Full wwPDB X-ray Structure Validation Report (i)

Jan 18, 2021 – 10:30 AM EST

PDB ID	:	6VLH
Title	:	HIV Integrase Core domain (IN) in complex with dimer-spanning ligand
Authors	:	Gorman, M.A.; Parker, M.W.
Deposited on	:	2020-01-24
Resolution	:	2.04 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 (i)) were used in the production of this report:

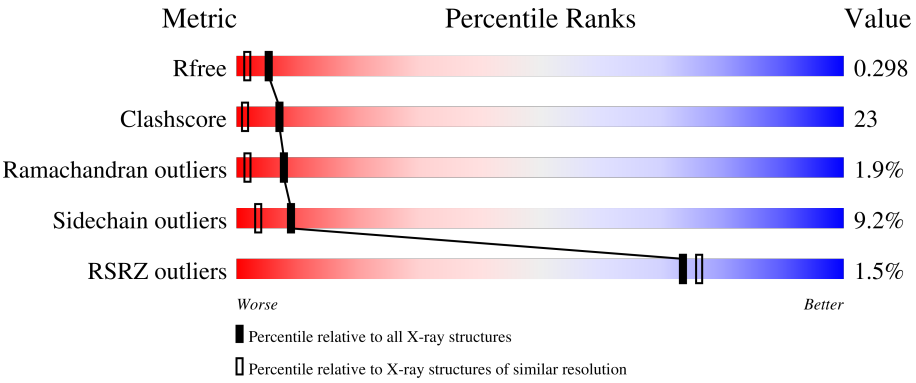
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.16
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.16

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 2.04 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	1692 (2.04-2.04)
Clashscore	141614	1773 (2.04-2.04)
Ramachandran outliers	138981	1752 (2.04-2.04)
Sidechain outliers	138945	1752 (2.04-2.04)
RSRZ outliers	127900	1672 (2.04-2.04)

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	164	2% 53% 24% 6% 16%
1	B	164	49% 30% • 17%

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	IOD	A	301	-	-	X	-
3	SO4	B	304	-	-	X	-
3	SO4	B	305	-	-	X	-

2 Entry composition (i)

There are 5 unique types of molecules in this entry. The entry contains 4413 atoms, of which 2147 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 Integrase.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	137	Total	C	H	N	O	S	0	0	0
			2105	672	1051	183	195	4			
1	B	136	Total	C	H	N	O	S	0	1	0
			2109	670	1059	183	194	3			

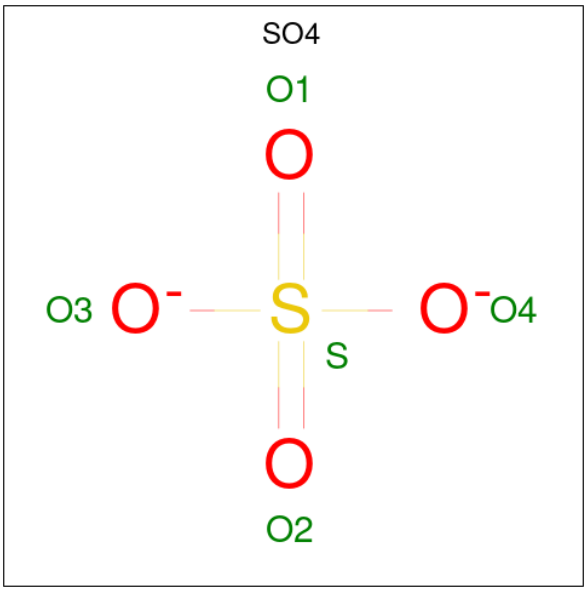
There are 14 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	48	GLY	-	expression tag	UNP F2WR39
A	49	SER	-	expression tag	UNP F2WR39
A	53	GLU	GLN	engineered mutation	UNP F2WR39
A	56	SER	CYS	engineered mutation	UNP F2WR39
A	131	GLU	TRP	engineered mutation	UNP F2WR39
A	185	LYS	PHE	engineered mutation	UNP F2WR39
A	209	GLU	GLN	engineered mutation	UNP F2WR39
B	48	GLY	-	expression tag	UNP F2WR39
B	49	SER	-	expression tag	UNP F2WR39
B	53	GLU	GLN	engineered mutation	UNP F2WR39
B	56	SER	CYS	engineered mutation	UNP F2WR39
B	131	GLU	TRP	engineered mutation	UNP F2WR39
B	185	LYS	PHE	engineered mutation	UNP F2WR39
B	209	GLU	GLN	engineered mutation	UNP F2WR39

- Molecule 2 is IODIDE ION (three-letter code: IOD) (formula: I).

