



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 27, 2014 – 03:03 AM GMT

PDB ID : 4J5P
Title : Crystal Structure of a Covalently Bound alpha-KetoheterocycleInhibitor (Ph
enhexyl/Oxadiazole/Pyridine)to a Humanized Variant of Fatty Acid Amide
Hydrolase
Authors : Otrubova, K.; Brown, M.; McCormick, M.S.; Han, G.W.; O'Neal, S.T.; Cra-
vatt, B.F.; Stevens, R.C.; Lichtman, A.H.; Boger, D.L.
Deposited on : 2013-02-08
Resolution : 2.30 Å(reported)

This is a full wwPDB 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/ValidationPDFNotes.html>

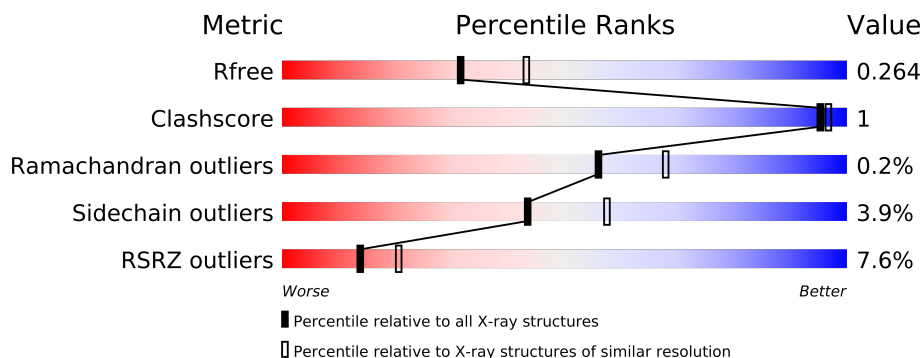
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.15 2013
Xtriage (Phenix) : dev-1323
EDS : stable22639
Percentile statistics : 21963
Refmac : 5.8.0049
CCP4 : 6.3.0 (Settle)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : stable22683

1 Overall quality at a glance

The reported resolution of this entry is 2.30 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}	66092	2929 (2.30-2.30)
Clashscore	79885	3679 (2.30-2.30)
Ramachandran outliers	78287	3642 (2.30-2.30)
Sidechain outliers	78261	3641 (2.30-2.30)
RSRZ outliers	66119	2930 (2.30-2.30)

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. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Mol	Chain	Length	Quality of chain
1	A	573	
1	B	573	

The following table lists non-polymeric compounds that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Geometry	Electron density
3	PEG	A	602	-	X
3	PEG	A	603	-	X
3	PEG	B	602	-	X
3	PEG	B	603	-	X
3	PEG	B	604	-	X

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 8787 atoms, of which 0 are hydrogen and 0 are deuterium.

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 Fatty-acid amide hydrolase 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	544	Total	C	N	O	S	0	0	0
			4198	2679	717	772	30			
1	B	545	Total	C	N	O	S	0	0	0
			4207	2684	719	774	30			

There are 58 discrepancies between the modelled and reference sequences:

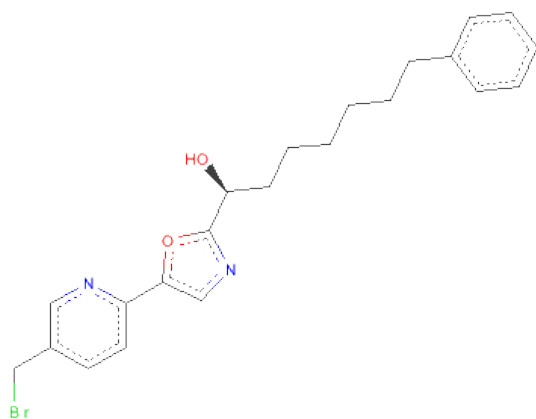
Chain	Residue	Modelled	Actual	Comment	Reference
A	7	MET	-	EXPRESSION TAG	UNP P97612
A	8	GLY	-	EXPRESSION TAG	UNP P97612
A	9	SER	-	EXPRESSION TAG	UNP P97612
A	10	SER	-	EXPRESSION TAG	UNP P97612
A	11	HIS	-	EXPRESSION TAG	UNP P97612
A	12	HIS	-	EXPRESSION TAG	UNP P97612
A	13	HIS	-	EXPRESSION TAG	UNP P97612
A	14	HIS	-	EXPRESSION TAG	UNP P97612
A	15	HIS	-	EXPRESSION TAG	UNP P97612
A	16	HIS	-	EXPRESSION TAG	UNP P97612
A	17	SER	-	EXPRESSION TAG	UNP P97612
A	18	SER	-	EXPRESSION TAG	UNP P97612
A	19	GLY	-	EXPRESSION TAG	UNP P97612
A	20	LEU	-	EXPRESSION TAG	UNP P97612
A	21	VAL	-	EXPRESSION TAG	UNP P97612
A	22	PRO	-	EXPRESSION TAG	UNP P97612
A	23	ARG	-	EXPRESSION TAG	UNP P97612
A	24	GLY	-	EXPRESSION TAG	UNP P97612
A	25	SER	-	EXPRESSION TAG	UNP P97612
A	26	HIS	-	EXPRESSION TAG	UNP P97612
A	27	MET	-	EXPRESSION TAG	UNP P97612
A	28	ALA	-	EXPRESSION TAG	UNP P97612
A	29	SER	-	EXPRESSION TAG	UNP P97612
A	192	PHE	LEU	ENGINEERED MUTATION	UNP P97612
A	194	TYR	PHE	ENGINEERED MUTATION	UNP P97612

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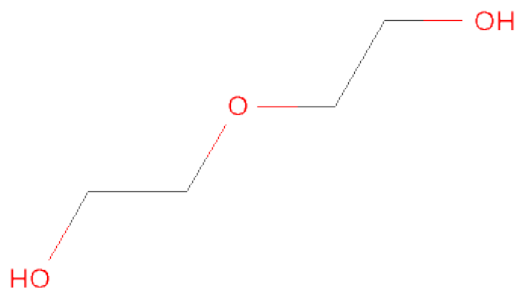
Chain	Residue	Modelled	Actual	Comment	Reference
A	377	THR	ALA	ENGINEERED MUTATION	UNP P97612
A	435	ASN	SER	ENGINEERED MUTATION	UNP P97612
A	491	VAL	ILE	ENGINEERED MUTATION	UNP P97612
A	495	MET	VAL	ENGINEERED MUTATION	UNP P97612
B	7	MET	-	EXPRESSION TAG	UNP P97612
B	8	GLY	-	EXPRESSION TAG	UNP P97612
B	9	SER	-	EXPRESSION TAG	UNP P97612
B	10	SER	-	EXPRESSION TAG	UNP P97612
B	11	HIS	-	EXPRESSION TAG	UNP P97612
B	12	HIS	-	EXPRESSION TAG	UNP P97612
B	13	HIS	-	EXPRESSION TAG	UNP P97612
B	14	HIS	-	EXPRESSION TAG	UNP P97612
B	15	HIS	-	EXPRESSION TAG	UNP P97612
B	16	HIS	-	EXPRESSION TAG	UNP P97612
B	17	SER	-	EXPRESSION TAG	UNP P97612
B	18	SER	-	EXPRESSION TAG	UNP P97612
B	19	GLY	-	EXPRESSION TAG	UNP P97612
B	20	LEU	-	EXPRESSION TAG	UNP P97612
B	21	VAL	-	EXPRESSION TAG	UNP P97612
B	22	PRO	-	EXPRESSION TAG	UNP P97612
B	23	ARG	-	EXPRESSION TAG	UNP P97612
B	24	GLY	-	EXPRESSION TAG	UNP P97612
B	25	SER	-	EXPRESSION TAG	UNP P97612
B	26	HIS	-	EXPRESSION TAG	UNP P97612
B	27	MET	-	EXPRESSION TAG	UNP P97612
B	28	ALA	-	EXPRESSION TAG	UNP P97612
B	29	SER	-	EXPRESSION TAG	UNP P97612
B	192	PHE	LEU	ENGINEERED MUTATION	UNP P97612
B	194	TYR	PHE	ENGINEERED MUTATION	UNP P97612
B	377	THR	ALA	ENGINEERED MUTATION	UNP P97612
B	435	ASN	SER	ENGINEERED MUTATION	UNP P97612
B	491	VAL	ILE	ENGINEERED MUTATION	UNP P97612
B	495	MET	VAL	ENGINEERED MUTATION	UNP P97612

