Full wwPDB X-ray Structure Validation Report (i)

Jun 14, 2020 – 09:56 pm BST

PDB ID	:	3D59
Title	:	Crystal structure of human plasma platelet activating factor acetylhydrolase
Authors	:	Samanta, U.; Bahnson, B.J.
Deposited on	:	2008-05-16
Resolution	:	1.50 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 (i) symbol.

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

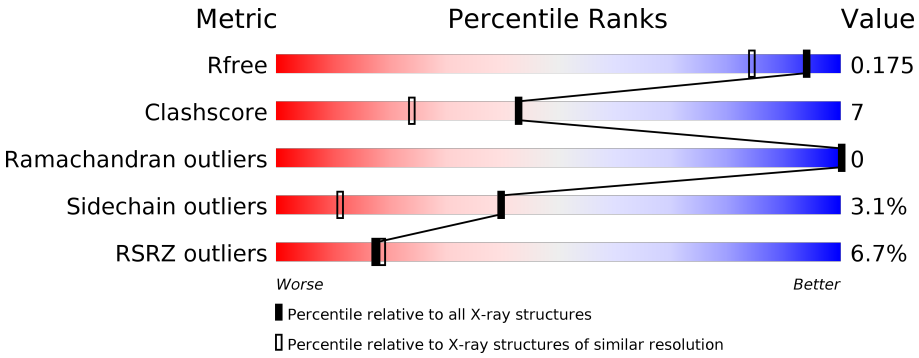
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.11
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, 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 1.50 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	2936 (1.50-1.50)
Clashscore	141614	3144 (1.50-1.50)
Ramachandran outliers	138981	3066 (1.50-1.50)
Sidechain outliers	138945	3064 (1.50-1.50)
RSRZ outliers	127900	2884 (1.50-1.50)

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	383	5% 84% 12%
1	B	383	8% 84% 13%

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
2	ACT	A	16	-	-	X	-
2	ACT	A	22	-	-	-	X
2	ACT	A	24	-	-	X	-
2	ACT	A	33	-	-	X	-
2	ACT	A	36	-	-	X	-
2	ACT	B	23	-	-	X	-
2	ACT	B	38	-	-	-	X

2 Entry composition

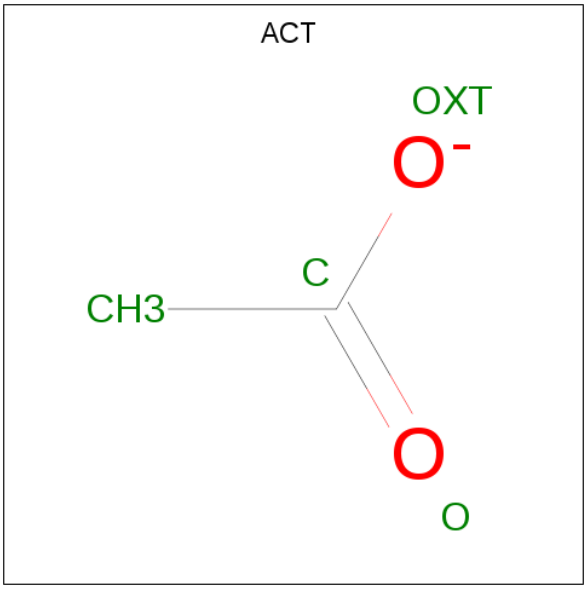
There are 4 unique types of molecules in this entry. The entry contains 6692 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Platelet-activating factor acetylhydrolase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	372	Total	C	N	O	S	0	27	0
			3065	1967	516	568	14			
1	B	374	Total	C	N	O	S	0	11	0
			2990	1913	514	550	13			

- Molecule 2 is ACETATE ION (three-letter code: ACT) (formula: $C_2H_3O_2$).