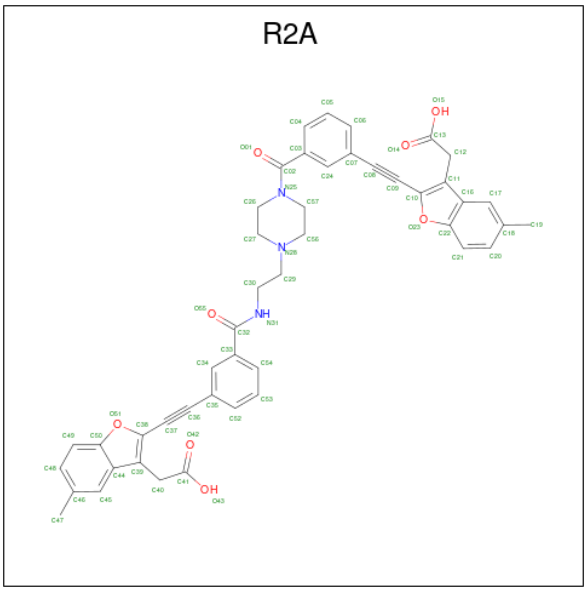
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	B	2	Total	I	0	0
			2	2		
2	A	4	Total	I	0	0
			4	4		

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



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total O S 5 4 1	0	0
3	A	1	Total O S 5 4 1	0	0
3	A	1	Total O S 5 4 1	0	0
3	A	1	Total O S 5 4 1	0	0
3	B	1	Total O S 5 4 1	0	0
3	B	1	Total O S 5 4 1	0	0
3	B	1	Total O S 5 4 1	0	0
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 (2-{[3-(4-{2-[(3-{[3-(carboxymethyl)-5-methyl-1-benzofuran-2-yl]ethynyl}benzene-1-carbonyl)amino]ethyl}piperazine-1-carbonyl)phenyl]ethynyl}-5-methyl-1-benzofuran-3-yl)acetic acid (three-letter code: R2A) (formula: $C_{46}H_{39}N_3O_8$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	B	1	Total	C	H	N	O	0	0
			94	46	37	3	8		

- Molecule 5 is water.

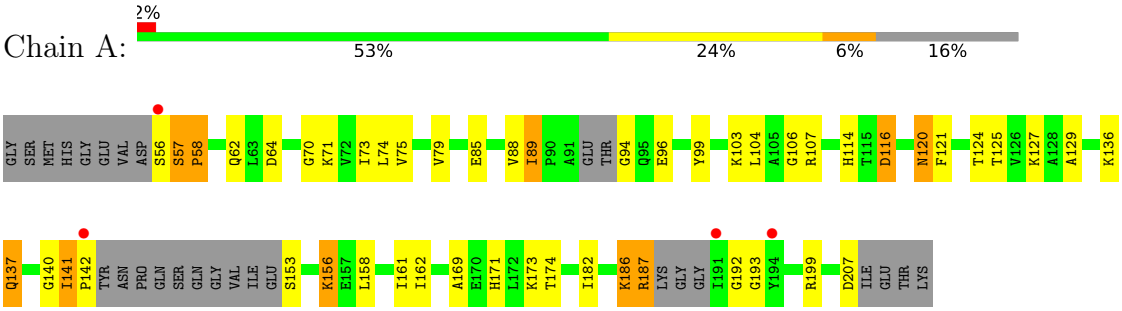
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	23	Total	O	0	0
			23	23		
5	B	31	Total	O	0	0
			31	31		

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.

