-CA-C	-5.31	101.31	111.40
1	A	106	THR	CB-CA-C	-5.11	97.79	111.60

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	1403	0	1369	23	0
1	B	1425	0	1407	46	0
1	C	1385	0	1354	27	0
1	D	1421	0	1391	26	0
2	A	19	0	19	2	0
2	D	19	0	19	1	0
3	B	6	0	8	0	0
3	C	12	0	16	3	0
4	B	4	0	3	5	0
5	A	132	0	0	5	0
5	B	141	0	0	2	0
5	C	129	0	0	2	0
5	D	148	0	0	3	0
All	All	6244	0	5586	119	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 11.

All (119) 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:89:ALA:CB	1:D:115:HIS:HB3	1.69	1.22
1:D:89:ALA:HB2	1:D:115:HIS:HB3	1.18	1.14
1:D:89:ALA:HB2	1:D:115:HIS:CB	1.82	1.10
1:B:51:ARG:HG2	1:B:51:ARG:HH11	1.19	1.08
1:C:51:ARG:HH11	1:C:51:ARG:HG2	1.21	1.05
1:A:89:ALA:HB2	1:A:115:HIS:HB3	1.35	1.02
1:A:51:ARG:HH11	1:A:51:ARG:HG2	1.20	1.01
1:B:132:GLU:O	1:B:133:ASN:HB2	1.63	0.98
1:D:51:ARG:HG2	1:D:51:ARG:HH11	1.29	0.96
1:B:2:ALA:CB	1:B:37:ARG:H	1.87	0.88
1:B:2:ALA:H	1:B:3:SER:C	1.81	0.84
1:C:116:ARG:HH11	1:C:116:ARG:HG2	1.43	0.84
1:D:89:ALA:HB1	1:D:115:HIS:HB3	1.60	0.82
1:C:116:ARG:HH11	1:C:116:ARG:CG	1.94	0.81
1:C:51:ARG:CG	1:C:51:ARG:HH11	1.96	0.79
1:A:77[B]:CYS:SG	5:A:376:HOH:O	2.39	0.79
1:A:51:ARG:HH11	1:A:51:ARG:CG	1.99	0.75
1:C:51:ARG:NH1	1:C:51:ARG:HG2	1.99	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:51:ARG:NH1	1:A:51:ARG:HG2	1.96	0.74
1:A:29:SER:HA	1:A:146:ASP:HA	1.72	0.72
1:B:51:ARG:CG	1:B:51:ARG:HH11	2.02	0.69
1:C:120:TYR:HD2	1:C:145:VAL:CG1	2.06	0.69
1:A:89:ALA:CB	1:A:115:HIS:HB3	2.20	0.69
1:B:2:ALA:N	1:B:3:SER:HA	2.08	0.69
1:B:2:ALA:N	1:B:3:SER:CA	2.57	0.67
1:D:88:PRO:HB2	5:D:219:HOH:O	1.94	0.67
1:C:120:TYR:CD2	1:C:145:VAL:CG1	2.77	0.66
1:C:58:TYR:HE2	5:C:645:HOH:O	1.77	0.66
1:A:115:HIS:HB2	5:A:202:HOH:O	1.96	0.66
2:A:192:A8S:H4	2:A:192:A8S:O11	1.96	0.65
1:B:83:VAL:HG22	1:B:90:ASN:HD22	1.62	0.65
1:B:95:ARG:HD3	5:B:365:HOH:O	1.98	0.63
1:B:34:HIS:CE1	1:B:165:LYS:HE3	2.34	0.62
1:B:28:GLY:HA2	3:C:192:GOL:H11	1.80	0.62