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

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

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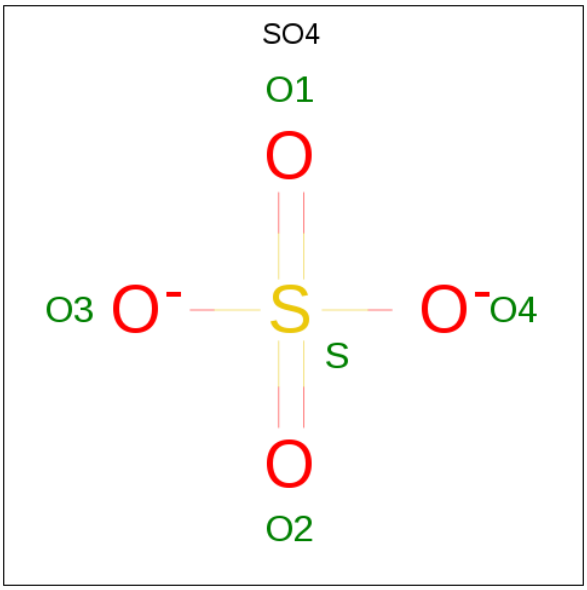
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	B	1	Total C O 4 2 2	0	0
2	B	1	Total C O 4 2 2	0	0
2	B	1	Total C O 4 2 2	0	0
2	B	1	Total C O 4 2 2	0	0

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



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	B	1	Total O S 5 4 1	0	0
3	B	1	Total O S 5 4 1	0	0

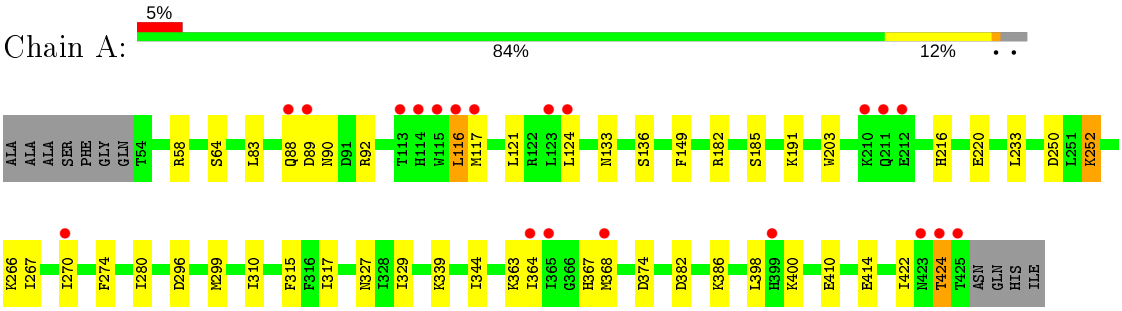
- Molecule 4 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	293	Total O 293 293	0	0
4	B	218	Total O 218 218	0	0

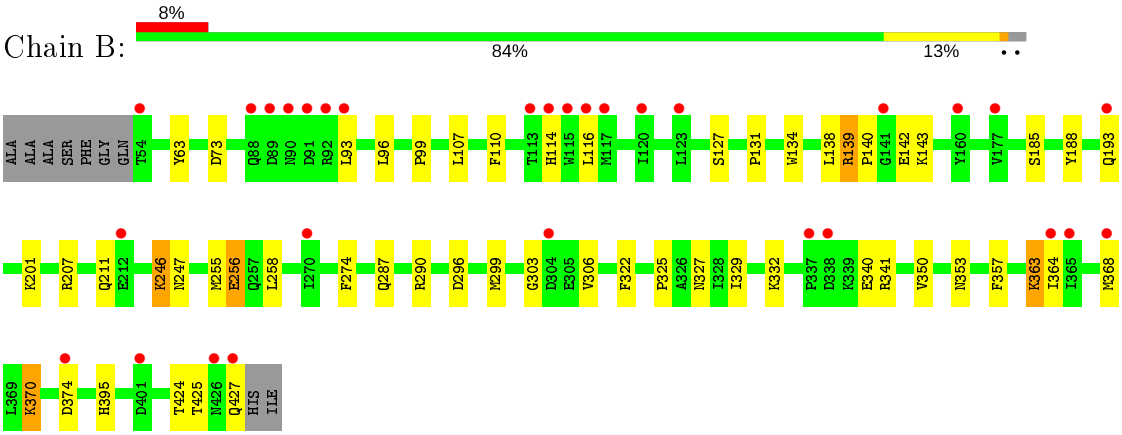
3 Residue-property plots (i)