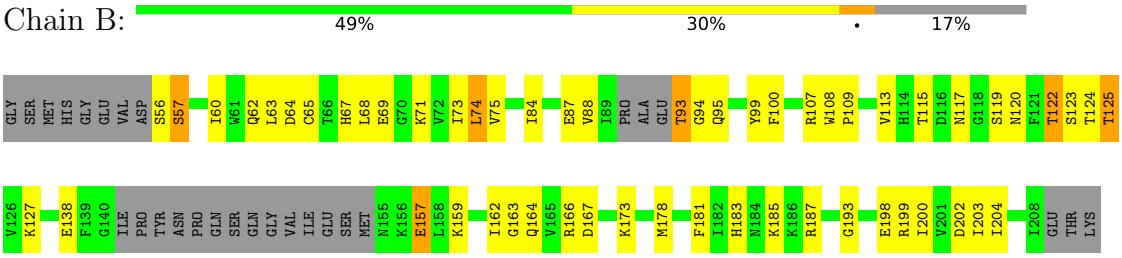
• Molecule 1: Integrase

Chain A:



• Molecule 1: Integrase

Chain B:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 43	Depositor
Cell constants a, b, c, α, β, γ	46.31Å 46.31Å 139.15Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	46.31 – 2.04 46.31 – 2.04	Depositor EDS
% Data completeness (in resolution range)	98.8 (46.31-2.04) 94.5 (46.31-2.04)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.19 (at 2.03Å)	Xtriage
Refinement program	PHENIX (1.13_2998-000)	Depositor
R, R_{free}	0.209 , 0.298 0.219 , 0.298	Depositor DCC
R_{free} test set	1845 reflections (9.95%)	wwPDB-VP
Wilson B-factor (Å^2)	29.6	Xtriage
Anisotropy	0.094	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.41 , 40.7	EDS
L-test for twinning[2]	$< \|L\| > = 0.50$, $< L^2 > = 0.33$	Xtriage
Estimated twinning fraction	0.480 for h,-k,-l	Xtriage
F_o,F_c correlation	0.95	EDS
Total number of atoms	4413	wwPDB-VP
Average B, all atoms (Å^2)	39.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 8.71% 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: CSO, IOD, SO4, R2A

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	0.69	0/1064	0.76	0/1434
1	B	0.64	0/1062	0.75	1/1430 (0.1%)
All	All	0.66	0/2126	0.75	1/2864 (0.0%)

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	B	74	LEU	CB-CG-CD2	-5.04	102.42	111.00

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	1054	1051	1063	48	0
1	B	1050	1059	1068	54	1
2	A	4	0	0	4	0
2	B	2	0	0	1	0
3	A	20	0	0	0	1
3	B	25	0	0	10	0
4	B	57	37	0	5	0
5	A	23	0	0	5	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	B	31	0	0	3	1
All	All	2266	2147	2131	99	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 23.