1:C:148:PRO:HG2	1:C:155:ASP:CB	2.29	0.62
1:B:51:ARG:HG2	1:B:51:ARG:NH1	1.99	0.61
1:B:115:HIS:H	4:B:192:ACY:H2	1.64	0.61
1:B:2:ALA:H	1:B:3:SER:CA	2.14	0.61
1:D:51:ARG:HH11	1:D:51:ARG:CG	2.07	0.61
1:B:82:ILE:HD13	1:B:91:THR:HB	1.81	0.61
1:C:148:PRO:HG2	1:C:155:ASP:CG	2.21	0.60
1:A:80:ASP:OD1	1:A:93:THR:HB	2.01	0.60
1:C:50:ARG:NH1	1:C:101:ASP:OD1	2.33	0.60
1:D:89:ALA:HB2	1:D:115:HIS:HB2	1.81	0.58
1:A:120:TYR:HD2	1:A:145:VAL:HG13	1.69	0.57
1:B:2:ALA:HB2	1:B:37:ARG:H	1.69	0.57
1:A:89:ALA:HB2	1:A:115:HIS:CB	2.23	0.57
1:C:116:ARG:HG2	1:C:116:ARG:NH1	2.12	0.56
1:B:120:TYR:CD2	1:B:145:VAL:HG13	2.41	0.55
1:D:24:GLN:O	1:D:24:GLN:HG2	2.07	0.55
1:B:84:ILE:O	1:B:84:ILE:HG23	2.05	0.55
1:B:131:LYS:O	1:B:132:GLU:HB2	2.06	0.54
1:B:120:TYR:HD2	1:B:145:VAL:HG13	1.73	0.54
1:B:27:PRO:HA	1:C:33:LEU:HD13	1.90	0.54
1:A:95:ARG:HD3	5:A:208:HOH:O	2.07	0.53
1:B:105:VAL:HG22	1:B:125:THR:HG22	1.89	0.53
1:A:154:ASP:O	1:A:158:MET:HG3	2.09	0.52
1:B:2:ALA:HB2	1:B:36:GLN:HA	1.90	0.52
1:A:115:HIS:HD2	1:A:117:LEU:H	1.57	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:130:GLU:O	1:A:130:GLU:HG2	2.09	0.51
2:D:192:A8S:H4	2:D:192:A8S:O11	2.10	0.51
1:B:114:GLU:HG3	4:B:192:ACY:H2	1.92	0.51
1:B:1:MET:HG3	1:B:35:ALA:O	2.11	0.51
1:C:148:PRO:HG2	1:C:155:ASP:HB2	1.92	0.50
1:B:155:ASP:OD1	1:B:157:ARG:HD2	2.11	0.50
1:A:120:TYR:CD2	1:A:145:VAL:HG13	2.45	0.50
1:C:120:TYR:HD2	1:C:145:VAL:HG11	1.75	0.50
1:C:120:TYR:CD2	1:C:145:VAL:HG12	2.46	0.50
1:B:83:VAL:CG2	1:B:90:ASN:ND2	2.76	0.49
1:C:51:ARG:CG	1:C:51:ARG:NH1	2.66	0.49
1:D:114:GLU:HA	1:D:114:GLU:OE1	2.12	0.49
1:D:110:ILE:HG21	1:D:115:HIS:NE2	2.29	0.48
1:D:169:GLN:O	1:D:173:THR:HG23	2.14	0.48
1:B:115:HIS:HB2	4:B:192:ACY:H1	1.96	0.47
1:C:13:LEU:HG	1:C:140:LEU:HD11	1.97	0.47
1:C:87:LEU:HB2	1:D:88:PRO:HB3	1.97	0.47
1:B:33:LEU:HD23	1:B:142:SER:HB3	1.97	0.47
1:D:24:GLN:HB3	5:D:487:HOH:O	2.13	0.47
1:C:120:TYR:HD2	1:C:145:VAL:HG12	1.78	0.47
1:D:83:VAL:HG12	1:D:84:ILE:N	2.29	0.47
