



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 14, 2017 – 10:00 am GMT

PDB ID : 2ZYH
Title : mutant A. Fulgidus lipase S136A complexed with fatty acid fragment
Authors : Chen, C.K.; Ko, T.P.; Guo, R.T.; Wang, A.H.
Deposited on : 2009-01-22
Resolution : 1.83 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 : 1.7.2 (RC1), CSD as538be (2017)
Xtriage (Phenix) : 1.9-1692
EDS : trunk28620
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)
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) : recalc28949

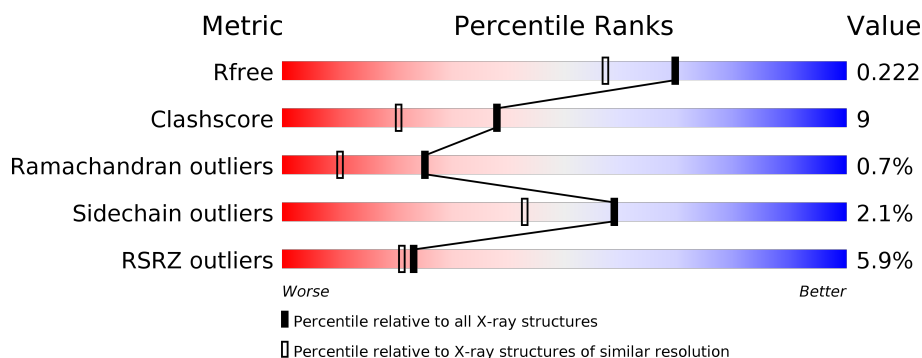
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.83 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}	100719	2964 (1.86-1.82)
Clashscore	112137	3197 (1.86-1.82)
Ramachandran outliers	110173	3164 (1.86-1.82)
Sidechain outliers	110143	3165 (1.86-1.82)
RSRZ outliers	101464	2973 (1.86-1.82)

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	475	<div> <div>8%</div> <div> <div></div> <div>83%</div> <div>11%</div> <div>• •</div> </div> </div>
1	B	475	<div> <div>3%</div> <div> <div></div> <div>83%</div> <div>12%</div> <div>• •</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 criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	R16	A	500	-	-	-	X
2	R16	B	500	-	-	-	X

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 8462 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.

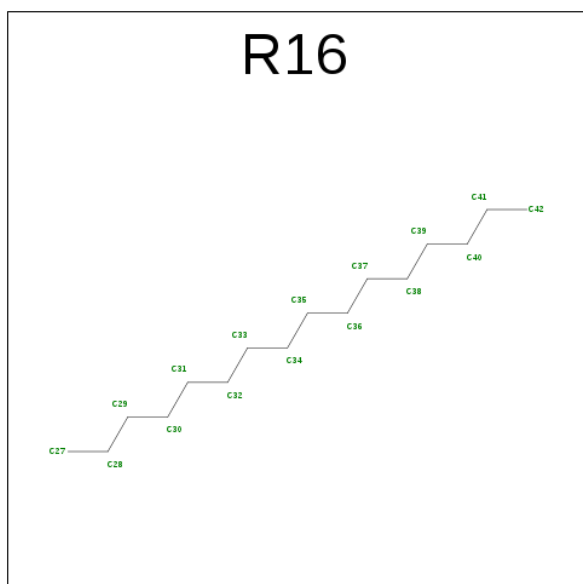
- Molecule 1 is a protein called Lipase, putative.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	456	Total	C	N	O	S	0	0	0
			3601	2320	595	674	12			
1	B	456	Total	C	N	O	S	0	0	0
			3601	2320	595	674	12			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	136	ALA	SER	ENGINEERED	UNP O28511
A	475	VAL	-	EXPRESSION TAG	UNP O28511
B	136	ALA	SER	ENGINEERED	UNP O28511
B	475	VAL	-	EXPRESSION TAG	UNP O28511

- Molecule 2 is HEXADECANE (three-letter code: R16) (formula: $C_{16}H_{34}$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total C 16 16	0	0
2	B	1	Total C 16 16	0	0

- Molecule 3 is CALCIUM ION (three-letter code: CA) (formula: Ca).