All (99) 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:57:SER:HB2	1:A:58:PRO:HD3	1.47	0.96
1:A:173:LYS:HE2	2:A:301:IOD:I	2.40	0.92
1:A:99:TYR:OH	1:B:87:GLU:OE2	1.91	0.86
1:A:85:GLU:OE1	1:A:107:ARG:NH1	2.12	0.82
1:A:96:GLU:N	1:A:96:GLU:OE1	2.13	0.81
1:B:93:THR:OG1	1:B:94:GLY:N	2.15	0.78
1:A:103:LYS:O	5:A:401:HOH:O	2.01	0.78
1:A:114:HIS:ND1	1:A:140:GLY:O	2.17	0.78
1:A:199:ARG:NH2	5:A:402:HOH:O	2.19	0.75
1:A:57:SER:CB	1:A:58:PRO:HD3	2.18	0.74
1:A:57:SER:CB	1:A:58:PRO:CD	2.66	0.73
1:A:57:SER:HB2	1:A:58:PRO:CD	2.19	0.72
1:B:107:ARG:O	5:B:401:HOH:O	2.09	0.70
1:A:187:ARG:HD3	2:A:303:IOD:I	2.62	0.69
1:A:120:ASN:ND2	1:A:137:GLN:OE1	2.24	0.67
1:B:64:ASP:OD1	1:B:65:CSO:N	2.33	0.62
1:B:187:ARG:NH2	1:B:198:GLU:OE1	2.33	0.61
1:B:67:HIS:ND1	3:B:303:SO4:O1	2.30	0.61
1:B:115:THR:HG21	1:B:120:ASN:HD22	1.65	0.60
1:B:117:ASN:ND2	1:B:119:SER:OG	2.36	0.58
1:B:56:SER:O	1:B:57:SER:CB	2.51	0.58
1:B:57:SER:HB3	3:B:305:SO4:S	2.45	0.57
1:A:74:LEU:HD11	1:A:89:ILE:HD13	1.86	0.57
1:B:164:GLN:NE2	5:B:406:HOH:O	2.38	0.56
1:A:99:TYR:O	1:A:103:LYS:HG3	2.06	0.55
1:B:56:SER:O	1:B:57:SER:OG	2.24	0.55
1:B:124:THR:O	5:B:402:HOH:O	2.18	0.55
1:B:57:SER:HB3	3:B:305:SO4:O4	2.05	0.55
1:B:108:TRP:HB3	1:B:109:PRO:HD2	1.88	0.55
1:B:166:ARG:HB2	3:B:304:SO4:O4	2.08	0.54
1:B:199:ARG:NH1	1:B:202:ASP:OD2	2.39	0.54
1:B:57:SER:HB2	1:B:60:ILE:CD1	2.37	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:73:ILE:HG22	1:B:75:VAL:CG2	2.38	0.54
1:B:57:SER:OG	3:B:305:SO4:O1	2.16	0.53
1:A:74:LEU:CD1	1:A:89:ILE:HD13	2.39	0.53
1:A:58:PRO:O	5:A:403:HOH:O	2.19	0.52
1:B:99:TYR:HB2	4:B:308:R2A:C08	2.41	0.51
1:A:121:PHE:CD2	1:A:121:PHE:N	2.78	0.51
1:A:64:ASP:OD2	1:A:141:ILE:CD1	2.58	0.51
1:B:74:LEU:N	1:B:87:GLU:O	2.40	0.50
1:B:95:GLN:HG2	1:B:125:THR:HG21	1.93	0.50
1:A:120:ASN:HB3	1:A:137:GLN:HE22	1.78	0.49
1:B:162:ILE:HG22	3:B:304:SO4:O4	2.12	0.49
1:A:107:ARG:HD3	1:B:107:ARG:HD3	1.95	0.49
1:A:141:ILE:O	1:A:141:ILE:CG2	2.60	0.49
1:A:104:LEU:O	1:A:107:ARG:N	2.44	0.49
1:B:162:ILE:O	1:B:166:ARG:N	2.45	0.49
1:B:74:LEU:HD21	1:B:100:PHE:CD2	2.48	0.48
1:A:71:LYS:NZ	2:A:301:IOD:I	3.14	0.48
1:B:123:SER:OG	3:B:306:SO4:O1	2.21	0.48
1:B:166:ARG:O	1:B:166:ARG:NH1	2.44	0.48