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: Platelet-activating factor acetylhydrolase



- Molecule 1: Platelet-activating factor acetylhydrolase



4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α, β, γ	116.18Å 83.06Å 96.70Å 90.00° 115.09° 90.00°	Depositor
Resolution (Å)	10.00 – 1.50 28.78 – 1.40	Depositor EDS
% Data completeness (in resolution range)	91.5 (10.00-1.50) 79.7 (28.78-1.40)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.01 (at 1.40Å)	Xtriage
Refinement program	SHELXL-97	Depositor
R, R_{free}	0.131 , 0.191 0.133 , 0.175	Depositor DCC
R_{free} test set	6763 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å^2)	16.7	Xtriage
Anisotropy	0.271	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.41 , 74.2	EDS
L-test for twinning[2]	$< \|L\| > = 0.49$, $< L^2 > = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.98	EDS
Total number of atoms	6692	wwPDB-VP
Average B, all atoms (Å^2)	27.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.83% 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: SO4, ACT

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	0.58	0/3229	1.10	1/4364 (0.0%)
1	B	0.57	0/3086	1.07	3/4175 (0.1%)
All	All	0.58	0/6315	1.08	4/8539 (0.0%)

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	83	LEU	CA-CB-CG	5.80	128.65	115.30
1	B	341	ARG	NE-CZ-NH2	-5.53	117.54	120.30
1	B	188	TYR	CG-CD1-CE1	5.43	125.64	121.30
1	B	73	ASP	CB-CG-OD1	5.36	123.13	118.30

