Full wwPDB X-ray Structure Validation Report (i)

Jun 23, 2024 – 01:03 PM EDT

PDB ID	:	5F8U
Title	:	Ligand occupancy in crystal structure of beta1-adrenergic receptor previously submitted by Huang et al
Authors	:	Leslie, A.G.W.; Warne, A.; Tate, C.G.
Deposited on	:	2015-12-09
Resolution	:	3.35 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:

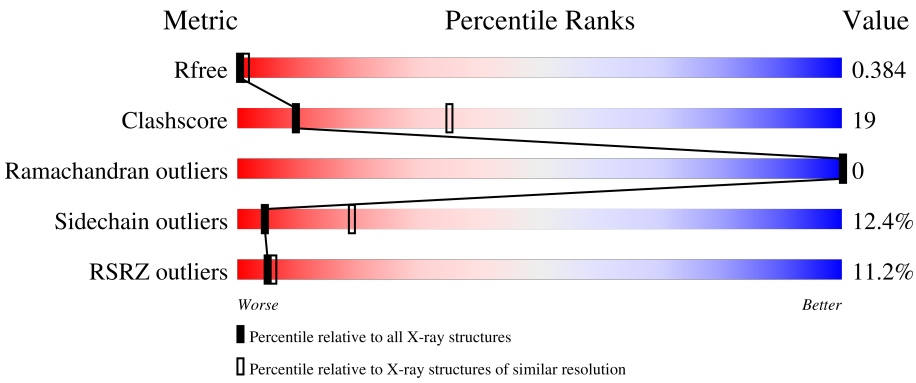
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.37.1
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.37.1

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 3.35 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	1558 (3.42-3.30)
Clashscore	141614	1627 (3.42-3.30)
Ramachandran outliers	138981	1599 (3.42-3.30)
Sidechain outliers	138945	1598 (3.42-3.30)
RSRZ outliers	127900	1507 (3.42-3.30)

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 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% 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	313	10%, 52%, 32%, •, 12%
1	B	313	10%, 52%, 32%, •, 12%

2 Entry composition (i)

There are 2 unique types of molecules in this entry. The entry contains 4432 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 Beta-1 adrenergic receptor.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	B	276	2195	1455	358	364	18	0	0	0
1	A	276	2195	1455	358	364	18	0	0	0

There are 90 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	31	MET	-	initiating methionine	UNP P07700
B	32	GLY	-	expression tag	UNP P07700
B	68	SER	ARG	engineered mutation	UNP P07700
B	90	VAL	MET	engineered mutation	UNP P07700
B	116	LEU	CYS	engineered mutation	UNP P07700
B	227	ALA	TYR	engineered mutation	UNP P07700
B	?	-	CYS	deletion	UNP P07700
B	?	-	GLU	deletion	UNP P07700
B	?	-	GLY	deletion	UNP P07700
B	?	-	ARG	deletion	UNP P07700
B	?	-	PHE	deletion	UNP P07700
B	?	-	TYR	deletion	UNP P07700
B	?	-	GLY	deletion	UNP P07700
B	?	-	SER	deletion	UNP P07700
B	?	-	GLN	deletion	UNP P07700
B	?	-	GLU	deletion	UNP P07700
B	?	-	GLN	deletion	UNP P07700
B	?	-	PRO	deletion	UNP P07700
B	?	-	GLN	deletion	UNP P07700
B	?	-	PRO	deletion	UNP P07700
B	?	-	PRO	deletion	UNP P07700
B	?	-	PRO	deletion	UNP P07700
B	?	-	LEU	deletion	UNP P07700
B	?	-	PRO	deletion	UNP P07700
B	?	-	GLN	deletion	UNP P07700

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Chain	Residue	Modelled	Actual	Comment	Reference
B	?	-	HIS	deletion	UNP P07700
B	?	-	GLN	deletion	UNP P07700
B	?	-	PRO	deletion	UNP P07700
B	?	-	ILE	deletion	UNP P07700
B	?	-	LEU	deletion	UNP P07700
B	?	-	GLY	deletion	UNP P07700
B	?	-	ASN	deletion	UNP P07700
B	?	-	GLY	deletion	UNP P07700
B	?	-	ARG	deletion	UNP P07700
B	?	-	THR	deletion	UNP P07700
B	?	-	SER	deletion	UNP P07700
B	282	LEU	ALA	engineered mutation	UNP P07700
B	327	ALA	PHE	engineered mutation	UNP P07700
B	338	MET	PHE	engineered mutation	UNP P07700
B	358	ALA	CYS	engineered mutation	UNP P07700
B	369	HIS	-	expression tag	UNP P07700
B	370	HIS	-	expression tag	UNP P07700
B	371	HIS	-	expression tag	UNP P07700
B	372	HIS	-	expression tag	UNP P07700
B	373	HIS	-	expression tag	UNP P07700
A	31	MET	-	initiating methionine	UNP P07700
A	32	GLY	-	expression tag	UNP P07700
A	68	SER	ARG	engineered mutation	UNP P07700
A	90	VAL	MET	engineered mutation	UNP P07700
A	116	LEU	CYS	engineered mutation	UNP P07700
A	227	ALA	TYR	engineered mutation	UNP P07700
A	?	-	CYS	deletion	UNP P07700
A	?	-	GLU	deletion	UNP P07700
A	?	-	GLY	deletion	UNP P07700
A	?	-	ARG	deletion	UNP P07700
A	?	-	PHE	deletion	UNP P07700
A	?	-	TYR	deletion	UNP P07700
A	?	-	GLY	deletion	UNP P07700
A	?	-	SER	deletion	UNP P07700
A	?	-	GLN	deletion	UNP P07700
A	?	-	GLU	deletion	UNP P07700
A	?	-	GLN	deletion	UNP P07700
A	?	-	PRO	deletion	UNP P07700
A	?	-	GLN	deletion	UNP P07700
A	?	-	PRO	deletion	UNP P07700
A	?	-	PRO	deletion	UNP P07700
A	?	-	PRO	deletion	UNP P07700