1:A:62:GLN:HG3	1:A:79:VAL:CG2	2.44	0.47
1:B:123:SER:N	1:B:127:LYS:HE2	2.29	0.47
1:A:62:GLN:NE2	1:A:142:PRO:O	2.47	0.47
1:A:187:ARG:HG3	1:A:192:GLY:HA3	1.97	0.47
1:A:158:LEU:O	1:A:162:ILE:HG13	2.15	0.47
1:A:153:SER:O	1:A:156:LYS:HB3	2.15	0.46
1:B:122:THR:HG23	1:B:122:THR:O	2.14	0.46
1:B:187:ARG:NH1	1:B:198:GLU:OE2	2.45	0.46
1:B:173:LYS:HD3	2:B:301:IOD:I	2.84	0.46
1:B:163:GLY:HA2	3:B:304:SO4:O3	2.15	0.46
1:A:106:GLY:HA3	5:A:401:HOH:O	2.16	0.46
1:A:94:GLY:O	1:A:125:THR:HB	2.16	0.46
1:B:99:TYR:HB2	4:B:308:R2A:C09	2.47	0.45
1:A:107:ARG:HD3	1:B:107:ARG:CD	2.46	0.45
1:A:141:ILE:HG22	1:A:141:ILE:O	2.16	0.45
1:B:178:MET:O	1:B:181:PHE:HB3	2.17	0.45
1:A:96:GLU:HB2	4:B:308:R2A:O55	2.17	0.45
1:B:167:ASP:OD1	1:B:167:ASP:N	2.46	0.45
1:A:57:SER:OG	1:A:58:PRO:HD2	2.17	0.44
1:A:121:PHE:O	1:A:127:LYS:NZ	2.40	0.44
1:B:181:PHE:O	1:B:185:LYS:HG2	2.17	0.44
1:B:57:SER:CB	3:B:305:SO4:O1	2.66	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:187:ARG:HH22	1:B:198:GLU:CD	2.21	0.44
1:B:69:GLU:OE1	1:B:71:LYS:NZ	2.51	0.44
1:B:73:ILE:HG22	1:B:75:VAL:HG23	1.99	0.44
1:B:157:GLU:OE2	1:B:183:HIS:HD2	2.02	0.43
1:B:63:LEU:HA	1:B:63:LEU:HD12	1.92	0.43
1:B:73:ILE:HG12	1:B:88:VAL:HG22	2.01	0.43
1:A:129:ALA:HB2	4:B:308:R2A:C48	2.48	0.43
1:B:63:LEU:HD22	1:B:113:VAL:HG11	1.99	0.43
1:B:119:SER:O	1:B:122:THR:HG22	2.18	0.43
1:A:174:THR:OG1	4:B:308:R2A:C10	2.67	0.43
1:A:88:VAL:HG11	2:A:301:IOD:I	2.89	0.42
1:A:70:GLY:O	1:A:71:LYS:HG3	2.19	0.42
1:A:89:ILE:HG23	1:A:96:GLU:HG3	2.01	0.42
1:A:57:SER:OG	1:A:58:PRO:CD	2.68	0.42
1:B:199:ARG:HD2	1:B:199:ARG:HA	1.78	0.42
1:B:60:ILE:HG13	3:B:305:SO4:O4	2.20	0.42
1:B:68:LEU:HD13	1:B:159:LYS:HE2	2.02	0.41
1:B:187:ARG:HD3	1:B:193:GLY:O	2.20	0.41
1:A:161:ILE:O	1:A:162:ILE:C	2.55	0.41
1:B:123:SER:O	1:B:127:LYS:HG3	2.20	0.41
1:A:73:ILE:HG22	1:A:75:VAL:HG22	2.02	0.41
1:B:200:ILE:O	1:B:204:ILE:HD12	2.20	0.41
1:A:116:ASP:HB3	1:A:141:ILE:HB	2.03	0.41
1:A:182:ILE:O	1:A:186:LYS:HB3	2.21	0.41
1:A:127:LYS:HA	5:A:422:HOH:O	2.22	0.40
1:A:169:ALA:HB1	1:A:174:THR:HG21	2.03	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)
5:B:425:HOH:O	5:B:426:HOH:O[4_555]	1.91	0.29
1:B:122:THR:OG1	3:A:308:SO4:O3[3_554]	2.06	0.14