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

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	3065	0	3026	44	0
1	B	2990	0	2912	38	0
2	A	68	0	51	14	0
2	B	48	0	36	6	0
3	B	10	0	0	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	A	293	0	0	3	0
4	B	218	0	0	3	0
All	All	6692	0	6025	84	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 (84) 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:299:MET:H	1:B:327:ASN:HD21	1.19	0.88
1:A:203:TRP:H	2:A:16:ACT:H1	1.40	0.85
1:A:422:ILE:HG22	1:A:424:THR:HG22	1.57	0.84
1:A:299:MET:H	1:A:327:ASN:HD21	1.25	0.82
1:A:90:ASN:HD22	1:A:133:ASN:HD21	1.30	0.80
1:B:138:LEU:HD22	1:B:258:LEU:HD23	1.63	0.79
1:A:364:ILE:O	1:A:368:MET:HG3	1.83	0.78
1:B:350:VAL:H	1:B:353:ASN:HD22	1.29	0.77
1:A:116:LEU:HD13	1:A:116:LEU:H	1.51	0.76
1:B:364:ILE:O	1:B:368:MET:HG3	1.88	0.72
1:B:357:PHE:CZ	2:B:23:ACT:H2	2.26	0.70
1:B:114:HIS:CD2	1:B:116:LEU:H	2.11	0.68
1:A:317[B]:ILE:HD13	1:A:344:ILE:HD11	1.73	0.68
1:A:124:LEU:HD22	2:A:24:ACT:H3	1.77	0.67
1:B:107:LEU:HD22	2:B:23:ACT:H1	1.77	0.67
1:B:299:MET:H	1:B:327:ASN:ND2	1.95	0.63
1:B:114:HIS:HD2	1:B:116:LEU:H	1.47	0.63
1:B:350:VAL:H	1:B:353:ASN:ND2	1.96	0.62
1:A:58:ARG:H	2:A:33:ACT:H3	1.64	0.62
1:A:203:TRP:H	2:A:16:ACT:CH3	2.13	0.61
1:A:299:MET:H	1:A:327:ASN:ND2	1.99	0.59
1:A:266:LYS:HD3	1:A:398:LEU:HD23	1.85	0.58
1:A:182:ARG:HH12	2:A:36:ACT:H3	1.69	0.58
1:A:382[B]:ASP:OD1	1:A:386:LYS:HE3	2.04	0.57
1:B:134:TRP:HE1	2:B:13:ACT:C	2.18	0.56
1:B:207:ARG:HD2	3:B:1:SO4:O4	2.05	0.56
1:A:58:ARG:H	2:A:33:ACT:CH3	2.17	0.56
1:A:266:LYS:HD3	1:A:398:LEU:CD2	2.40	0.52
1:A:116:LEU:HD22	1:A:117:MET:H	1.75	0.52
1:A:315:PHE:CE2	1:A:317[B]:ILE:HD11	2.45	0.52
1:B:424:THR:HG22	4:B:542:HOH:O	2.10	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:414[A]:GLU:HG2	4:A:583:HOH:O	2.09	0.51
1:B:142:GLU:HG2	1:B:143:LYS:N	2.24	0.51
1:B:107:LEU:HD13	2:B:23:ACT:CH3	2.40	0.51
1:B:363[A]:LYS:HG2	1:B:364:ILE:N	2.26	0.51
1:A:89[B]:ASP:OD1	1:A:136:SER:OG	2.30	0.50
2:A:11:ACT:OXT	2:A:15:ACT:O	2.29	0.50
1:A:367:HIS:HE1	1:A:374:ASP:OD1	1.94	0.50
1:A:191:LYS:HZ1	2:A:28:ACT:C	2.24	0.49
1:A:203:TRP:HB2	2:A:16:ACT:H1	1.95	0.49
1:A:116:LEU:CD1	1:A:116:LEU:H	2.22	0.48
1:B:340:GLU:HG2	1:B:395:HIS:CE1	2.48	0.48
1:A:252:LYS:HD3	1:A:252:LYS:HA	1.49	0.47
1:B:139:ARG:HG2	1:B:139:ARG:NH1	2.30	0.47
1:A:400:LYS:HE2	4:A:626:HOH:O	2.15	0.47
1:B:63:TYR:HE1	1:B:139:ARG:HE	1.61	0.47
1:A:317[B]:ILE:HD13	1:A:344:ILE:CD1	2.44	0.47
1:B:332:LYS:HD3	1:B:332:LYS:HA	1.60	0.47
1:A:90:ASN:ND2	1:A:133:ASN:HD21	2.08	0.46
1:B:424:THR:HA	4:B:542:HOH:O	2.15	0.46
1:A:88:GLN:HG3	1:A:89[A]:ASP:OD2	2.15	0.46
1:B:93:LEU:HB3	1:B:131:PRO:HA	1.96	0.46
1:B:322:PHE:HD1	2:B:14:ACT:H3	1.81	0.46
1:A:410:GLU:O	2:A:39:ACT:OXT	2.32	0.46
1:A:149:PHE:HA	1:A:270:ILE:O	2.16	0.46
2:A:19:ACT:H2	4:A:662:HOH:O	2.16	0.46
1:B:139:ARG:NH1	1:B:140:PRO:O	2.48	0.46
1:B:139:ARG:NH2	1:B:142:GLU:OE1	2.49	0.45
1:A:280:ILE:HG23	1:A:310:ILE:HD11	1.98	0.45
1:B:287:GLN:NE2	1:B:290[B]:ARG:NH1	2.64	0.45
1:A:203:TRP:N	2:A:16:ACT:H1	2.20	0.45
1:A:64:SER:OG	1:A:90:ASN:HB2	2.17	0.45
1:A:233:LEU:HD11	1:A:267[A]:ILE:HD13	1.98	0.45
1:A:124:LEU:HD22	2:A:24:ACT:CH3	2.45	0.44
1:A:182:ARG:HH12	2:A:36:ACT:CH3	2.29	0.43
1:B:325:PRO:O	1:B:329:ILE:HG13	2.19	0.43
1:A:364:ILE:N	1:A:364:ILE:HD12	2.33	0.43
1:A:310:ILE:O	1:A:339[B]:LYS:NZ	2.50	0.43
1:B:96:LEU:HD23	1:B:99:PRO:HA	2.01	0.42
1:B:201:LYS:NZ	4:B:640:HOH:O	2.53	0.42
1:B:246:LYS:HD3	1:B:247:ASN:O	2.19	0.42
1:B:303:GLY:O	1:B:306:VAL:HG12	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:287:GLN:NE2	1:B:290[B]:ARG:HH12	2.18	0.42
1:B:255:MET:CE	1:B:258:LEU:HD12	2.50	0.42
1:A:117:MET:O	1:A:121:LEU:HG	2.21	0.41
1:A:116:LEU:CD2	1:A:117:MET:H	2.33	0.41
1:B:110:PHE:O	2:B:34:ACT:OXT	2.38	0.41
1:B:425:THR:HG23	1:B:427:GLN:H	1.84	0.41
1:A:216:HIS:NE2	1:A:220[B]:GLU:OE2	2.54	0.41
1:A:329:ILE:HA	1:A:329:ILE:HD12	1.91	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	394/383 (103%)	384 (98%)	10 (2%)	0	100	100
1	B	378/383 (99%)	368 (97%)	10 (3%)	0	100	100
All	All	772/766 (101%)	752 (97%)	20 (3%)	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	344/329 (105%)	335 (97%)	9 (3%)	46	16