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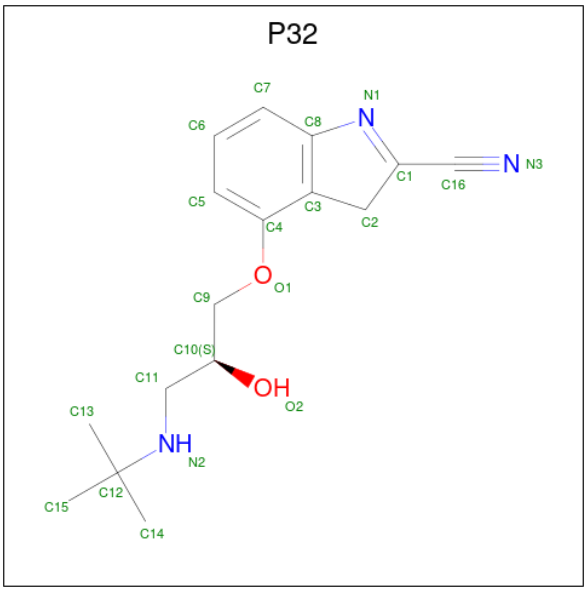
Chain	Residue	Modelled	Actual	Comment	Reference
A	?	-	LEU	deletion	UNP P07700
A	?	-	PRO	deletion	UNP P07700
A	?	-	GLN	deletion	UNP P07700
A	?	-	HIS	deletion	UNP P07700
A	?	-	GLN	deletion	UNP P07700
A	?	-	PRO	deletion	UNP P07700
A	?	-	ILE	deletion	UNP P07700
A	?	-	LEU	deletion	UNP P07700
A	?	-	GLY	deletion	UNP P07700
A	?	-	ASN	deletion	UNP P07700
A	?	-	GLY	deletion	UNP P07700
A	?	-	ARG	deletion	UNP P07700
A	?	-	THR	deletion	UNP P07700
A	?	-	SER	deletion	UNP P07700
A	282	LEU	ALA	engineered mutation	UNP P07700
A	327	ALA	PHE	engineered mutation	UNP P07700
A	338	MET	PHE	engineered mutation	UNP P07700
A	358	ALA	CYS	engineered mutation	UNP P07700
A	369	HIS	-	expression tag	UNP P07700
A	370	HIS	-	expression tag	UNP P07700
A	371	HIS	-	expression tag	UNP P07700
A	372	HIS	-	expression tag	UNP P07700
A	373	HIS	-	expression tag	UNP P07700

- Molecule 2 is 4-{[(2S)-3-(tert-butylamino)-2-hydroxypropyl]oxy}-3H-indole-2-carbonitrile (three-letter code: P32) (formula: $C_{16}H_{21}N_3O_2$).



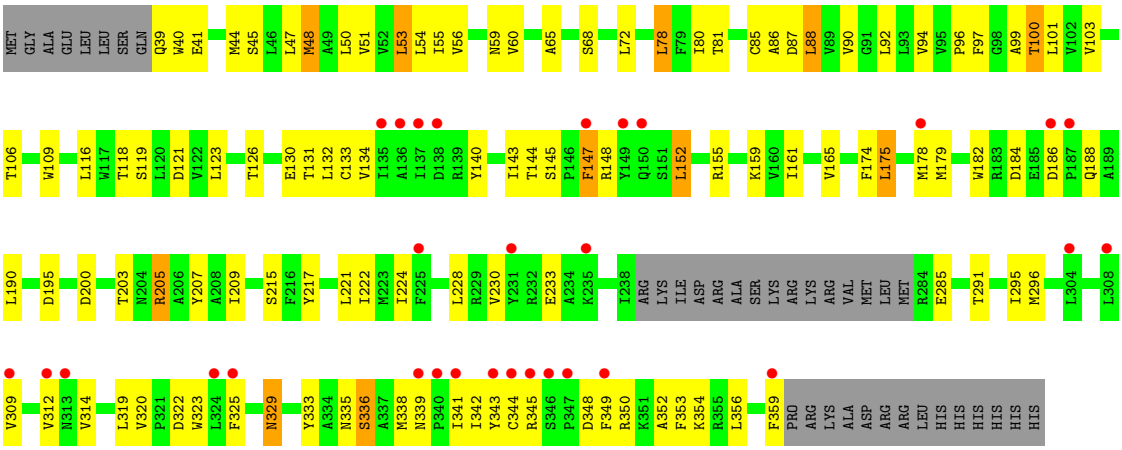
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	N	O		
2	B	1	21	16	3	2	0	0
			Total	C	N	O		
2	A	1	21	16	3	2	0	0

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 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.

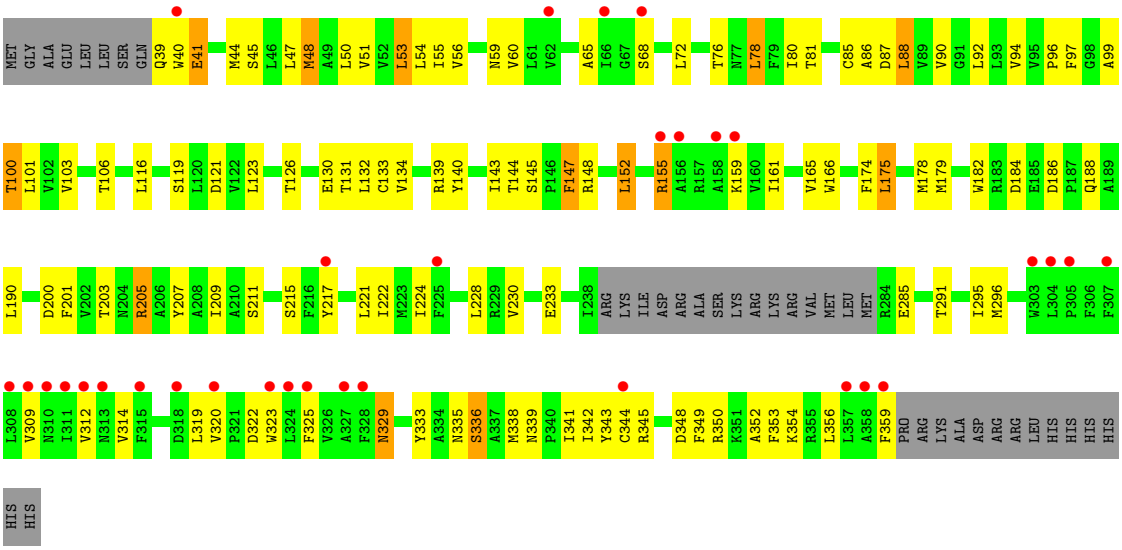
• Molecule 1: Beta-1 adrenergic receptor