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	128/164 (78%)	112 (88%)	13 (10%)	3 (2%)	6 1
1	B	130/164 (79%)	119 (92%)	9 (7%)	2 (2%)	10 3
All	All	258/328 (79%)	231 (90%)	22 (8%)	5 (2%)	8 2

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	57	SER
1	A	58	PRO
1	B	57	SER
1	A	193	GLY
1	B	203	ILE

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	110/132 (83%)	97 (88%)	13 (12%)	5 1
1	B	109/132 (83%)	102 (94%)	7 (6%)	17 9
All	All	219/264 (83%)	199 (91%)	20 (9%)	9 3

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

Mol	Chain	Res	Type
1	A	56	SER
1	A	89	ILE
1	A	116	ASP
1	A	120	ASN
1	A	124	THR
1	A	136	LYS
1	A	137	GLN

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Mol	Chain	Res	Type
1	A	141	ILE
1	A	156	LYS
1	A	171	HIS
1	A	186	LYS
1	A	187	ARG
1	A	207	ASP
1	B	62	GLN
1	B	84	ILE
1	B	93	THR
1	B	122	THR
1	B	125	THR
1	B	138	GLU
1	B	157	GLU

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

Mol	Chain	Res	Type
1	A	120	ASN
1	A	137	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)

2 non-standard protein/DNA/RNA residues 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	$\#\|Z\| > 2$
1	CSO	A	65	1	3,6,7	0.66	0	0,6,8	0.00	-
1	CSO	B	65	1	3,6,7	0.87	0	0,6,8	0.00	-

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
1	CSO	A	65	1	-	0/1/5/7	-
1	CSO	B	65	1	-	0/1/5/7	-

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
1	B	65	CSO	1	0

5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

5.6 Ligand geometry (i)

Of 16 ligands modelled in this entry, 6 are monoatomic - leaving 10 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	$\#\|Z\| > 2$
3	SO4	B	304	-	4,4,4	0.21	0	6,6,6	0.17	0
3	SO4	B	305	-	4,4,4	0.18	0	6,6,6	0.45	0
3	SO4	A	308	-	4,4,4	0.31	0	6,6,6	0.32	0
3	SO4	A	305	-	4,4,4	0.17	0	6,6,6	0.17	0
4	R2A	B	308	-	47,63,63	2.08	8 (17%)	61,89,89	2.06	14 (22%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\|>2$	Counts	RMSZ	$\#\|Z\|>2$
3	SO4	B	306	-	4,4,4	0.17	0	6,6,6	0.21	0
3	SO4	B	303	-	4,4,4	0.18	0	6,6,6	0.15	0
3	SO4	A	307	-	4,4,4	0.17	0	6,6,6	0.19	0
3	SO4	B	307	-	4,4,4	0.18	0	6,6,6	0.38	0
3	SO4	A	306	-	4,4,4	0.20	0	6,6,6	0.58	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
4	R2A	B	308	-	-	1/26/46/46	0/7/7/7

All (8) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	B	308	R2A	C32-N31	7.10	1.49	1.33
4	B	308	R2A	C02-N25	6.29	1.48	1.34
4	B	308	R2A	C35-C36	4.63	1.55	1.44
4	B	308	R2A	C16-C22	-4.56	1.33	1.43
4	B	308	R2A	C33-C32	3.65	1.57	1.50
4	B	308	R2A	C03-C02	2.36	1.53	1.50
4	B	308	R2A	C07-C08	2.23	1.49	1.44
4	B	308	R2A	C40-C39	2.01	1.55	1.52

All (14) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
4	B	308	R2A	C10-C11-C16	-7.27	100.44	109.56
4	B	308	R2A	C18-C17-C16	-6.03	114.83	121.64
4	B	308	R2A	C38-C39-C44	-4.67	103.70	109.56
4	B	308	R2A	C29-C30-N31	4.59	120.39	111.60
4	B	308	R2A	C56-C57-N25	3.78	118.55	110.44
4	B	308	R2A	C29-N28-C56	3.74	120.81	111.23
4	B	308	R2A	C27-C26-N25	3.40	117.73	110.44
4	B	308	R2A	C03-C02-N25	2.87	122.36	118.72
4	B	308	R2A	C33-C32-N31	2.53	122.53	117.09
4	B	308	R2A	C17-C16-C11	-2.46	129.92	134.17
4	B	308	R2A	C30-C29-N28	2.21	118.38	112.88
4	B	308	R2A	C20-C18-C17	2.20	121.11	118.40
4	B	308	R2A	C40-C39-C38	2.13	130.59	127.36

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
4	B	308	R2A	C30-N31-C32	2.02	126.69	122.08

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	B	308	R2A	N28-C29-C30-N31

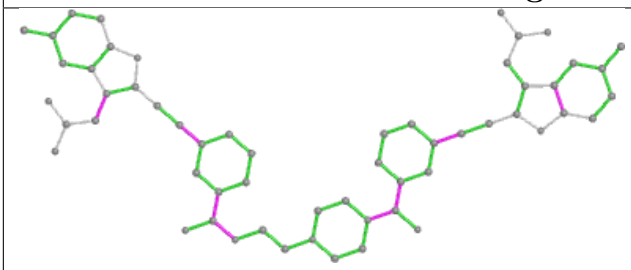
There are no ring outliers.