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

- Molecule 4 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	579	Total O 579 579	0	0
4	B	647	Total O 647 647	0	0

4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	91.20Å 107.87Å 118.90Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	30.00 – 1.83 29.91 – 1.82	Depositor EDS
% Data completeness (in resolution range)	95.2 (30.00-1.83) 94.9 (29.91-1.82)	Depositor EDS
R_{merge}	0.05	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	5.70 (at 1.83Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.187 , 0.223 0.187 , 0.222	Depositor DCC
R_{free} test set	4979 reflections (5.04%)	DCC
Wilson B-factor (Å ²)	20.3	Xtriage
Anisotropy	0.546	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 62.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	8462	wwPDB-VP
Average B, all atoms (Å ²)	28.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 16.80% 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, 0.333 respectively for untwinned datasets, and 0.375, 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: R16, CA

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	0.93	1/3688 (0.0%)	0.82	1/5007 (0.0%)
1	B	0.97	0/3688	0.84	3/5007 (0.1%)
All	All	0.95	1/7376 (0.0%)	0.83	4/10014 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	458	ALA	CA-CB	5.62	1.64	1.52

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	213	LEU	CA-CB-CG	7.66	132.92	115.30
1	A	357	LEU	CA-CB-CG	6.19	129.53	115.30
1	B	285	ARG	NE-CZ-NH1	-5.10	117.75	120.30
1	B	328	ARG	NE-CZ-NH1	5.02	122.81	120.30

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	3601	0	3554	74	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	B	3601	0	3554	56	1
2	A	16	0	34	0	0
2	B	16	0	34	1	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
4	A	579	0	0	16	0
4	B	647	0	0	11	1
All	All	8462	0	7176	125	1

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 9.