Chain B:



• Molecule 1: Beta-1 adrenergic receptor

Chain A:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α, β, γ	229.66Å 79.59Å 69.04Å 90.00° 101.83° 90.00°	Depositor
Resolution (Å)	67.57 – 3.35 67.57 – 3.35	Depositor EDS
% Data completeness (in resolution range)	76.5 (67.57-3.35) 76.5 (67.57-3.35)	Depositor EDS
R_{merge}	0.14	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	6.64 (at 3.33Å)	Xtriage
Refinement program	REFMAC 5.8.0047	Depositor
R, R_{free}	0.344 , 0.382 0.350 , 0.384	Depositor DCC
R_{free} test set	677 reflections (4.98%)	wwPDB-VP
Wilson B-factor (Å^2)	65.3	Xtriage
Anisotropy	0.172	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.27 , 64.3	EDS
L-test for twinning[2]	$< \|L\| > = 0.47$, $< L^2 > = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.73	EDS
Total number of atoms	4432	wwPDB-VP
Average B, all atoms (Å^2)	80.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.84% 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 (i)

5.1 Standard geometry (i)

Bond lengths and bond angles in the following residue types are not validated in this section: P32

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	0/2250	0.80	1/3070 (0.0%)
1	B	0.66	0/2250	0.80	0/3070
All	All	0.66	0/4500	0.80	1/6140 (0.0%)

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	1
1	B	0	1
All	All	0	2

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	155	ARG	NE-CZ-NH1	5.32	122.96	120.30

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	39	GLN	Peptide
1	B	39	GLN	Peptide

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	2195	0	2267	93	2
1	B	2195	0	2267	92	2
2	A	21	0	21	3	0
2	B	21	0	21	2	0
All	All	4432	0	4576	175	2

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 19.