6 monomers are involved in 16 short contacts:

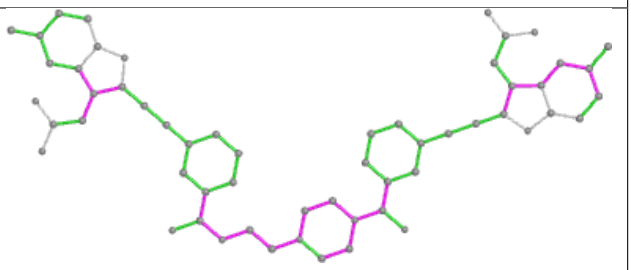
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	304	SO4	3	0
3	B	305	SO4	5	0
3	A	308	SO4	0	1
4	B	308	R2A	5	0
3	B	306	SO4	1	0
3	B	303	SO4	1	0

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.

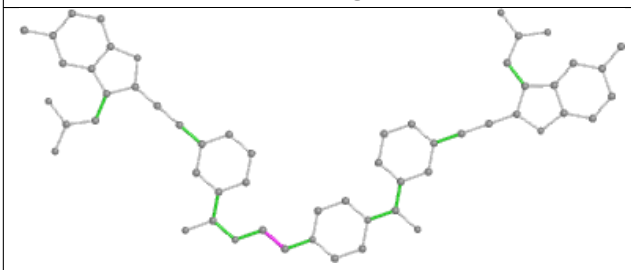
Ligand R2A B 308



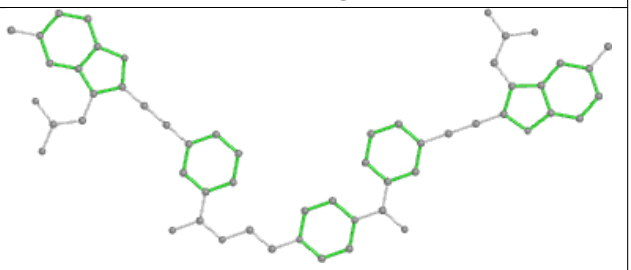
Bond lengths



Bond angles



Torsions



Rings

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	136/164 (82%)	0.13	4 (2%) 51 56	18, 35, 59, 67	0
1	B	135/164 (82%)	-0.02	0 100 100	19, 32, 56, 66	0
All	All	271/328 (82%)	0.06	4 (1%) 73 76	18, 34, 57, 67	0

All (4) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	191	ILE	3.6
1	A	142	PRO	3.6
1	A	194	TYR	2.6
1	A	56	SER	2.1

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

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
1	CSO	B	65	7/8	0.91	0.08	33,40,48,53	0
1	CSO	A	65	7/8	0.94	0.10	40,43,51,58	0

6.3 Carbohydrates

There are no monosaccharides in this entry.