All (125) 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:A:218:GLU:HG2	1:B:191:LEU:HD13	1.34	1.09
1:A:81:GLU:HA	4:A:530:HOH:O	1.54	1.06
1:A:186:LEU:HD21	1:A:397:ALA:HB2	1.51	0.93
4:A:684:HOH:O	1:B:191:LEU:HD12	1.71	0.89
1:A:185:ALA:O	1:A:186:LEU:HD23	1.77	0.84
1:A:218:GLU:CG	1:B:191:LEU:HD13	2.10	0.82
1:A:94:THR:HA	1:A:97:LYS:HE2	1.62	0.81
1:B:395:GLU:HG2	4:B:1001:HOH:O	1.82	0.80
1:B:286:VAL:HG21	1:B:304:PHE:HE1	1.51	0.75
1:A:191:LEU:HB3	1:A:194:GLU:OE1	1.89	0.72
1:A:82:PHE:HB2	4:A:515:HOH:O	1.89	0.72
1:A:186:LEU:HD22	4:A:1176:HOH:O	1.88	0.72
1:B:191:LEU:HB2	1:B:192:PRO:HD3	1.70	0.71
1:B:186:LEU:O	1:B:372:GLU:HG3	1.90	0.71
1:B:189:LEU:HD23	1:B:189:LEU:H	1.56	0.70
1:A:186:LEU:CD2	1:A:397:ALA:HB2	2.22	0.70
1:A:475:VAL:CG2	4:A:910:HOH:O	2.41	0.68
1:B:184:LYS:HA	1:B:184:LYS:HE3	1.73	0.68
1:A:186:LEU:HB3	1:A:187:PRO:CD	2.23	0.68
1:A:83:GLY:HA2	1:A:86:ILE:HD11	1.76	0.67
1:B:191:LEU:HB2	1:B:192:PRO:CD	2.25	0.66
1:B:282:LYS:HG3	1:B:292:VAL:HG21	1.78	0.65
1:A:183:PRO:O	1:A:188:ALA:HB2	1.96	0.64
1:B:20:GLU:HB3	4:B:1141:HOH:O	1.96	0.64
1:A:218:GLU:HG2	1:B:191:LEU:CD1	2.21	0.64
1:A:74:LEU:HD11	1:A:82:PHE:HD2	1.63	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:295:ARG:HG2	1:B:295:ARG:NH1	2.13	0.64
1:A:82:PHE:CZ	1:A:86:ILE:HG12	2.33	0.64
1:B:295:ARG:HG2	1:B:295:ARG:HH11	1.63	0.63
1:A:285:ARG:HE	1:A:287:LYS:HZ1	1.46	0.62
1:A:83:GLY:HA2	1:A:86:ILE:CD1	2.29	0.62
1:A:67:LEU:HD21	1:A:86:ILE:HD13	1.80	0.62
1:B:396:ARG:NE	4:B:1165:HOH:O	2.32	0.62
1:B:275:ARG:HH22	1:B:303:GLN:NE2	1.98	0.61
1:B:424:MET:HE3	1:B:425:PRO:HD2	1.82	0.60
1:A:285:ARG:HE	1:A:287:LYS:NZ	1.99	0.60
1:B:34:SER:H	1:B:37:GLN:HE22	1.50	0.59
1:A:20:GLU:OE1	1:A:20:GLU:HA	2.03	0.58
1:A:278:ARG:NH1	4:A:1047:HOH:O	2.35	0.58
1:B:184:LYS:HB2	4:B:999:HOH:O	2.03	0.58
1:A:194:GLU:HB3	1:B:225:GLU:OE1	2.03	0.58
1:B:89:ILE:HG23	1:B:336:LEU:HD13	1.84	0.58
1:A:475:VAL:HG23	4:A:910:HOH:O	2.03	0.58
1:A:89:ILE:HG21	1:A:336:LEU:HD13	1.86	0.57
1:B:295:ARG:NH1	4:B:808:HOH:O	2.38	0.57
1:A:475:VAL:HG21	4:A:910:HOH:O	2.01	0.56
1:B:286:VAL:CG2	1:B:304:PHE:HE1	2.17	0.56
1:A:74:LEU:HD11	1:A:82:PHE:CD2	2.41	0.55
1:A:20:GLU:HG3	4:A:481:HOH:O	2.05	0.55
1:B:295:ARG:HH11	1:B:295:ARG:CG	2.21	0.53
1:B:463:ARG:HG2	1:B:463:ARG:NH1	2.24	0.53
1:B:81:GLU:HB3	1:B:84:LEU:HD12	1.90	0.53
1:A:34:SER:H	1:A:37:GLN:HE22	1.57	0.53
1:A:73:MET:HA	1:A:78:LEU:HB2	1.90	0.53
1:A:275:ARG:HH22	1:A:303:GLN:NE2	2.06	0.52
1:A:186:LEU:HB3	1:A:187:PRO:HD3	1.90	0.52
1:B:225:GLU:HG2	4:B:914:HOH:O	2.09	0.52
1:A:72:ASP:O	1:A:76:SER:HB3	2.10	0.51
1:A:82:PHE:CE1	1:A:86:ILE:HG12	2.46	0.51
1:B:240:GLN:NE2	1:B:323:ASP:H	2.09	0.50
1:A:189:LEU:HD21	4:A:673:HOH:O	2.11	0.50
1:A:186:LEU:HD21	1:A:397:ALA:CB	2.34	0.49
