Full wwPDB X-ray Structure Validation Report (i)

Jun 12, 2024 – 07:50 PM EDT

PDB ID	:	1JFR
Title	:	CRYSTAL STRUCTURE OF THE STREPTOMYCES EXFOLIATUS LIPASE AT 1.9A RESOLUTION: A MODEL FOR A FAMILY OF PLATELET-ACTIVATING FACTOR ACETYLHYDROLASES
Authors	:	Wei, Y.; Derewenda, Z.S.
Deposited on	:	1997-07-11
Resolution	:	1.90 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 types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

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

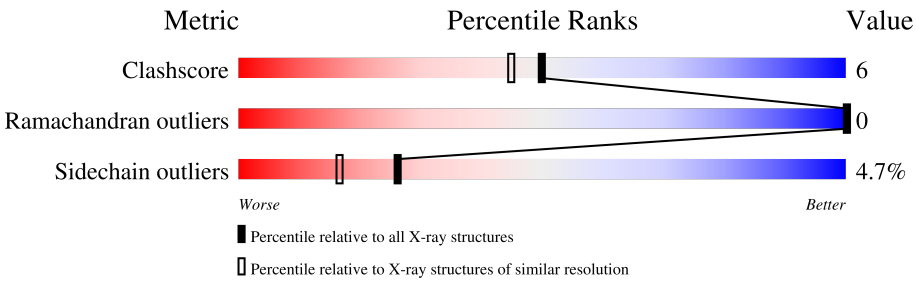
MolProbity	:	4.02b-467
Xtriage (Phenix)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36.2

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 1.90 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))
Clashscore	141614	6847 (1.90-1.90)
Ramachandran outliers	138981	6760 (1.90-1.90)
Sidechain outliers	138945	6760 (1.90-1.90)

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 of 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%

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	262	85% 12% •••
1	B	262	85% 12% •••

2 Entry composition (i)

There are 2 unique types of molecules in this entry. The entry contains 4536 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.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	260	1962	1232	339	387	4	0	0	0
1	B	260	1962	1232	339	387	4	0	0	0

- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
2	A	309	309	309	0	0
2	B	303	303	303	0	0

3 Residue-property plots (i)

These plots are drawn for all protein, RNA, DNA and oligosaccharide 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. 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. 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.

Note EDS was not executed.

• Molecule 1: LIPASE

Chain A: 85% 12% •••

• Molecule 1: LIPASE

Chain B: 85% 12% •••

4 Data and refinement statistics (i)

Xtriage (Phenix) and EDS were not executed - this section is therefore incomplete.

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	77.50Å 53.00Å 81.10Å 90.00° 95.80° 90.00°	Depositor
Resolution (Å)	8.00 – 1.90	Depositor
% Data completeness (in resolution range)	(Not available) (8.00-1.90)	Depositor
R_{merge}	0.04	Depositor
R_{sym}	0.04	Depositor
Refinement program	SHELX-90	Depositor
R, R_{free}	0.140 , 0.186	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	4536	wwPDB-VP
Average B, all atoms (Å^2)	23.0	wwPDB-VP

5 Model quality (i)

5.1 Standard geometry (i)

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	0.71	4/2012 (0.2%)	1.31	20/2747 (0.7%)
1	B	0.68	2/2012 (0.1%)	1.11	11/2747 (0.4%)
All	All	0.69	6/4024 (0.1%)	1.21	31/5494 (0.6%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand.A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	2

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	262	SER	C-OXT	15.98	1.53	1.23
1	A	262	SER	CA-C	-13.51	1.17	1.52
1	A	20	ARG	CD-NE	-11.44	1.27	1.46
1	B	262	SER	CA-C	-10.97	1.24	1.52
1	A	170	LEU	CA-CB	7.57	1.71	1.53
1	A	144	ARG	CD-NE	-5.53	1.37	1.46