All (175) 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:147:PHE:C	1:B:147:PHE:CD1	2.43	0.90
1:A:147:PHE:C	1:A:147:PHE:CD1	2.43	0.89
1:B:59:ASN:HB2	1:B:88:LEU:HD13	1.65	0.78
1:A:51:VAL:HA	1:A:54:LEU:HD12	1.67	0.76
1:B:51:VAL:HA	1:B:54:LEU:HD12	1.68	0.76
1:A:59:ASN:HB2	1:A:88:LEU:HD13	1.67	0.75
1:A:309:VAL:HG13	1:A:320:VAL:HG11	1.68	0.74
1:B:309:VAL:HG13	1:B:320:VAL:HG11	1.69	0.73
1:A:186:ASP:OD2	1:A:188:GLN:NE2	2.23	0.72
1:B:147:PHE:CD1	1:B:147:PHE:O	2.46	0.68
1:A:147:PHE:CD1	1:A:147:PHE:O	2.47	0.68
1:B:80:ILE:HD12	1:B:343:TYR:OH	1.94	0.67
1:A:41:GLU:HG2	1:A:103:VAL:CG1	2.25	0.67
1:A:80:ILE:HD12	1:A:343:TYR:OH	1.95	0.67
1:B:41:GLU:HG2	1:B:103:VAL:CG1	2.25	0.66
1:B:186:ASP:OD2	1:B:188:GLN:NE2	2.29	0.66
1:A:184:ASP:OD1	1:A:205:ARG:NH2	2.29	0.66
1:A:147:PHE:CG	1:A:148:ARG:N	2.61	0.65
1:B:147:PHE:CG	1:B:148:ARG:N	2.59	0.65
1:A:53:LEU:HG	1:A:54:LEU:N	2.13	0.64
1:B:184:ASP:OD1	1:B:205:ARG:NH2	2.31	0.63
1:A:161:ILE:O	1:A:165:VAL:HG23	1.98	0.63
1:B:53:LEU:HG	1:B:54:LEU:N	2.13	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:161:ILE:O	1:B:165:VAL:HG23	1.99	0.62
1:A:87:ASP:OD2	1:A:339:ASN:ND2	2.32	0.62
1:B:87:ASP:OD2	1:B:339:ASN:ND2	2.33	0.62
1:B:148:ARG:C	1:A:148:ARG:HH21	2.03	0.62
1:A:65:ALA:HB2	1:A:353:PHE:CD1	2.37	0.60
1:A:201:PHE:HB2	2:A:400:P32:H151	1.84	0.60
1:B:132:LEU:HD22	1:B:296:MET:HG2	1.84	0.60
1:B:65:ALA:HB2	1:B:353:PHE:CD1	2.36	0.59
1:B:121:ASP:OD1	1:B:121:ASP:C	2.41	0.59
1:A:130:GLU:O	1:A:134:VAL:HG23	2.03	0.59
1:A:211:SER:OG	2:A:400:P32:N1	2.31	0.59
1:B:148:ARG:CZ	1:A:152:LEU:HB2	2.33	0.59
1:B:350:ARG:O	1:B:354:LYS:HG3	2.02	0.59
1:A:132:LEU:HD22	1:A:296:MET:HG2	1.83	0.59
1:B:130:GLU:O	1:B:134:VAL:HG23	2.04	0.58
1:B:56:VAL:O	1:B:60:VAL:HG23	2.03	0.57
1:A:56:VAL:O	1:A:60:VAL:HG23	2.03	0.57
1:A:121:ASP:OD1	1:A:121:ASP:C	2.41	0.57
1:B:81:THR:O	1:B:85:CYS:SG	2.50	0.57
1:A:350:ARG:O	1:A:354:LYS:HG3	2.03	0.56
1:B:72:LEU:HD11	1:B:352:ALA:HB3	1.87	0.56
1:A:126:THR:OG1	1:A:215:SER:HB3	2.06	0.56
1:B:205:ARG:HB3	1:B:314:VAL:HG13	1.88	0.56
1:B:309:VAL:CG1	1:B:320:VAL:HG11	2.36	0.56
1:A:81:THR:O	1:A:85:CYS:SG	2.50	0.56
1:A:72:LEU:HD11	1:A:352:ALA:HB3	1.88	0.55
1:B:65:ALA:HB2	1:B:353:PHE:CE1	2.41	0.55
1:A:309:VAL:CG1	1:A:320:VAL:HG11	2.34	0.55
1:A:65:ALA:HB2	1:A:353:PHE:CE1	2.41	0.55
1:A:205:ARG:HB3	1:A:314:VAL:HG13	1.87	0.54
1:A:352:ALA:O	1:A:356:LEU:HG	2.06	0.54
1:B:174:PHE:O	1:B:178:MET:HG2	2.06	0.54
1:B:152:LEU:HB2	1:A:148:ARG:CZ	2.38	0.54
1:A:205:ARG:O	1:A:209:ILE:HD12	2.08	0.54
1:A:143:ILE:HG23	1:A:144:THR:HG23	1.89	0.54
1:A:174:PHE:O	1:A:178:MET:HG2	2.08	0.54
1:A:48:MET:HA	1:A:51:VAL:HG22	1.89	0.54
1:B:121:ASP:CG	2:B:400:P32:HA	2.11	0.53
1:B:147:PHE:CZ	1:A:147:PHE:HE2	2.25	0.53
1:B:205:ARG:O	1:B:209:ILE:HD12	2.08	0.53
1:B:48:MET:HA	1:B:51:VAL:HG22	1.89	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:72:LEU:HD11	1:A:352:ALA:CB	2.38	0.53
1:B:143:ILE:HG23	1:B:144:THR:HG23	1.91	0.53
1:B:72:LEU:HD11	1:B:352:ALA:CB	2.37	0.53
1:B:94:VAL:HG11	1:B:333:TYR:HE2	1.74	0.53
1:B:126:THR:OG1	1:B:215:SER:HB3	2.08	0.53
1:A:65:ALA:HA	1:A:356:LEU:HD11	1.91	0.53
1:B:147:PHE:HE2	1:A:147:PHE:CZ	2.27	0.52
1:B:352:ALA:O	1:B:356:LEU:HG	2.08	0.52
1:A:94:VAL:HG11	1:A:333:TYR:HE2	1.74	0.52
1:A:65:ALA:HA	1:A:356:LEU:CD1	2.40	0.52
1:B:65:ALA:HA	1:B:356:LEU:HD11	1.91	0.51
1:B:65:ALA:HA	1:B:356:LEU:CD1	2.40	0.51
1:B:78:LEU:HD21	1:B:159:LYS:HE2	1.93	0.51
1:A:78:LEU:O	1:A:81:THR:HB	2.11	0.51
1:B:97:PHE:N	1:B:97:PHE:CD2	2.78	0.51
1:B:182:TRP:HE3	1:B:203:THR:HG22	1.76	0.51
1:A:335:ASN:HA	1:A:338:MET:SD	2.51	0.51
1:B:335:ASN:HA	1:B:338:MET:SD	2.51	0.50
1:A:78:LEU:HD21	1:A:159:LYS:HE2	1.94	0.50
1:A:97:PHE:CD2	1:A:97:PHE:N	2.80	0.50
1:A:182:TRP:HE3	1:A:203:THR:HG22	1.77	0.50
1:B:147:PHE:CE2	1:B:148:ARG:HG2	2.47	0.50
1:B:148:ARG:HH21	1:A:148:ARG:C	2.14	0.49
1:B:78:LEU:O	1:B:81:THR:HB	2.12	0.49
1:B:100:THR:HG21	1:B:109:TRP:CZ2	2.47	0.49
1:A:175:LEU:O	1:A:179:MET:HG3	2.13	0.49
1:A:147:PHE:CE2	1:A:148:ARG:HG2	2.48	0.49
1:A:295:ILE:HD13	1:A:342:ILE:HD13	1.95	0.49
1:B:133:CYS:SG	1:B:222:ILE:HG22	2.53	0.48
1:B:295:ILE:HD13	1:B:342:ILE:HD13	1.96	0.48
1:B:341:ILE:O	1:B:344:CYS:HB2	2.14	0.47
1:B:140:TYR:HA	1:B:230:VAL:HG22	1.97	0.47
1:A:123:LEU:HD12	1:A:123:LEU:O	2.15	0.47
1:B:147:PHE:HZ	1:A:147:PHE:HE2	1.60	0.47
1:A:133:CYS:SG	1:A:222:ILE:HG22	2.54	0.47
1:B:92:LEU:O	1:B:96:PRO:HG2	2.15	0.47
1:B:175:LEU:O	1:B:179:MET:HG3	2.14	0.47
1:B:123:LEU:HD12	1:B:123:LEU:O	2.14	0.47
1:B:147:PHE:HE2	1:A:147:PHE:HZ	1.61	0.47
1:A:92:LEU:O	1:A:96:PRO:HG2	2.15	0.47
1:A:224:ILE:O	1:A:228:LEU:HG	2.15	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:341:ILE:O	1:A:344:CYS:HB2	2.14	0.46
1:A:201:PHE:HB2	2:A:400:P32:C15	2.44	0.46
1:B:68:SER:HB2	1:B:356:LEU:CD1	2.46	0.46
1:B:224:ILE:O	1:B:228:LEU:HG	2.16	0.46
1:B:94:VAL:HG11	1:B:333:TYR:CE2	2.51	0.46
1:A:140:TYR:HA	1:A:230:VAL:HG22	1.97	0.46
1:A:68:SER:HB2	1:A:356:LEU:CD1	2.46	0.45
1:A:186:ASP:O	1:A:190:LEU:HG	2.16	0.45
1:B:48:MET:HG2	1:B:99:ALA:CB	2.47	0.45
1:B:96:PRO:O	1:B:100:THR:HG23	2.16	0.45
1:B:329:ASN:C	1:B:329:ASN:HD22	2.19	0.45
1:B:295:ILE:CD1	1:B:342:ILE:HG21	2.46	0.45
1:A:87:ASP:HA	1:A:336:SER:OG	2.16	0.45
1:B:87:ASP:HA	1:B:336:SER:OG	2.17	0.45
1:B:182:TRP:CE3	1:B:203:THR:HG22	2.51	0.45
1:A:86:ALA:O	1:A:90:VAL:HG23	2.17	0.44
1:B:350:ARG:HG2	1:B:354:LYS:HE3	1.98	0.44
1:A:207:TYR:C	1:A:207:TYR:CD2	2.91	0.44
1:A:295:ILE:CD1	1:A:342:ILE:HG21	2.47	0.44
1:A:41:GLU:HG2	1:A:103:VAL:HG12	1.98	0.44
1:B:186:ASP:O	1:B:190:LEU:HG	2.17	0.44
1:B:207:TYR:CD2	1:B:207:TYR:C	2.90	0.44
1:A:285:GLU:H	1:A:285:GLU:CD	2.20	0.44
1:A:47:LEU:C	1:A:47:LEU:HD13	2.38	0.44
1:A:94:VAL:HG11	1:A:333:TYR:CE2	2.52	0.44
1:A:96:PRO:O	1:A:100:THR:HG23	2.17	0.44
1:A:350:ARG:HG2	1:A:354:LYS:HE3	1.99	0.44
1:A:312:VAL:CG1	1:A:319:LEU:HD23	2.48	0.43
1:A:291:THR:O	1:A:295:ILE:HG12	2.19	0.43
1:B:295:ILE:HD11	1:B:342:ILE:HG21	2.00	0.43
1:B:65:ALA:CB	1:B:353:PHE:CE1	3.01	0.43
1:A:186:ASP:OD2	1:A:188:GLN:CD	2.57	0.43
1:B:47:LEU:C	1:B:47:LEU:HD13	2.38	0.43
1:B:119:SER:HB3	1:B:174:PHE:CD2	2.54	0.43
1:A:182:TRP:CE3	1:A:203:THR:HG22	2.53	0.43
1:B:147:PHE:CD2	1:B:148:ARG:N	2.87	0.43
1:B:285:GLU:H	1:B:285:GLU:CD	2.21	0.43
1:A:65:ALA:CB	1:A:353:PHE:CE1	3.01	0.43
1:B:55:ILE:O	1:B:59:ASN:ND2	2.51	0.43
1:B:291:THR:O	1:B:295:ILE:HG12	2.19	0.43
1:A:55:ILE:O	1:A:59:ASN:ND2	2.52	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:86:ALA:O	1:B:90:VAL:HG23	2.18	0.43
1:A:329:ASN:C	1:A:329:ASN:HD22	2.21	0.43
1:B:312:VAL:CG1	1:B:319:LEU:HD23	2.49	0.42
1:A:295:ILE:HD11	1:A:342:ILE:HG21	2.01	0.42
1:B:148:ARG:NH2	1:A:152:LEU:HB2	2.34	0.42
1:B:217:TYR:O	1:B:221:LEU:HG	2.19	0.42
1:B:118:THR:HG23	2:B:400:P32:H131	2.00	0.42
1:A:41:GLU:HG2	1:A:103:VAL:HG13	1.99	0.42
1:B:329:ASN:ND2	1:B:333:TYR:CE1	2.88	0.42
1:A:295:ILE:CD1	1:A:342:ILE:HD13	2.49	0.42
1:A:48:MET:HG2	1:A:99:ALA:CB	2.50	0.42
1:A:147:PHE:CD2	1:A:148:ARG:N	2.88	0.41
1:B:100:THR:HG21	1:B:109:TRP:HZ2	1.83	0.41
1:B:41:GLU:HG2	1:B:103:VAL:HG12	1.99	0.41
1:B:295:ILE:CD1	1:B:342:ILE:HD13	2.50	0.41
1:A:60:VAL:HG23	1:A:88:LEU:HD11	2.01	0.41
1:B:60:VAL:HG23	1:B:88:LEU:HD11	2.01	0.41
1:B:140:TYR:O	1:B:143:ILE:HG22	2.20	0.41
1:A:140:TYR:O	1:A:143:ILE:HG22	2.21	0.41
1:A:209:ILE:HD11	1:A:314:VAL:HG11	2.03	0.41
1:A:119:SER:HB3	1:A:174:PHE:CD2	2.56	0.41
1:A:123:LEU:HD11	1:A:166:TRP:CE3	2.56	0.41
1:A:76:THR:OG1	1:A:139:ARG:NH2	2.54	0.41
1:B:97:PHE:N	1:B:97:PHE:HD2	2.18	0.40
1:B:148:ARG:NH1	1:A:152:LEU:HD12	2.37	0.40
1:A:97:PHE:N	1:A:97:PHE:HD2	2.19	0.40
1:B:94:VAL:CG1	1:B:333:TYR:CE2	3.05	0.40
1:A:217:TYR:O	1:A:221:LEU:HG	2.22	0.40
1:B:209:ILE:HD11	1:B:314:VAL:HG11	2.04	0.40