6.4 Ligands (i)

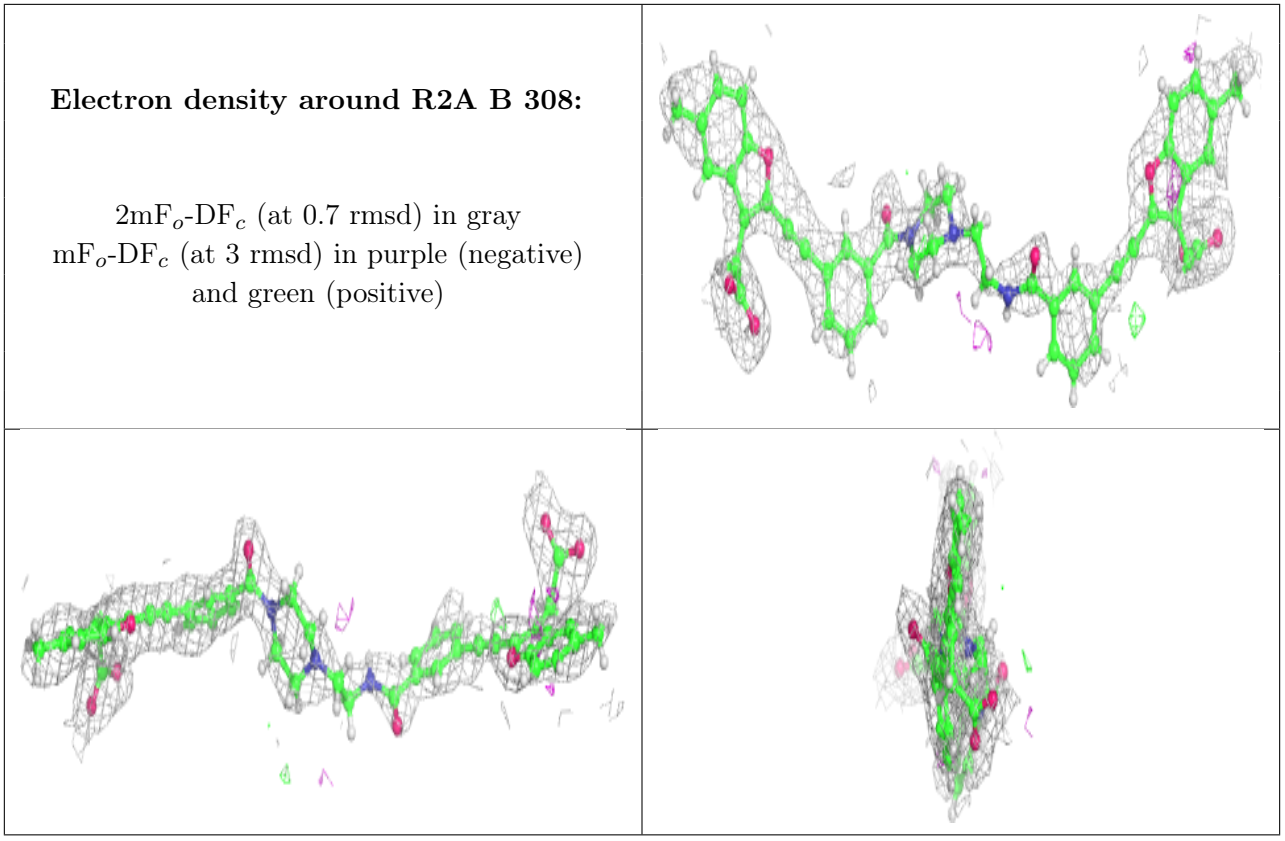
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95^{th} percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' 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
3	SO4	A	306	5/5	0.86	0.18	53,60,72,80	0
4	R2A	B	308	57/57	0.87	0.23	27,49,64,73	0
3	SO4	B	304	5/5	0.93	0.14	49,51,67,75	0
2	IOD	B	302	1/1	0.96	0.09	58,58,58,58	0
3	SO4	B	306	5/5	0.96	0.09	35,38,44,47	0
3	SO4	A	305	5/5	0.96	0.10	46,55,59,67	0
2	IOD	A	304	1/1	0.97	0.06	78,78,78,78	0
3	SO4	A	307	5/5	0.97	0.12	48,49,56,63	0
2	IOD	A	303	1/1	0.97	0.08	56,56,56,56	0
3	SO4	A	308	5/5	0.98	0.11	29,31,40,54	0
3	SO4	B	303	5/5	0.98	0.09	49,50,53,72	0
2	IOD	A	302	1/1	0.98	0.09	46,46,46,46	0
3	SO4	B	307	5/5	0.98	0.09	33,33,43,46	0
3	SO4	B	305	5/5	0.98	0.07	33,35,44,47	0
2	IOD	B	301	1/1	0.99	0.07	52,52,52,52	0
2	IOD	A	301	1/1	0.99	0.04	57,57,57,57	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 R2A B 308:

$2mF_o$-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

There are no such residues in this entry.