All (31) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	144	ARG	CD-NE-CZ	26.01	160.02	123.60
1	A	144	ARG	NE-CZ-NH1	-18.44	111.08	120.30
1	A	20	ARG	CB-CG-CD	16.51	154.52	111.60
1	B	144	ARG	NE-CZ-NH1	12.62	126.61	120.30
1	A	20	ARG	CG-CD-NE	11.83	136.64	111.80
1	A	262	SER	CA-C-O	-10.59	97.85	120.10
1	B	262	SER	CA-C-O	9.94	140.97	120.10
1	A	113	ARG	NE-CZ-NH1	9.40	125.00	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	B	144	ARG	CD-NE-CZ	9.35	136.69	123.60
1	A	144	ARG	NH1-CZ-NH2	8.61	128.87	119.40
1	A	113	ARG	CD-NE-CZ	7.68	134.35	123.60
1	B	144	ARG	NE-CZ-NH2	-7.23	116.69	120.30
1	B	20	ARG	NE-CZ-NH2	6.93	123.76	120.30
1	A	99	ARG	NE-CZ-NH2	-6.75	116.92	120.30
1	B	246	ARG	NE-CZ-NH2	6.62	123.61	120.30
1	A	99	ARG	NE-CZ-NH1	6.37	123.49	120.30
1	B	99	ARG	NE-CZ-NH1	6.17	123.39	120.30
1	A	262	SER	CB-CA-C	6.06	121.61	110.10
1	A	28	THR	N-CA-CB	5.86	121.42	110.30
1	B	12	THR	N-CA-CB	-5.83	99.22	110.30
1	A	229	ARG	NE-CZ-NH1	5.63	123.11	120.30
1	B	101	ARG	NE-CZ-NH1	5.58	123.09	120.30
1	B	113	ARG	CD-NE-CZ	5.54	131.36	123.60
1	A	236	ARG	NE-CZ-NH1	5.44	123.02	120.30
1	A	28	THR	CB-CA-C	-5.25	97.42	111.60
1	A	7	ARG	NE-CZ-NH2	5.22	122.91	120.30
1	A	117	ARG	NE-CZ-NH2	-5.18	117.71	120.30
1	A	222	TYR	CA-CB-CG	-5.09	103.73	113.40
1	B	170	LEU	CA-CB-CG	5.08	126.98	115.30
1	A	113	ARG	NE-CZ-NH2	-5.07	117.77	120.30
1	A	202	LEU	CA-CB-CG	5.03	126.86	115.30

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	20	ARG	Sidechain
1	A	28	THR	Mainchain

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	1962	0	1914	20	0
1	B	1962	0	1914	25	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	A	309	0	0	7	0
2	B	303	0	0	6	0
All	All	4536	0	3828	45	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 6.