- Molecule 2 is (1S)-1-{5-[5-(BROMOMETHYL)PYRIDIN-2-YL]-1,3-OXAZOL-2-YL}-7-PHENYLHEPTAN-1-OL (three-letter code: BR1) (formula: C₂₂H₂₅BrN₂O₂).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	N	O	0	0
			26	22	2	2		
2	B	1	Total	C	N	O	0	0
			26	22	2	2		

- Molecule 3 is DI(HYDROXYETHYL)ETHER (three-letter code: PEG) (formula: C₄H₁₀O₃).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			7	4	3		
3	A	1	Total	C	O	0	0
			7	4	3		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	B	1	Total	C	O	0	0
			7	4	3		
3	B	1	Total	C	O	0	0
			7	4	3		
3	B	1	Total	C	O	0	0
			7	4	3		

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

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	B	1	Total	Cl	0	0
			1	1		

- Molecule 5 is water.

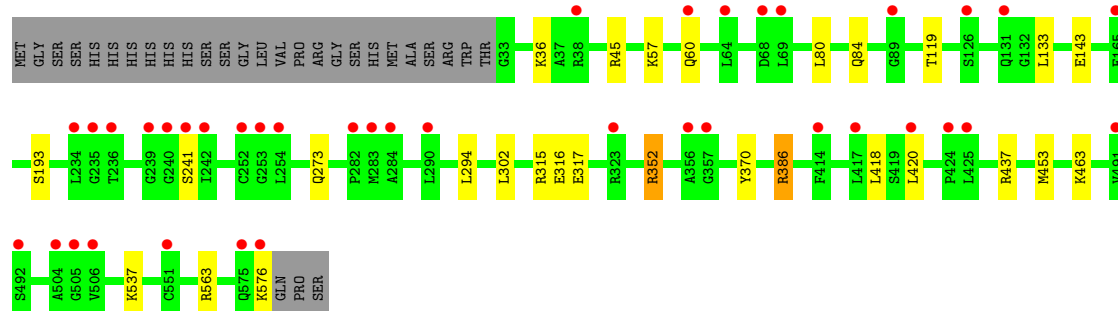
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	124	Total	O	0	0
			124	124		
5	B	170	Total	O	0	0
			170	170		

3 Residue-property plots

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.

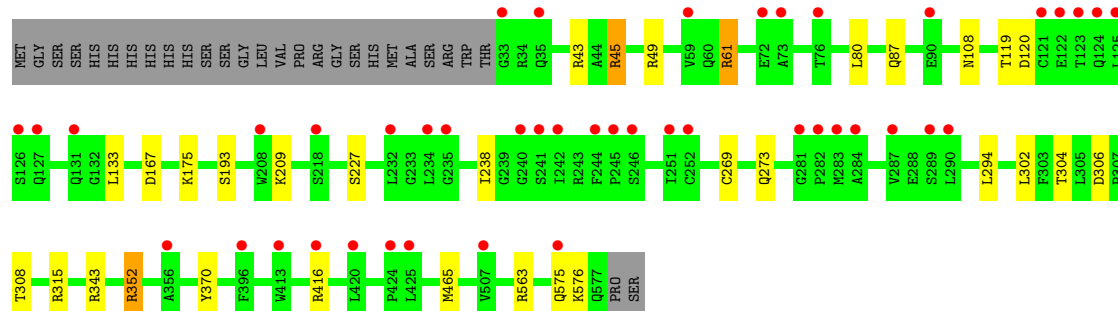
- Molecule 1: Fatty-acid amide hydrolase 1