1:D:51:ARG:HG2	1:D:51:ARG:NH1	2.09	0.46
1:B:120:TYR:HD2	1:B:145:VAL:CG1	2.28	0.45
1:B:83:VAL:CG2	1:B:90:ASN:HD22	2.29	0.45
1:B:5:LEU:HD12	1:C:27:PRO:HG2	1.97	0.45
1:D:1:MET:CE	1:D:1:MET:HA	2.46	0.45
1:A:83:VAL:HG21	2:A:192:A8S:H14A	1.98	0.45
1:B:83:VAL:HG22	1:B:90:ASN:ND2	2.30	0.45
1:B:84:ILE:HA	1:B:84:ILE:HD12	1.71	0.45
1:B:88:PRO:O	1:B:89:ALA:C	2.55	0.45
1:C:116:ARG:NH1	1:C:116:ARG:CG	2.64	0.44
1:B:28:GLY:CA	3:C:192:GOL:H11	2.46	0.44
1:D:131:LYS:HB2	1:D:136:TRP:CZ3	2.53	0.43
1:D:131:LYS:HB2	1:D:136:TRP:HZ3	1.83	0.43
1:C:150:GLY:O	1:C:153:GLU:N	2.51	0.43
1:D:131:LYS:O	1:D:132:GLU:C	2.51	0.43
1:D:23:TYR:CD1	1:D:144:VAL:HG21	2.53	0.43
1:A:68:GLU:O	1:A:71:PHE:HB2	2.19	0.43
1:B:28:GLY:HA2	3:C:192:GOL:C1	2.49	0.43
1:C:158:MET:HB3	5:C:650:HOH:O	2.18	0.43
1:D:121:LYS:HE3	5:D:232:HOH:O	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:51:ARG:NH1	1:A:51:ARG:CG	2.68	0.43
1:B:132:GLU:O	1:B:133:ASN:CB	2.45	0.43
1:B:43[A]:GLU:H	1:B:43[A]:GLU:CD	2.22	0.43
1:B:75:VAL:HG13	5:B:225:HOH:O	2.19	0.43
1:B:17:ILE:HG22	1:C:24[A]:GLN:HG2	2.00	0.42
1:D:51:ARG:NH1	1:D:51:ARG:CG	2.75	0.42
1:D:83:VAL:CG1	1:D:84:ILE:N	2.81	0.42
1:B:92:SER:CB	4:B:192:ACY:H3	2.50	0.42
1:B:27:PRO:HG2	1:C:5:LEU:HD12	2.01	0.42
1:B:84:ILE:O	1:B:84:ILE:CG2	2.68	0.42
1:A:91:THR:HG22	5:A:382:HOH:O	2.19	0.42
1:C:42:PRO:HG3	1:C:128:ARG:HB2	2.01	0.42
1:D:110:ILE:HG21	1:D:115:HIS:CE1	2.54	0.42
1:A:118:THR:HB	5:A:387:HOH:O	2.21	0.41
1:A:61:PHE:HA	1:A:84:ILE:CD1	2.50	0.41
1:A:110:ILE:HG21	1:A:115:HIS:NE2	2.36	0.41
1:B:115:HIS:HB2	4:B:192:ACY:CH3	2.51	0.41
1:B:18:ALA:HA	1:B:22:THR:CG2	2.51	0.41
1:D:23:TYR:CD1	1:D:144:VAL:CG2	3.04	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	174/193 (90%)	169 (97%)	4 (2%)	1 (1%)	30	22
1	B	174/193 (90%)	166 (95%)	7 (4%)	1 (1%)	30	22
1	C	167/193 (86%)	162 (97%)	5 (3%)	0	100	100
1	D	178/193 (92%)	174 (98%)	3 (2%)	1 (1%)	30	22
All	All	693/772 (90%)	671 (97%)	19 (3%)	3 (0%)	39	33