All (2) 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:45:SER:OG	1:A:45:SER:OG[1_545]	1.91	0.29
1:B:195:ASP:OD1	1:A:188:GLN:NE2[4_546]	2.11	0.09

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	272/313 (87%)	268 (98%)	4 (2%)	0	100	100
1	B	272/313 (87%)	269 (99%)	3 (1%)	0	100	100
All	All	544/626 (87%)	537 (99%)	7 (1%)	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	238/271 (88%)	208 (87%)	30 (13%)	4	18
1	B	238/271 (88%)	209 (88%)	29 (12%)	5	19
All	All	476/542 (88%)	417 (88%)	59 (12%)	4	19

All (59) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	40	TRP
1	B	44	MET
1	B	48	MET
1	B	50	LEU
1	B	53	LEU
1	B	78	LEU
1	B	88	LEU
1	B	100	THR

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Mol	Chain	Res	Type
1	B	101	LEU
1	B	106	THR
1	B	116	LEU
1	B	131	THR
1	B	145	SER
1	B	147	PHE
1	B	152	LEU
1	B	155	ARG
1	B	175	LEU
1	B	200	ASP
1	B	205	ARG
1	B	233	GLU
1	B	322	ASP
1	B	323	TRP
1	B	325	PHE
1	B	329	ASN
1	B	336	SER
1	B	345	ARG
1	B	348	ASP
1	B	349	PHE
1	B	359	PHE
1	A	40	TRP
1	A	41	GLU
1	A	44	MET
1	A	48	MET
1	A	50	LEU
1	A	53	LEU
1	A	78	LEU
1	A	88	LEU
1	A	100	THR
1	A	101	LEU
1	A	106	THR
1	A	116	LEU
1	A	131	THR
1	A	145	SER
1	A	147	PHE
1	A	152	LEU
1	A	155	ARG
1	A	175	LEU
1	A	200	ASP
1	A	205	ARG
1	A	233	GLU

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Mol	Chain	Res	Type
1	A	322	ASP
1	A	323	TRP
1	A	325	PHE
1	A	329	ASN
1	A	336	SER
1	A	345	ARG
1	A	348	ASP
1	A	349	PHE
1	A	359	PHE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	188	GLN
1	A	188	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 monosaccharides in this entry.