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	B	321/329 (98%)	308 (96%)	13 (4%)	31 6
All	All	665/658 (101%)	643 (97%)	22 (3%)	40 10

All (22) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	92	ARG
1	A	116	LEU
1	A	185[A]	SER
1	A	185[B]	SER
1	A	252	LYS
1	A	274	PHE
1	A	296	ASP
1	A	363	LYS
1	A	424	THR
1	B	127	SER
1	B	139	ARG
1	B	185[A]	SER
1	B	185[B]	SER
1	B	193	GLN
1	B	211	GLN
1	B	246	LYS
1	B	256[A]	GLU
1	B	274	PHE
1	B	296	ASP
1	B	363[A]	LYS
1	B	370	LYS
1	B	374	ASP

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (12) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	90	ASN
1	A	100	ASN
1	A	119	ASN
1	A	135	ASN
1	A	241	HIS
1	A	327	ASN
1	A	367	HIS
1	A	415	ASN
1	B	60	ASN

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Mol	Chain	Res	Type
1	B	114	HIS
1	B	327	ASN
1	B	353	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

31 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	ACT	A	15	-	1,3,3	1.35	0	0,3,3	0.00	-
2	ACT	A	33	-	1,3,3	1.13	0	0,3,3	0.00	-
3	SO4	B	2	-	4,4,4	0.86	0	6,6,6	1.44	1 (16%)
2	ACT	A	28	-	1,3,3	1.78	0	0,3,3	0.00	-
2	ACT	B	18	-	1,3,3	1.54	0	0,3,3	0.00	-
2	ACT	A	25	-	1,3,3	1.58	0	0,3,3	0.00	-
2	ACT	B	37	-	1,3,3	1.66	0	0,3,3	0.00	-
2	ACT	B	26	-	1,3,3	1.26	0	0,3,3	0.00	-
2	ACT	A	24	-	1,3,3	2.13	1 (100%)	0,3,3	0.00	-
2	ACT	B	34	-	1,3,3	1.60	0	0,3,3	0.00	-