1:A:423:ILE:O	1:A:423:ILE:HG22	2.11	0.49
1:A:76:SER:HB2	4:A:923:HOH:O	2.12	0.48
1:A:77:GLY:C	1:A:79:GLY:N	2.62	0.48
1:A:191:LEU:HB3	1:A:194:GLU:CD	2.34	0.48
1:B:146:VAL:HG11	1:B:174:ILE:HD12	1.96	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:423:ILE:O	1:A:423:ILE:CG2	2.61	0.48
1:B:246:LYS:HE3	1:B:291:GLU:OE2	2.12	0.48
1:B:240:GLN:HG3	1:B:322:ARG:HA	1.96	0.48
1:B:89:ILE:HG22	1:B:90:ILE:HG13	1.95	0.48
1:B:105:ARG:HE	1:B:105:ARG:HB2	1.45	0.47
1:A:77:GLY:O	1:A:78:LEU:C	2.51	0.47
1:A:85:ASN:CG	1:A:423:ILE:HG23	2.35	0.47
1:A:75:PHE:CZ	1:A:86:ILE:HD12	2.49	0.47
1:B:424:MET:CE	1:B:425:PRO:HD2	2.45	0.47
1:A:191:LEU:HD13	1:A:194:GLU:OE2	2.15	0.46
1:A:194:GLU:O	1:A:194:GLU:CD	2.53	0.46
1:A:198:TYR:O	1:A:199:ASN:HB2	2.16	0.46
1:A:85:ASN:HB3	1:A:423:ILE:HG23	1.98	0.46
1:B:153:ALA:HB1	1:B:174:ILE:HD11	1.97	0.46
1:B:338:VAL:CG1	1:B:424:MET:HE1	2.46	0.46
1:B:53:GLU:HG2	4:B:539:HOH:O	2.16	0.46
1:A:73:MET:HG2	1:A:79:GLY:HA3	1.97	0.46
1:B:292:VAL:HG22	1:B:293:ARG:N	2.31	0.46
1:A:231:LYS:HG2	4:A:1091:HOH:O	2.15	0.46
1:A:85:ASN:OD1	1:A:423:ILE:HG23	2.16	0.46
1:A:191:LEU:HD22	1:A:194:GLU:OE2	2.16	0.45
1:A:186:LEU:O	1:A:188:ALA:N	2.49	0.45
1:A:411:LYS:NZ	4:A:1178:HOH:O	2.49	0.45
1:A:182:ASN:O	1:A:185:ALA:HB2	2.17	0.45
1:A:186:LEU:CB	1:A:187:PRO:CD	2.93	0.45
1:B:150:PRO:HD2	1:B:151:GLU:OE1	2.16	0.45
1:B:342:ILE:HD12	1:B:342:ILE:C	2.37	0.45
1:B:120:GLU:HG2	4:B:540:HOH:O	2.16	0.44
1:A:192:PRO:O	1:A:193:GLU:HB3	2.17	0.44
1:A:189:LEU:N	1:A:189:LEU:HD23	2.32	0.44
1:A:371:GLU:O	1:A:374:GLY:N	2.50	0.44
1:B:389:GLU:HG2	4:B:1169:HOH:O	2.16	0.44
1:A:182:ASN:O	1:A:185:ALA:CB	2.65	0.44
1:B:396:ARG:NH2	1:B:417:GLU:OE1	2.52	0.43
1:B:231:LYS:HE3	4:B:1003:HOH:O	2.19	0.43
1:A:182:ASN:OD1	1:A:184:LYS:HB2	2.19	0.42
1:A:342:ILE:HG23	1:A:342:ILE:O	2.18	0.42
1:A:370:ASP:HB2	1:A:394:ILE:HD11	2.01	0.42
1:B:286:VAL:HG21	1:B:304:PHE:CE1	2.41	0.42
1:B:338:VAL:HG12	1:B:424:MET:HE1	2.02	0.42
1:A:462:ASP:N	1:A:462:ASP:OD1	2.51	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:218:GLU:OE2	1:B:191:LEU:HD22	2.18	0.42
1:A:246:LYS:NZ	4:A:1112:HOH:O	2.53	0.42
1:A:76:SER:O	1:A:78:LEU:N	2.47	0.42
1:A:77:GLY:O	1:A:79:GLY:N	2.53	0.41
1:B:151:GLU:H	1:B:151:GLU:CD	2.23	0.41
1:A:406:ARG:HH22	1:A:416:ARG:HB2	1.86	0.41
1:A:82:PHE:O	1:A:86:ILE:HG13	2.20	0.41
1:B:343:LEU:O	1:B:344:PRO:C	2.58	0.41
1:A:473:TYR:HB2	4:A:541:HOH:O	2.19	0.41
1:B:91:ASP:OD2	1:B:94:THR:OG1	2.35	0.41
1:B:20:GLU:N	4:B:951:HOH:O	2.54	0.41
1:A:186:LEU:HB3	4:A:1176:HOH:O	2.21	0.40
1:B:191:LEU:CB	1:B:192:PRO:CD	2.97	0.40
1:B:39:GLU:OE2	1:B:324:ASP:OD2	2.39	0.40
1:B:358:LEU:HD21	2:B:500:R16:H331	2.02	0.40
1:A:105:ARG:HG2	1:A:109:GLU:OE2	2.20	0.40
1:B:250:LYS:HE3	1:B:252:LEU:HD13	2.03	0.40