5.6 Ligand geometry (i)

2 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	P32	B	400	-	22,22,22	3.20	4 (18%)	25,31,31	2.91	6 (24%)
2	P32	A	400	-	22,22,22	3.17	4 (18%)	25,31,31	2.78	8 (32%)

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	P32	B	400	-	-	9/11/21/21	0/2/2/2
2	P32	A	400	-	-	4/11/21/21	0/2/2/2

All (8) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	400	P32	C16-C1	-10.06	1.33	1.44
2	B	400	P32	C16-C1	-10.02	1.33	1.44
2	B	400	P32	C8-C3	7.81	1.51	1.39
2	A	400	P32	C4-C3	7.56	1.50	1.40
2	A	400	P32	C8-C3	6.50	1.49	1.39
2	B	400	P32	C4-C3	6.15	1.48	1.40
2	B	400	P32	C2-C3	-4.18	1.44	1.50
2	A	400	P32	C2-C3	-2.64	1.46	1.50

All (14) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	B	400	P32	C2-C1-N1	8.09	124.02	114.31
2	B	400	P32	C8-N1-C1	-7.35	101.82	107.41
2	A	400	P32	C11-N2-C12	7.09	124.10	116.54
2	B	400	P32	C11-N2-C12	6.82	123.81	116.54
2	A	400	P32	C2-C1-N1	6.31	121.88	114.31
2	A	400	P32	C8-N1-C1	-5.45	103.26	107.41
2	A	400	P32	C7-C8-C3	-4.95	116.00	121.58
2	A	400	P32	O1-C4-C3	4.16	121.71	115.71
2	B	400	P32	C7-C8-C3	-3.65	117.47	121.58
2	B	400	P32	O1-C4-C3	2.86	119.84	115.71
2	A	400	P32	C7-C8-N1	2.47	135.27	128.29
2	A	400	P32	C7-C6-C5	2.38	123.62	120.25
2	B	400	P32	C7-C8-N1	2.20	134.52	128.29
2	A	400	P32	O1-C4-C5	-2.03	119.57	123.97

There are no chirality outliers.

All (13) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	B	400	P32	O2-C10-C11-N2
2	B	400	P32	C9-C10-C11-N2
2	B	400	P32	C11-C10-C9-O1
2	B	400	P32	C15-C12-N2-C11
2	B	400	P32	C13-C12-N2-C11
2	A	400	P32	C11-C10-C9-O1
2	B	400	P32	C14-C12-N2-C11
2	B	400	P32	O2-C10-C9-O1
2	A	400	P32	O2-C10-C9-O1
2	A	400	P32	C5-C4-O1-C9
2	A	400	P32	C3-C4-O1-C9
2	B	400	P32	C5-C4-O1-C9
2	B	400	P32	C3-C4-O1-C9

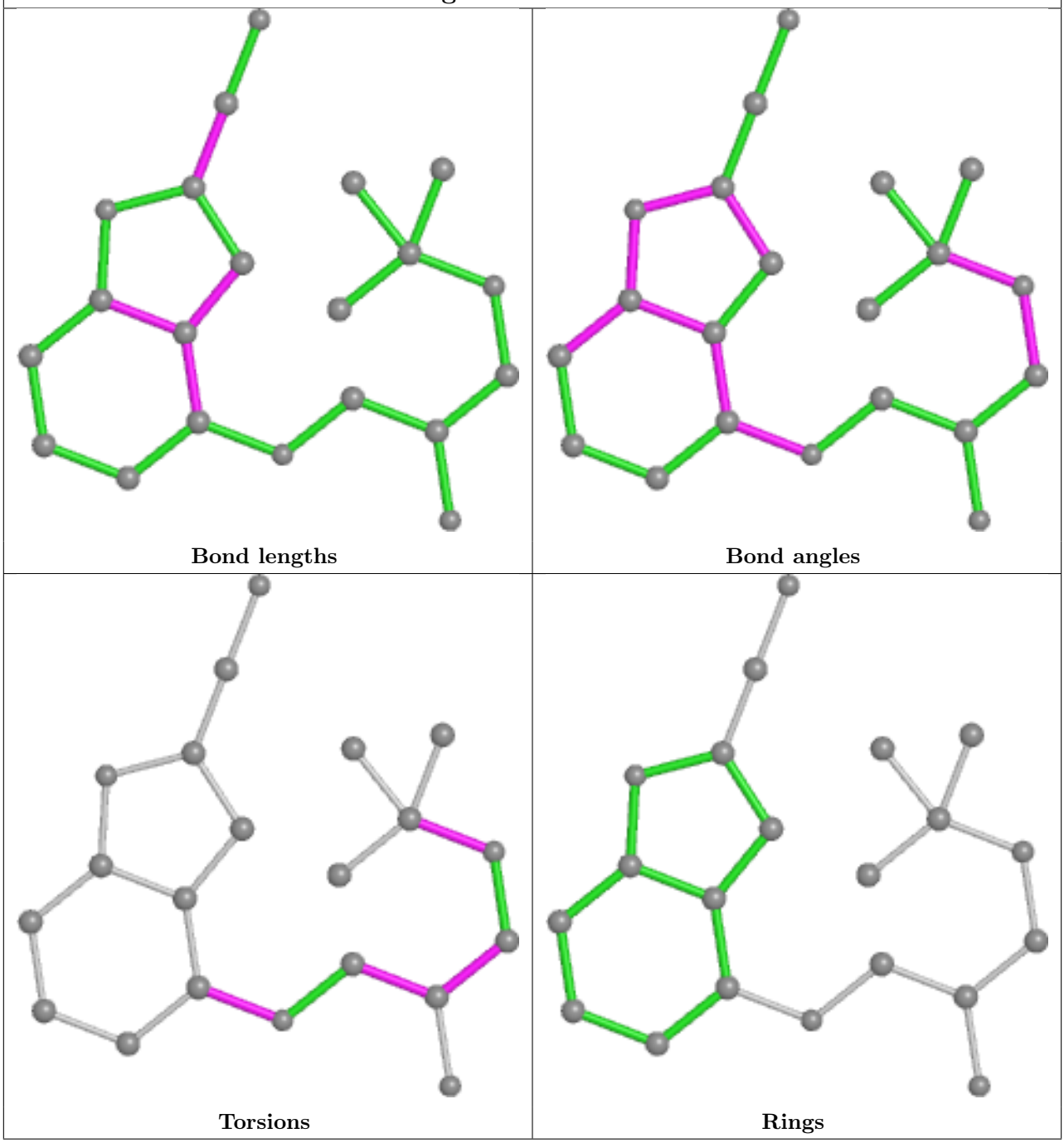
There are no ring outliers.