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\|>2$	Counts	RMSZ	$\#\|Z\|>2$
2	ACT	A	19	-	1,3,3	1.68	0	0,3,3	0.00	-
2	ACT	B	38	-	1,3,3	2.26	1 (100%)	0,3,3	0.00	-
2	ACT	B	23	-	1,3,3	1.92	0	0,3,3	0.00	-
2	ACT	A	36	-	1,3,3	1.42	0	0,3,3	0.00	-
2	ACT	A	22	-	1,3,3	2.17	1 (100%)	0,3,3	0.00	-
2	ACT	B	21	-	1,3,3	2.13	1 (100%)	0,3,3	0.00	-
2	ACT	A	32	-	1,3,3	1.54	0	0,3,3	0.00	-
2	ACT	A	30	-	1,3,3	1.91	0	0,3,3	0.00	-
2	ACT	A	20	-	1,3,3	1.55	0	0,3,3	0.00	-
2	ACT	B	17	-	1,3,3	1.50	0	0,3,3	0.00	-
2	ACT	A	12	-	1,3,3	1.75	0	0,3,3	0.00	-
2	ACT	A	35	-	1,3,3	0.91	0	0,3,3	0.00	-
2	ACT	B	13	-	1,3,3	2.64	1 (100%)	0,3,3	0.00	-
2	ACT	A	11	-	1,3,3	1.79	0	0,3,3	0.00	-
3	SO4	B	1	-	4,4,4	1.10	0	6,6,6	1.78	1 (16%)
2	ACT	B	27	-	1,3,3	1.23	0	0,3,3	0.00	-
2	ACT	A	39	-	1,3,3	2.32	1 (100%)	0,3,3	0.00	-
2	ACT	A	29	-	1,3,3	1.90	0	0,3,3	0.00	-
2	ACT	B	31	-	1,3,3	1.58	0	0,3,3	0.00	-
2	ACT	A	16	-	1,3,3	1.13	0	0,3,3	0.00	-
2	ACT	B	14	-	1,3,3	0.67	0	0,3,3	0.00	-

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	13	ACT	CH3-C	2.64	1.52	1.48
2	A	39	ACT	CH3-C	2.32	1.51	1.48
2	B	38	ACT	CH3-C	2.26	1.51	1.48
2	A	22	ACT	CH3-C	2.17	1.51	1.48
2	B	21	ACT	CH3-C	2.13	1.51	1.48
2	A	24	ACT	CH3-C	2.13	1.51	1.48

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	B	1	SO4	O4-S-O3	4.10	126.56	109.06
3	B	2	SO4	O4-S-O3	3.23	122.85	109.06

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

14 monomers are involved in 21 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	15	ACT	1	0
2	A	33	ACT	2	0
2	A	28	ACT	1	0
2	A	24	ACT	2	0
2	B	34	ACT	1	0
2	A	19	ACT	1	0
2	B	23	ACT	3	0
2	A	36	ACT	2	0
2	B	13	ACT	1	0
2	A	11	ACT	1	0
3	B	1	SO4	1	0
2	A	39	ACT	1	0
2	A	16	ACT	4	0
2	B	14	ACT	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, 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	372/383 (97%)	0.06	20 (5%)	25	28	12, 20, 44, 84	3 (0%)
1	B	374/383 (97%)	0.21	30 (8%)	12	13	13, 25, 52, 80	5 (1%)
All	All	746/766 (97%)	0.14	50 (6%)	17	19	12, 22, 50, 84	8 (1%)

All (50) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	91	ASP	11.0
1	B	90	ASN	9.3
1	A	116	LEU	8.7
1	B	92	ARG	8.1
1	B	54	THR	8.0
1	A	425	THR	7.8
1	B	116	LEU	7.1
1	A	115	TRP	6.7
1	B	88	GLN	6.5
1	B	114	HIS	6.5
1	A	114	HIS	6.5
1	B	89	ASP	6.5
1	B	115	TRP	6.4
1	B	93	LEU	5.9
1	A	423	ASN	4.5
1	B	141	GLY	4.5
1	B	364	ILE	4.3
1	B	117	MET	4.1
1	A	113	THR	4.0
1	A	123	LEU	4.0
1	A	364	ILE	3.9
1	B	337	PRO	3.7
1	B	113	THR	3.6
1	B	123	LEU	3.5