Chain A: 



- Molecule 1: Fatty-acid amide hydrolase 1

Chain B: 



4 Data and refinement statistics

Property	Value	Source
Space group	P 32 2 1	Depositor
Cell constants a, b, c, α , β , γ	104.07Å 104.07Å 261.03Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	33.38 – 2.30 33.38 – 2.30	Depositor EDS
% Data completeness (in resolution range)	97.2 (33.38-2.30) 97.3 (33.38-2.30)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.13	Depositor
$\langle I/\sigma(I) \rangle$ ¹	48.72 (at 2.29Å)	Xtriage
Refinement program	REFMAC 5.7.0029	Depositor
R, R_{free}	0.220 , 0.265 0.225 , 0.264	Depositor DCC
R_{free} test set	3602 reflections (5.30%)	DCC
Wilson B-factor (Å ²)	55.3	Xtriage
Anisotropy	0.295	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 40.3	EDS
Estimated twinning fraction	0.000 for -h,-k,l	Xtriage
L-test for twinning	$\langle L \rangle = 0.54$, $\langle L^2 \rangle = 0.38$	Xtriage
Outliers	0 of 71606 reflections	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	8787	wwPDB-VP
Average B, all atoms (Å ²)	61.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.16% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: PEG, BR1, CL

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	0.79	0/4292	0.87	7/5822 (0.1%)
1	B	0.84	1/4301 (0.0%)	0.89	6/5834 (0.1%)
All	All	0.82	1/8593 (0.0%)	0.88	13/11656 (0.1%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	227	SER	CB-OG	-5.83	1.34	1.42

All (13) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	343	ARG	NE-CZ-NH2	-7.18	116.71	120.30
1	A	315	ARG	NE-CZ-NH2	6.93	123.77	120.30
1	A	45	ARG	NE-CZ-NH2	6.44	123.52	120.30
1	B	45	ARG	NE-CZ-NH2	6.37	123.48	120.30
1	A	386	ARG	NE-CZ-NH1	6.19	123.40	120.30
1	A	352	ARG	NE-CZ-NH1	6.00	123.30	120.30
1	B	49	ARG	CG-CD-NE	-5.47	100.31	111.80
1	A	437	ARG	NE-CZ-NH1	-5.44	117.58	120.30
1	B	315	ARG	NE-CZ-NH1	5.41	123.01	120.30
1	A	453	MET	CG-SD-CE	5.19	108.50	100.20
1	B	43	ARG	NE-CZ-NH1	-5.07	117.76	120.30
1	A	352	ARG	NE-CZ-NH2	-5.04	117.78	120.30
1	B	352	ARG	NE-CZ-NH1	-5.01	117.80	120.30

There are no chirality outliers.

There are no planarity outliers.

5.2 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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	4198	0	0	2	0
1	B	4207	0	0	10	0
2	A	26	0	22	1	0
2	B	26	0	22	2	0
3	A	14	0	20	0	0
3	B	21	0	30	0	0
4	B	1	0	0	0	0
5	A	124	0	0	0	0
5	B	170	0	0	5	0
All	All	8787	0	94	11	0

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 1.

All (11) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:238:ILE:N	2:B:601:BR1:H9	1.89	0.70
1:A:241:SER:N	2:A:601:BR1:H9	1.93	0.66
1:B:45:ARG:NH2	5:B:763:HOH:O	2.41	0.52
1:B:61:ARG:N	5:B:719:HOH:O	2.42	0.51
1:B:209:LYS:NZ	5:B:822:HOH:O	2.45	0.47
1:A:463:LYS:NZ	1:B:304:THR:O	2.48	0.47
1:B:87:GLN:NE2	5:B:714:HOH:O	2.50	0.44
1:B:269:CYS:N	2:B:601:BR1:C21	2.81	0.44
1:B:108:ASN:ND2	5:B:767:HOH:O	2.51	0.44
1:B:167:ASP:OD1	1:B:175:LYS:NZ	2.52	0.42
1:B:306:ASP:OD2	1:B:308:THR:OG1	2.38	0.41