All (45) 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:20:ARG:HD3	2:A:546:HOH:O	1.53	1.05
1:B:12:THR:HG22	1:B:15:SER:H	1.40	0.85
1:A:13:ASN:HD21	1:A:221:LYS:NZ	1.87	0.72
1:A:205:ARG:HG2	1:A:205:ARG:HH11	1.62	0.64
1:B:113:ARG:HG2	1:B:113:ARG:HH11	1.63	0.63
1:B:95:GLN:NE2	2:B:561:HOH:O	2.31	0.63
1:A:3:ASN:N	2:A:459:HOH:O	2.32	0.63
1:B:3:ASN:N	2:B:546:HOH:O	2.34	0.60
1:A:20:ARG:CD	2:A:546:HOH:O	2.23	0.60
1:B:157:ASN:H	1:B:185:HIS:HD2	1.49	0.59
1:A:13:ASN:HD21	1:A:221:LYS:HZ1	1.52	0.58
1:B:246:ARG:CZ	1:B:246:ARG:HA	2.35	0.57
1:B:64:THR:HA	1:B:92:THR:HB	1.87	0.56
1:B:12:THR:HG22	1:B:15:SER:N	2.15	0.55
1:A:113:ARG:NH2	2:A:467:HOH:O	2.40	0.55
1:A:205:ARG:NH1	1:A:248:SER:O	2.42	0.53
1:B:245:PRO:O	1:B:246:ARG:NH1	2.42	0.53
1:A:64:THR:HA	1:A:92:THR:HB	1.91	0.53
1:A:157:ASN:H	1:A:185:HIS:HD2	1.58	0.51
1:B:13:ASN:HD21	1:B:221:LYS:NZ	2.09	0.51
1:A:128:MET:HG2	1:A:151:ILE:HB	1.92	0.51
1:B:244:ILE:HG13	1:B:246:ARG:NH1	2.27	0.50
1:A:58:VAL:HG12	1:A:85:PHE:HB3	1.94	0.50
1:B:132:MET:HG3	2:B:343:HOH:O	2.12	0.50
1:B:242:CYS:HA	1:B:243:PRO:C	2.32	0.50
1:B:130:HIS:HD2	2:B:269:HOH:O	1.97	0.47
1:A:130:HIS:HD2	2:A:270:HOH:O	1.98	0.47
1:B:13:ASN:HD21	1:B:221:LYS:HZ1	1.64	0.46
1:B:246:ARG:NE	1:B:247:PRO:HD3	2.32	0.45
1:A:144:ARG:HD3	2:A:263:HOH:O	2.17	0.45
1:A:205:ARG:HH11	1:A:205:ARG:CG	2.30	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:95:GLN:HB3	1:A:96:PRO:HD2	2.00	0.44
1:B:12:THR:HG23	1:B:14:ALA:H	1.82	0.44
1:B:63:PHE:CD2	1:B:64:THR:HG23	2.53	0.44
1:A:113:ARG:NE	2:A:518:HOH:O	2.51	0.44
1:A:242:CYS:HA	1:A:243:PRO:C	2.37	0.44
1:B:185:HIS:HE1	2:B:468:HOH:O	2.01	0.43
1:B:157:ASN:H	1:B:185:HIS:CD2	2.34	0.43
1:B:246:ARG:HB3	1:B:247:PRO:HD2	2.00	0.43
1:B:244:ILE:HA	1:B:245:PRO:HD3	1.87	0.43
1:B:12:THR:HG21	2:B:499:HOH:O	2.19	0.42
1:B:43:ILE:HG21	1:B:116:VAL:HG21	2.02	0.42
1:A:43:ILE:HG21	1:A:116:VAL:HG21	2.02	0.40
1:A:95:GLN:HB3	1:A:96:PRO:CD	2.51	0.40
1:B:113:ARG:HG2	1:B:113:ARG:NH1	2.34	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	258/262 (98%)	253 (98%)	5 (2%)	0	100	100
1	B	258/262 (98%)	255 (99%)	3 (1%)	0	100	100
All	All	516/524 (98%)	508 (98%)	8 (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	213/213 (100%)	203 (95%)	10 (5%)	26	16
1	B	213/213 (100%)	203 (95%)	10 (5%)	26	16
All	All	426/426 (100%)	406 (95%)	20 (5%)	26	16

All (20) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	20	ARG
1	A	28	THR
1	A	34	VAL
1	A	144	ARG
1	A	197	LEU
1	A	202	LEU
1	A	205	ARG
1	A	214	THR
1	A	246	ARG
1	A	249	LEU
1	B	12	THR
1	B	19	SER
1	B	113	ARG
1	B	117	ARG
1	B	145	THR
1	B	158	THR
1	B	161	THR
1	B	170	LEU
1	B	197	LEU
1	B	249	LEU

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

Mol	Chain	Res	Type
1	A	13	ASN
1	A	130	HIS
1	A	185	HIS
1	B	13	ASN
1	B	130	HIS
1	B	185	HIS
1	B	213	ASN

5.3.3 RNA (i)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains (i)

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

5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

5.6 Ligand geometry (i)

There are no ligands in this entry.

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 (i)

6.1 Protein, DNA and RNA chains (i)

EDS was not executed - this section is therefore empty.

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

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates (i)

EDS was not executed - this section is therefore empty.

6.4 Ligands (i)

EDS was not executed - this section is therefore empty.

6.5 Other polymers (i)

EDS was not executed - this section is therefore empty.