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	131	LYS
1	B	133	ASN
1	D	148	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	156/171 (91%)	144 (92%)	12 (8%)	16	10
1	B	160/171 (94%)	145 (91%)	15 (9%)	11	6
1	C	154/171 (90%)	141 (92%)	13 (8%)	14	8
1	D	157/171 (92%)	145 (92%)	12 (8%)	16	10
All	All	627/684 (92%)	575 (92%)	52 (8%)	14	8

All (52) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	13	LEU
1	A	49	VAL
1	A	51	ARG
1	A	56	GLN
1	A	84	ILE
1	A	93	THR
1	A	106	THR
1	A	130	GLU
1	A	132	GLU
1	A	145	VAL
1	A	147	MET
1	A	171	LEU
1	B	13	LEU
1	B	22	THR
1	B	33	LEU
1	B	50	ARG
1	B	51	ARG

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Mol	Chain	Res	Type
1	B	75	VAL
1	B	84	ILE
1	B	87	LEU
1	B	90	ASN
1	B	91	THR
1	B	96	LEU
1	B	114	GLU
1	B	116	ARG
1	B	145	VAL
1	B	157	ARG
1	C	11	SER
1	C	13	LEU
1	C	24[A]	GLN
1	C	24[B]	GLN
1	C	33	LEU
1	C	50	ARG
1	C	51	ARG
1	C	56	GLN
1	C	87	LEU
1	C	96	LEU
1	C	114	GLU
1	C	116	ARG
1	C	157	ARG
1	D	12	GLU
1	D	13	LEU
1	D	33	LEU
1	D	51	ARG
1	D	54	LYS
1	D	56	GLN
1	D	75	VAL
1	D	85	SER
1	D	106	THR
1	D	131	LYS
1	D	145	VAL
1	D	151	ASN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	90	ASN
1	B	90	ASN
1	C	119	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 ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry ⓘ

6 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$
2	A8S	A	192	-	13,19,19	2.40	5 (38%)	12,29,29	2.02	4 (33%)
4	ACY	B	192	-	1,3,3	1.25	0	0,3,3	0.00	-
3	GOL	B	3968	-	5,5,5	0.28	0	5,5,5	0.55	0
3	GOL	C	192	-	5,5,5	0.38	0	5,5,5	0.40	0
3	GOL	C	3968	-	5,5,5	0.34	0	5,5,5	0.23	0
2	A8S	D	192	-	13,19,19	2.50	6 (46%)	12,29,29	2.07	3 (25%)

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	A8S	A	192	-	-	0/8/34/34	0/1/1/1
4	ACY	B	192	-	-	0/0/0/0	0/0/0/0
3	GOL	B	3968	-	-	0/4/4/4	0/0/0/0
3	GOL	C	192	-	-	0/4/4/4	0/0/0/0

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	GOL	C	3968	-	-	0/4/4/4	0/0/0/0
2	A8S	D	192	-	-	0/8/34/34	0/1/1/1

All (11) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	192	A8S	C4-C3	-2.64	1.40	1.45
2	A	192	A8S	C9-C10	-2.20	1.40	1.45
2	A	192	A8S	C4-C3	-2.19	1.41	1.45
2	D	192	A8S	C9-C10	-2.17	1.40	1.45
2	D	192	A8S	C11-C10	2.38	1.53	1.50
2	D	192	A8S	C2-C3	3.17	1.39	1.35
2	A	192	A8S	C2-C3	3.73	1.40	1.35
2	A	192	A8S	C4-C5	4.04	1.40	1.32
2	D	192	A8S	C4-C5	4.09	1.40	1.32
2	A	192	A8S	C9-C8	5.27	1.39	1.33
2	D	192	A8S	C9-C8	5.44	1.40	1.33

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	192	A8S	C6-C3-C2	-3.94	116.44	125.17
2	A	192	A8S	C6-C3-C2	-3.71	116.95	125.17
2	D	192	A8S	C8-C9-C10	-3.20	120.46	123.87
2	A	192	A8S	O10-C10-C11	-2.92	116.83	120.80
2	A	192	A8S	C8-C9-C10	-2.40	121.31	123.87
2	D	192	A8S	C11-C10-C9	3.30	121.53	117.60
2	A	192	A8S	C11-C10-C9	3.56	121.83	117.60

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

4 monomers are involved in 11 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	192	A8S	2	0
4	B	192	ACY	5	0
3	C	192	GOL	3	0
2	D	192	A8S	1	0

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	176/193 (91%)	0.86	25 (14%) 4 4	17, 26, 38, 42	0
1	B	175/193 (90%)	0.74	20 (11%) 7 7	13, 23, 40, 50	0
1	C	174/193 (90%)	0.72	23 (13%) 4 5	14, 24, 41, 54	0
1	D	180/193 (93%)	0.86	26 (14%) 3 4	15, 23, 38, 45	0
All	All	705/772 (91%)	0.80	94 (13%) 4 5	13, 24, 39, 54	0