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Mol	Chain	Res	Type	RSRZ
1	A	424	THR	3.5
1	B	427	GLN	3.4
1	B	120	ILE	3.3
1	B	365	ILE	3.2
1	B	212	GLU	3.1
1	B	368	MET	3.0
1	B	193	GLN	2.9
1	A	210	LYS	2.8
1	A	124	LEU	2.7
1	A	117	MET	2.6
1	A	211	GLN	2.6
1	B	426	ASN	2.4
1	B	338	ASP	2.3
1	A	88	GLN	2.3
1	A	365	ILE	2.3
1	A	399	HIS	2.2
1	B	160	TYR	2.2
1	A	89[A]	ASP	2.2
1	B	177[A]	VAL	2.2
1	B	374	ASP	2.1
1	A	212	GLU	2.1
1	A	368	MET	2.1
1	B	304[A]	ASP	2.1
1	B	401	ASP	2.1
1	A	270	ILE	2.0
1	B	270	ILE	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
2	ACT	B	38	4/4	0.44	0.43	93,101,102,106	0
2	ACT	A	22	4/4	0.46	0.46	77,91,93,95	0
2	ACT	B	23	4/4	0.64	0.40	105,113,117,121	0
2	ACT	B	34	4/4	0.68	0.20	48,67,74,76	0
2	ACT	A	39	4/4	0.68	0.32	44,51,58,61	0
2	ACT	A	32	4/4	0.73	0.21	63,64,65,66	0
2	ACT	A	19	4/4	0.74	0.23	66,72,86,86	0
2	ACT	B	37	4/4	0.74	0.27	67,68,77,81	0
2	ACT	B	31	4/4	0.74	0.35	76,77,80,85	0
2	ACT	A	28	4/4	0.75	0.25	51,70,85,102	0
2	ACT	A	30	4/4	0.75	0.39	78,80,81,86	0
2	ACT	A	33	4/4	0.76	0.20	41,53,58,89	0
2	ACT	A	35	4/4	0.77	0.35	49,66,76,78	0
2	ACT	B	13	4/4	0.78	0.24	62,72,74,78	0
2	ACT	A	20	4/4	0.79	0.26	50,52,59,65	0
2	ACT	A	36	4/4	0.80	0.18	59,66,67,70	0
2	ACT	A	29	4/4	0.83	0.30	40,41,47,49	0
2	ACT	A	24	4/4	0.83	0.24	79,104,105,113	0
2	ACT	A	16	4/4	0.84	0.23	46,60,71,72	0
2	ACT	B	17	4/4	0.86	0.16	57,61,63,63	0
2	ACT	B	27	4/4	0.89	0.25	51,59,62,69	0
2	ACT	B	21	4/4	0.90	0.14	35,42,42,55	0
2	ACT	B	26	4/4	0.91	0.13	49,53,59,61	0
2	ACT	B	18	4/4	0.92	0.14	39,39,43,44	0
2	ACT	A	12	4/4	0.93	0.16	48,53,59,62	0
2	ACT	A	25	4/4	0.93	0.09	32,40,43,45	0
3	SO4	B	2	5/5	0.94	0.14	46,47,51,55	0
2	ACT	A	15	4/4	0.94	0.23	57,57,63,77	0
3	SO4	B	1	5/5	0.95	0.11	58,66,79,86	0
2	ACT	A	11	4/4	0.95	0.17	43,54,55,56	0
2	ACT	B	14	4/4	0.95	0.13	29,36,36,47	0

6.5 Other polymers

There are no such residues in this entry.