All (1) 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)
1:B:194:GLU:OE1	4:B:814:HOH:O[4_566]	2.17	0.03

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	454/475 (96%)	431 (95%)	18 (4%)	5 (1%)	17	5
1	B	454/475 (96%)	443 (98%)	10 (2%)	1 (0%)	51	34
All	All	908/950 (96%)	874 (96%)	28 (3%)	6 (1%)	25	10

All (6) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	77	GLY
1	A	185	ALA
1	A	186	LEU
1	A	192	PRO
1	B	363	LYS
1	A	187	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	387/400 (97%)	376 (97%)	11 (3%)	49	30
1	B	387/400 (97%)	382 (99%)	5 (1%)	73	63
All	All	774/800 (97%)	758 (98%)	16 (2%)	59	43

All (16) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	20	GLU
1	A	72	ASP
1	A	189	LEU
1	A	194	GLU
1	A	252	LEU
1	A	285	ARG
1	A	342	ILE
1	A	353	GLU
1	A	357	LEU
1	A	389	GLU
1	A	417	GLU
1	B	184	LYS
1	B	189	LEU
1	B	213	LEU
1	B	295	ARG
1	B	423	ILE

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (14) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	37	GLN
1	A	48	ASN
1	A	206	ASN
1	A	240	GLN
1	A	303	GLN
1	A	399	ASN
1	A	469	GLN
1	B	37	GLN
1	B	48	ASN
1	B	199	ASN
1	B	240	GLN
1	B	303	GLN
1	B	399	ASN
1	B	469	GLN

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](#)

Of 4 ligands modelled in this entry, 2 are monoatomic - leaving 2 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	R16	A	500	-	15,15,15	0.34	0	14,14,14	0.50	0
2	R16	B	500	-	15,15,15	0.35	0	14,14,14	0.45	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	R16	A	500	-	-	0/13/13/13	0/0/0/0
2	R16	B	500	-	-	0/13/13/13	0/0/0/0

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

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
2	B	500	R16	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	456/475 (96%)	0.22	39 (8%) 11 10	14, 23, 67, 79	0
1	B	456/475 (96%)	-0.08	15 (3%) 47 44	13, 22, 39, 77	0
All	All	912/950 (96%)	0.07	54 (5%) 23 21	13, 22, 50, 79	0

All (54) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	188	ALA	14.9
1	B	189	LEU	11.2
1	A	191	LEU	8.4
1	A	186	LEU	7.7
1	A	192	PRO	7.5
1	B	188	ALA	7.5
1	A	80	SER	7.2
1	A	78	LEU	7.0
1	A	189	LEU	5.7
1	B	187	PRO	5.5
1	A	374	GLY	5.3
1	B	191	LEU	5.1
1	A	79	GLY	5.0
1	A	371	GLU	4.7
1	A	187	PRO	4.7
1	A	87	SER	4.6
1	A	86	ILE	4.5
1	B	190	GLY	4.1
1	A	183	PRO	4.0
1	A	77	GLY	3.8
1	A	93	GLU	3.8
1	B	192	PRO	3.7
1	A	190	GLY	3.7
1	B	371	GLU	3.6

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Mol	Chain	Res	Type	RSRZ
1	A	185	ALA	3.5
1	A	194	GLU	3.5
1	A	423	ILE	3.4
1	B	194	GLU	3.2
1	A	88	GLN	3.2
1	A	193	GLU	3.1
1	B	374	GLY	3.0
1	A	20	GLU	2.9
1	A	92	PRO	2.8
1	B	372	GLU	2.8
1	A	475	VAL	2.8
1	B	186	LEU	2.7
1	A	82	PHE	2.6
1	A	91	ASP	2.6
1	B	422	SER	2.4
1	A	308	PHE	2.4
1	A	81	GLU	2.3
1	A	85	ASN	2.3
1	A	21	ASP	2.2
1	A	100	SER	2.2
1	B	349	PRO	2.2
1	A	419	VAL	2.2
1	B	185	ALA	2.2
1	B	475	VAL	2.2
1	A	422	SER	2.1
1	A	349	PRO	2.1
1	A	104	GLU	2.1
1	A	151	GLU	2.1
1	A	96	ASP	2.0
1	A	352	LYS	2.0

6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates ⓘ

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
2	R16	A	500	16/16	0.91	0.25	5.62	35,37,38,39	0
2	R16	B	500	16/16	0.88	0.22	5.42	23,33,36,36	0
3	CA	B	700	1/1	1.00	0.04	-1.80	17,17,17,17	0
3	CA	A	700	1/1	0.99	0.05	-2.35	20,20,20,20	0

6.5 Other polymers [i](#)

There are no such residues in this entry.