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	542/573 (95%)	523 (96%)	18 (3%)	1 (0%)	56	68
1	B	543/573 (95%)	524 (96%)	18 (3%)	1 (0%)	56	68
All	All	1085/1146 (95%)	1047 (96%)	36 (3%)	2 (0%)	56	68

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	193	SER
1	A	193	SER

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	462/487 (95%)	441 (96%)	21 (4%)	38	50
1	B	463/487 (95%)	448 (97%)	15 (3%)	51	67
All	All	925/974 (95%)	889 (96%)	36 (4%)	43	57

All (36) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	36	LYS
1	A	57	LYS
1	A	60	GLN
1	A	80	LEU
1	A	84	GLN
1	A	119	THR
1	A	133	LEU

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Mol	Chain	Res	Type
1	A	143	GLU
1	A	273	GLN
1	A	294	LEU
1	A	302	LEU
1	A	316	GLU
1	A	317	GLU
1	A	352	ARG
1	A	370	TYR
1	A	386	ARG
1	A	418	LEU
1	A	420	LEU
1	A	537	LYS
1	A	563	ARG
1	A	576	LYS
1	B	61	ARG
1	B	80	LEU
1	B	119	THR
1	B	120	ASP
1	B	133	LEU
1	B	273	GLN
1	B	294	LEU
1	B	302	LEU
1	B	352	ARG
1	B	370	TYR
1	B	416	ARG
1	B	465	MET
1	B	563	ARG
1	B	575	GLN
1	B	576	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

5.3.3 RNA ⓘ

There are no RNA chains 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 8 ligands modelled in this entry, 1 is monoatomic - leaving 7 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	BR1	A	601	1	28,28,29	1.40	2 (7%)	30,36,37	1.83	3 (10%)
3	PEG	A	602	-	6,6,6	0.43	0	5,5,5	0.50	0
3	PEG	A	603	-	6,6,6	0.72	0	5,5,5	0.34	0
2	BR1	B	601	1	28,28,29	1.24	3 (10%)	30,36,37	1.68	5 (16%)
3	PEG	B	602	-	6,6,6	0.56	0	5,5,5	0.36	0
3	PEG	B	603	-	6,6,6	0.62	0	5,5,5	0.23	0
3	PEG	B	604	-	6,6,6	0.77	0	5,5,5	0.43	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	BR1	A	601	1	-	0/9/17/19	0/3/3/3
3	PEG	A	602	-	-	0/4/4/4	0/0/0/0
3	PEG	A	603	-	-	0/4/4/4	0/0/0/0
2	BR1	B	601	1	-	0/9/17/19	0/3/3/3
3	PEG	B	602	-	-	0/4/4/4	0/0/0/0
3	PEG	B	603	-	-	0/4/4/4	0/0/0/0
3	PEG	B	604	-	-	0/4/4/4	0/0/0/0

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	601	BR1	C16-C17	-5.03	1.43	1.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	601	BR1	C7-C8	-3.09	1.42	1.51
2	B	601	BR1	C16-C17	-2.99	1.45	1.50
2	A	601	BR1	C7-C8	-2.68	1.43	1.51
2	B	601	BR1	C21-C20	2.45	1.51	1.40

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	601	BR1	C21-C20-C22	-7.47	115.33	122.94
2	B	601	BR1	C21-C20-C22	-5.01	117.84	122.94
2	B	601	BR1	C18-C19-C20	-3.27	115.86	121.40
2	B	601	BR1	C5-C6-C7	-3.12	100.40	113.96
2	A	601	BR1	C18-C19-C20	-2.84	116.59	121.40
2	B	601	BR1	O1-C1-C14	-2.37	105.17	109.88
2	A	601	BR1	C5-C6-C7	-2.25	104.19	113.96
2	B	601	BR1	C15-C16-C17	-2.13	123.28	129.94