2 monomers are involved in 5 short contacts:

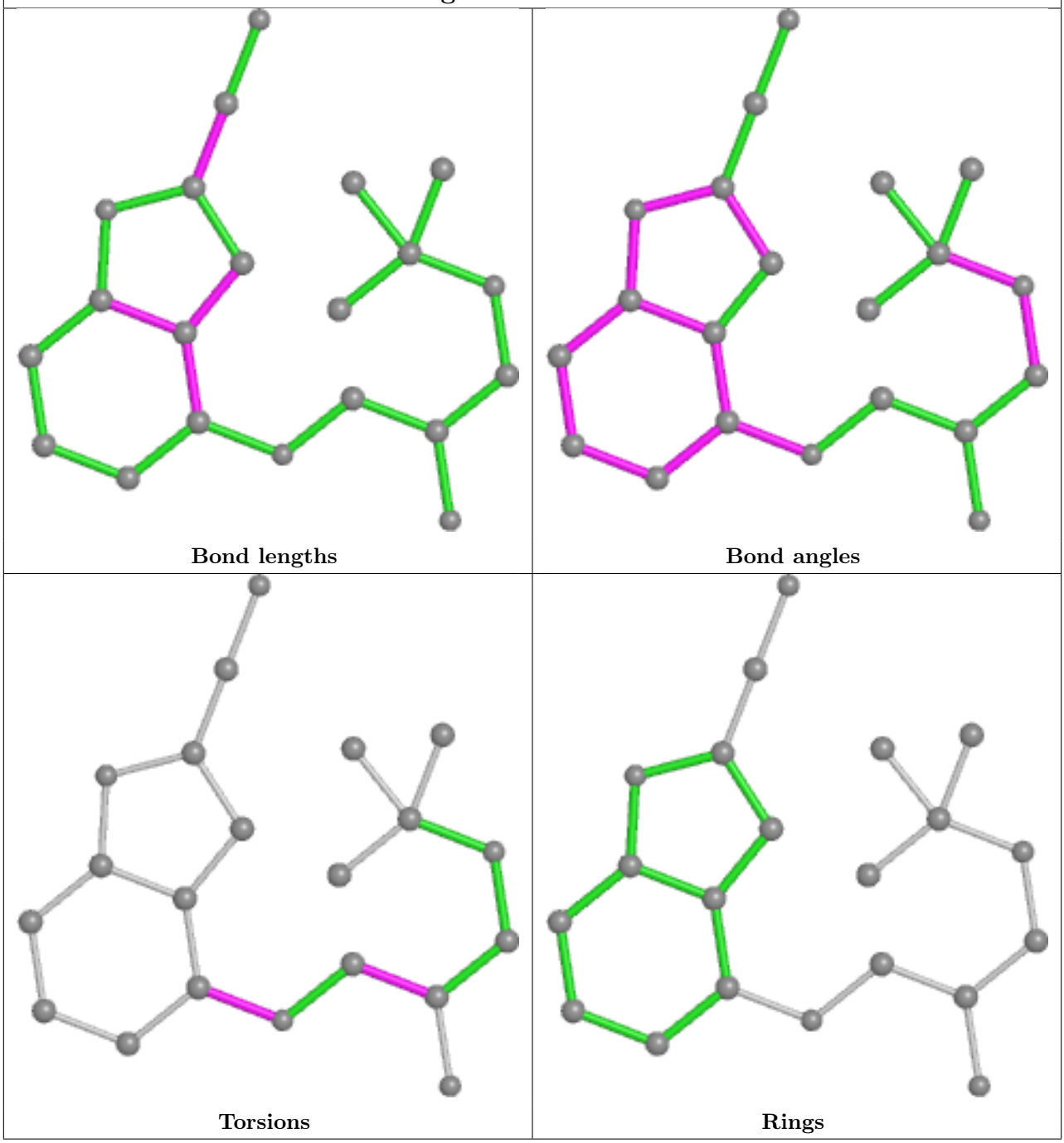
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	400	P32	2	0
2	A	400	P32	3	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less then 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

Ligand P32 B 400



Ligand P32 A 400



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)

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	276/313 (88%)	0.47	32 (11%)	4	5	35, 72, 142, 217	0
1	B	276/313 (88%)	0.52	30 (10%)	5	6	18, 70, 138, 247	0
All	All	552/626 (88%)	0.49	62 (11%)	5	6	18, 72, 142, 247	0

All (62) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	358	ALA	12.4
1	A	359	PHE	9.0
1	B	344	CYS	8.9
1	A	156	ALA	6.8
1	B	343	TYR	5.8
1	A	308	LEU	5.6
1	A	324	LEU	5.5
1	B	345	ARG	5.3
1	A	305	PRO	5.2
1	B	149	TYR	5.0
1	A	357	LEU	4.9
1	A	309	VAL	4.8
1	B	359	PHE	4.7
1	A	68	SER	4.4
1	A	159	LYS	4.1
1	B	324	LEU	4.0
1	B	304	LEU	3.9
1	A	344	CYS	3.8
1	B	235	LYS	3.6
1	A	217	TYR	3.6
1	A	328	PHE	3.6
1	B	186	ASP	3.6
1	B	308	LEU	3.6
1	A	307	PHE	3.4