All (94) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	27	PRO	6.6
1	D	150	GLY	6.5
1	D	149	GLU	6.3
1	D	152	SER	6.3
1	B	2	ALA	6.2
1	A	148	PRO	6.1
1	C	2	ALA	5.5
1	A	132	GLU	5.2
1	A	147	MET	5.0
1	A	154	ASP	5.0
1	D	151	ASN	5.0
1	D	132	GLU	4.8
1	D	27	PRO	4.8
1	A	25	LEU	4.8
1	B	154	ASP	4.7
1	D	70	ASN	4.6
1	D	114	GLU	4.6
1	A	24	GLN	4.5
1	D	24	GLN	4.3
1	C	153	GLU	4.3
1	B	117	LEU	4.1

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Mol	Chain	Res	Type	RSRZ
1	A	70	ASN	4.1
1	C	88	PRO	4.1
1	D	154	ASP	4.0
1	A	28	GLY	3.9
1	C	133	ASN	3.9
1	C	71	PHE	3.9
1	D	26	ASP	3.8
1	D	25	LEU	3.8
1	C	150	GLY	3.7
1	D	1	MET	3.7
1	C	87	LEU	3.6
1	C	74	ARG	3.6
1	C	140	LEU	3.5
1	C	179	ALA	3.4
1	B	114	GLU	3.4
1	A	114	GLU	3.4
1	A	26	ASP	3.4
1	D	133	ASN	3.3
1	B	87	LEU	3.3
1	C	149	GLU	3.2
1	C	70	ASN	3.1
1	D	153	GLU	3.1
1	D	69	GLN	3.1
1	D	147	MET	3.0
1	D	28	GLY	2.9
1	A	2	ALA	2.9
1	A	134	ARG	2.9
1	B	139	VAL	2.9
1	A	135	ILE	2.9
1	C	123	VAL	2.9
1	C	134	ARG	2.9
1	B	71	PHE	2.9
1	B	116	ARG	2.9
1	A	15	ASN	2.8
1	B	72	GLU	2.7
1	B	126	VAL	2.7
1	A	69	GLN	2.7
1	B	3	SER	2.7
1	D	168	LEU	2.7
1	D	123	VAL	2.7
1	D	71	PHE	2.7
1	A	133	ASN	2.6

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Mol	Chain	Res	Type	RSRZ
1	B	140	LEU	2.6
1	C	154	ASP	2.6
1	A	18	ALA	2.5
1	A	130	GLU	2.5
1	B	88	PRO	2.5
1	A	8	GLU	2.4
1	C	124	THR	2.4
1	B	69	GLN	2.4
1	B	180	ARG	2.4
1	B	164	VAL	2.4
1	C	132	GLU	2.4
1	D	139	VAL	2.3
1	C	155	ASP	2.3
1	A	12	GLU	2.3
1	C	138	VAL	2.3
1	B	124	THR	2.3
1	C	125	THR	2.2
1	B	1	MET	2.2
1	D	124	THR	2.2
1	D	164	VAL	2.2
1	D	111	ILE	2.2
1	A	178	MET	2.1
1	C	116	ARG	2.1
1	A	164	VAL	2.1
1	B	168	LEU	2.1
1	A	120	TYR	2.1
1	D	49	VAL	2.1
1	B	133	ASN	2.1
1	C	115	HIS	2.1
1	A	124	THR	2.0
1	C	139	VAL	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	GOL	C	3968	6/6	0.56	0.38	5.39	68,69,69,69	0
4	ACY	B	192	4/4	0.34	0.70	5.29	136,136,136,136	0
2	A8S	A	192	19/19	0.93	0.26	2.60	23,26,27,27	0
2	A8S	D	192	19/19	0.92	0.25	2.17	23,25,28,30	0
3	GOL	B	3968	6/6	0.72	0.24	2.09	43,48,50,51	0
3	GOL	C	192	6/6	0.73	0.22	0.95	42,47,49,51	0

6.5 Other polymers [i](#)

There are no such residues in this entry.