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

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	544/573 (94%)	0.25	39 (7%)	15 22	37, 57, 88, 136	0
1	B	545/573 (95%)	0.17	44 (8%)	12 18	39, 57, 98, 117	0
All	All	1089/1146 (95%)	0.21	83 (7%)	14 20	37, 57, 95, 136	0

All (83) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	123	THR	4.9
1	B	126	SER	4.7
1	A	242	ILE	4.4
1	B	124	GLN	4.3
1	B	127	GLN	4.2
1	A	254	LEU	4.2
1	B	125	LEU	4.2
1	A	253	GLY	4.1
1	A	69	LEU	4.1
1	A	64	LEU	4.0
1	B	33	GLY	3.9
1	A	506	VAL	3.9
1	A	323	ARG	3.8
1	B	290	LEU	3.7
1	B	575	GLN	3.7
1	A	576	LYS	3.6
1	A	240	GLY	3.4
1	A	504	ALA	3.4
1	A	282	PRO	3.3
1	A	290	LEU	3.3
1	B	284	ALA	3.2
1	A	68	ASP	3.2
1	B	245	PRO	3.1
1	A	235	GLY	3.1

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Mol	Chain	Res	Type	RSRZ
1	B	72	GLU	3.0
1	A	283	MET	3.0
1	B	232	LEU	3.0
1	A	38	ARG	3.0
1	B	282	PRO	3.0
1	B	242	ILE	2.9
1	A	131	GLN	2.9
1	B	251	ILE	2.9
1	A	234	LEU	2.8
1	A	414	PHE	2.8
1	B	90	GLU	2.8
1	A	417	LEU	2.8
1	B	425	LEU	2.7
1	B	252	CYS	2.7
1	A	165	GLU	2.7
1	B	283	MET	2.7
1	B	234	LEU	2.6
1	A	357	GLY	2.6
1	B	424	PRO	2.6
1	A	505	GLY	2.6
1	A	491	VAL	2.5
1	A	425	LEU	2.5
1	A	492	SER	2.5
1	A	239	GLY	2.5
1	A	252	CYS	2.5
1	B	208	TRP	2.5
1	B	240	GLY	2.4
1	B	131	GLN	2.4
1	B	281	GLY	2.4
1	B	507	VAL	2.4
1	B	420	LEU	2.3
1	A	60	GLN	2.3
1	A	126	SER	2.3
1	B	289	SER	2.3
1	A	420	LEU	2.3
1	B	122	GLU	2.3
1	A	551	CYS	2.2
1	B	241	SER	2.2
1	B	396	PHE	2.2
1	B	35	GLN	2.2
1	B	413	TRP	2.2
1	A	284	ALA	2.2

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Mol	Chain	Res	Type	RSRZ
1	A	356	ALA	2.2
1	B	246	SER	2.2
1	B	287	VAL	2.2
1	B	121	CYS	2.2
1	A	424	PRO	2.1
1	B	356	ALA	2.1
1	A	241	SER	2.1
1	A	575	GLN	2.1
1	B	76	THR	2.1
1	B	59	VAL	2.1
1	B	73	ALA	2.1
1	A	89	GLY	2.0
1	B	235	GLY	2.0
1	B	416	ARG	2.0
1	B	244	PHE	2.0
1	B	218	SER	2.0
1	A	236	THR	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 ⓘ

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	RSR	LLDF	B-factors(Å ²)	Q<0.9
3	PEG	B	602	7/7	0.21	6.94	68,76,81,82	0
3	PEG	B	604	7/7	0.11	4.96	62,69,78,84	0
3	PEG	A	603	7/7	0.16	2.87	54,59,75,76	0
3	PEG	A	602	7/7	0.17	2.79	69,69,74,74	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
3	PEG	B	603	7/7	0.15	2.77	82,93,106,107	0
2	BR1	A	601	26/27	0.22	0.76	48,68,77,81	0
2	BR1	B	601	26/27	0.20	0.72	49,62,68,71	0
4	CL	B	605	1/1	0.11	0.39	48,48,48,48	0

6.5 Other polymers ⓘ

There are no such residues in this entry.