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Mol	Chain	Res	Type	RSRZ
1	A	323	TRP	3.3
1	B	225	PHE	3.2
1	B	346	SER	3.2
1	A	40	TRP	3.2
1	B	136	ALA	3.1
1	A	312	VAL	3.0
1	B	312	VAL	2.9
1	A	310	ASN	2.8
1	B	150	GLN	2.8
1	A	62	VAL	2.8
1	A	315	PHE	2.8
1	B	137	ILE	2.8
1	A	225	PHE	2.8
1	B	147	PHE	2.8
1	A	318	ASP	2.8
1	A	325	PHE	2.7
1	A	155	ARG	2.7
1	B	341	ILE	2.7
1	A	313	ASN	2.6
1	A	304	LEU	2.6
1	B	339	ASN	2.6
1	A	66	ILE	2.5
1	B	309	VAL	2.5
1	B	325	PHE	2.3
1	A	303	TRP	2.3
1	B	347	PRO	2.3
1	B	231	TYR	2.3
1	A	327	ALA	2.3
1	B	138	ASP	2.3
1	B	187	PRO	2.3
1	A	311	ILE	2.2
1	B	178	MET	2.2
1	B	135	ILE	2.1
1	A	320	VAL	2.1
1	B	313	ASN	2.1
1	B	340	PRO	2.1
1	A	158	ALA	2.1
1	B	349	PHE	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 monosaccharides in this entry.

6.4 Ligands (i)

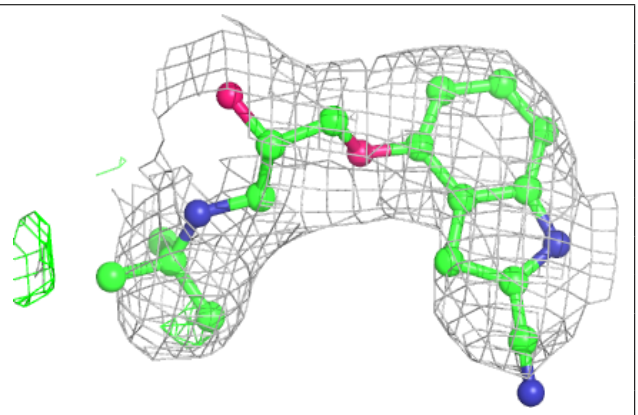
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

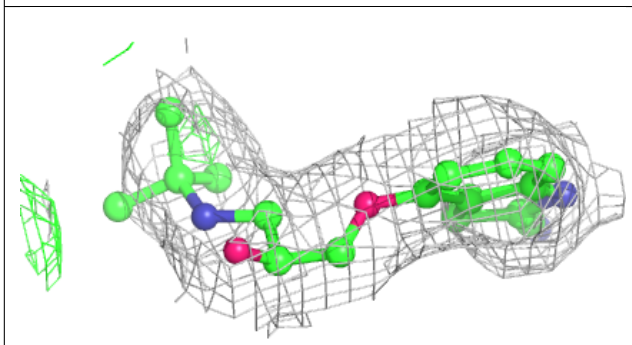
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
2	P32	A	400	21/21	0.92	0.33	31,38,43,48	21
2	P32	B	400	21/21	0.95	0.21	21,25,30,36	0

The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

Electron density around P32 A 400:

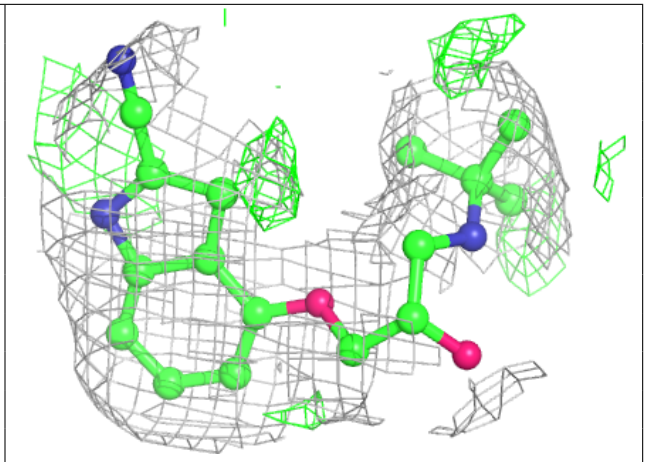
2mF$_o$-DF$_c$ (at 0.7 rmsd) in gray
mF$_o$-DF$_c$ (at 3 rmsd) in purple (negative) and green (positive)

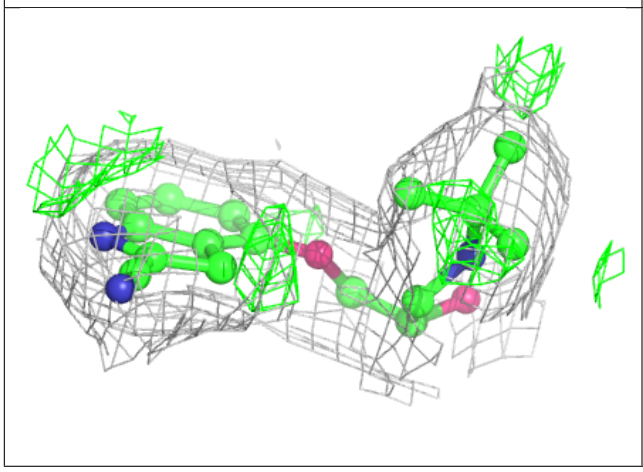


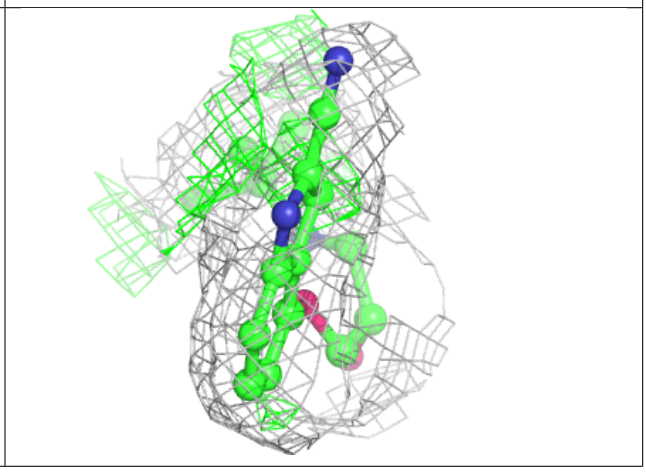


Electron density around P32 B 400:

$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)







6.5 Other polymers (i)

There are no such residues in this entry.