



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 10:52 AM GMT

PDB ID : 3NF8
Title : Structural basis for a new mechanism of inhibition of HIV integrase identified by fragment screening and structure based design
Authors : Peat, T.S.; Newman, J.; Deadman, J.J.; Rhodes, D.
Deposited on : 2010-06-09
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
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467
Mogul : 1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026688
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

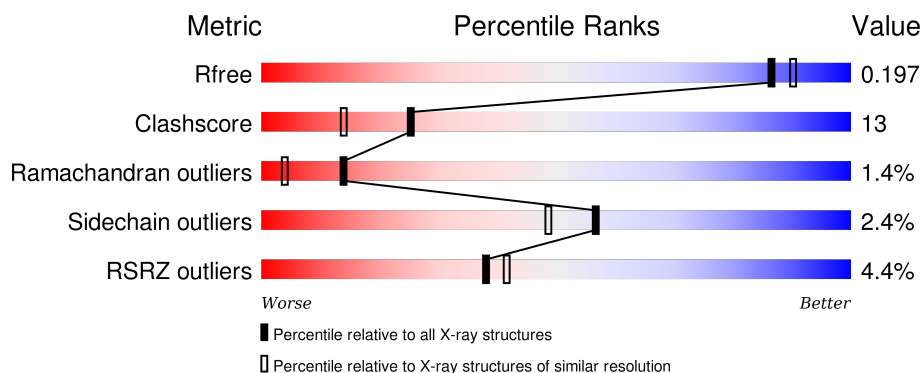
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.90 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))
R_{free}	91344	4755 (1.90-1.90)
Clashscore	102246	5398 (1.90-1.90)
Ramachandran outliers	100387	5338 (1.90-1.90)
Sidechain outliers	100360	5339 (1.90-1.90)
RSRZ outliers	91569	4766 (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 on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	183	<div> <div>4%</div> <div>64% 17% • 19%</div> </div>
1	B	183	<div> <div>3%</div> <div>62% 17% • 19%</div> </div>

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	SO4	A	5	-	-	X	-
2	SO4	B	3	-	-	X	-
3	CDQ	A	225	-	-	-	X

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 2737 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 Integrase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	149	Total	C	N	O	S	0	11	0
			1224	785	210	225	4			
1	B	149	Total	C	N	O	S	0	10	0
			1223	782	213	224	4			

There are 46 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	30	MET	-	EXPRESSION TAG	UNP Q76353
A	31	GLY	-	EXPRESSION TAG	UNP Q76353
A	32	SER	-	EXPRESSION TAG	UNP Q76353
A	33	SER	-	EXPRESSION TAG	UNP Q76353
A	34	HIS	-	EXPRESSION TAG	UNP Q76353
A	35	HIS	-	EXPRESSION TAG	UNP Q76353
A	36	HIS	-	EXPRESSION TAG	UNP Q76353
A	37	HIS	-	EXPRESSION TAG	UNP Q76353
A	38	HIS	-	EXPRESSION TAG	UNP Q76353
A	39	HIS	-	EXPRESSION TAG	UNP Q76353
A	40	SER	-	EXPRESSION TAG	UNP Q76353
A	41	SER	-	EXPRESSION TAG	UNP Q76353
A	42	GLY	-	EXPRESSION TAG	UNP Q76353
A	43	LEU	-	EXPRESSION TAG	UNP Q76353
A	44	VAL	-	EXPRESSION TAG	UNP Q76353
A	45	PRO	-	EXPRESSION TAG	UNP Q76353
A	46	ARG	-	EXPRESSION TAG	UNP Q76353
A	47	GLY	-	EXPRESSION TAG	UNP Q76353
A	48	SER	-	EXPRESSION TAG	UNP Q76353
A	49	HIS	-	EXPRESSION TAG	UNP Q76353
A	56	SER	CYS	ENGINEERED MUTATION	UNP Q76353
A	139	ASP	PHE	ENGINEERED MUTATION	UNP Q76353
A	185	HIS	PHE	ENGINEERED MUTATION	UNP Q76353
B	30	MET	-	EXPRESSION TAG	UNP Q76353
B	31	GLY	-	EXPRESSION TAG	UNP Q76353

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
B	32	SER	-	EXPRESSION TAG	UNP Q76353
B	33	SER	-	EXPRESSION TAG	UNP Q76353
B	34	HIS	-	EXPRESSION TAG	UNP Q76353
B	35	HIS	-	EXPRESSION TAG	UNP Q76353
B	36	HIS	-	EXPRESSION TAG	UNP Q76353
B	37	HIS	-	EXPRESSION TAG	UNP Q76353
B	38	HIS	-	EXPRESSION TAG	UNP Q76353
B	39	HIS	-	EXPRESSION TAG	UNP Q76353
B	40	SER	-	EXPRESSION TAG	UNP Q76353
B	41	SER	-	EXPRESSION TAG	UNP Q76353
B	42	GLY	-	EXPRESSION TAG	UNP Q76353
B	43	LEU	-	EXPRESSION TAG	UNP Q76353
B	44	VAL	-	EXPRESSION TAG	UNP Q76353
B	45	PRO	-	EXPRESSION TAG	UNP Q76353
B	46	ARG	-	EXPRESSION TAG	UNP Q76353
B	47	GLY	-	EXPRESSION TAG	UNP Q76353
B	48	SER	-	EXPRESSION TAG	UNP Q76353
B	49	HIS	-	EXPRESSION TAG	UNP Q76353
B	56	SER	CYS	ENGINEERED MUTATION	UNP Q76353
B	139	ASP	PHE	ENGINEERED MUTATION	UNP Q76353
B	185	HIS	PHE	ENGINEERED MUTATION	UNP Q76353

- Molecule 2 is SULFATE ION (three-letter code: SO4) (formula: O₄S).



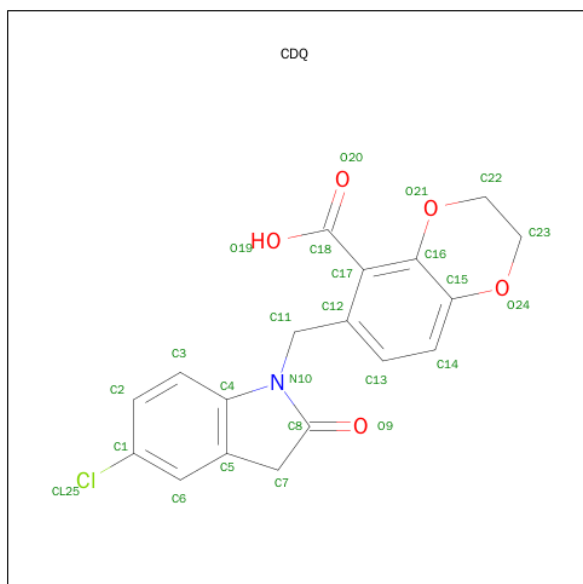
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	O	S	0	0
			5	4	1		

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	O	S	0	0
			5	4	1		
2	A	1	Total	O	S	0	0
			5	4	1		
2	B	1	Total	O	S	0	0
			5	4	1		
2	B	1	Total	O	S	0	0
			5	4	1		
2	B	1	Total	O	S	0	0
			5	4	1		

- Molecule 3 is 6-[(5-CHLORO-2-OXO-2,3-DIHYDRO-1H-INDOL-1-YL)METHYL]-2,3-DIHYDRO-1,4-BENZODIOXINE-5-CARBOXYLIC ACID (three-letter code: CDQ) (formula: $C_{18}H_{14}ClNO_5$).



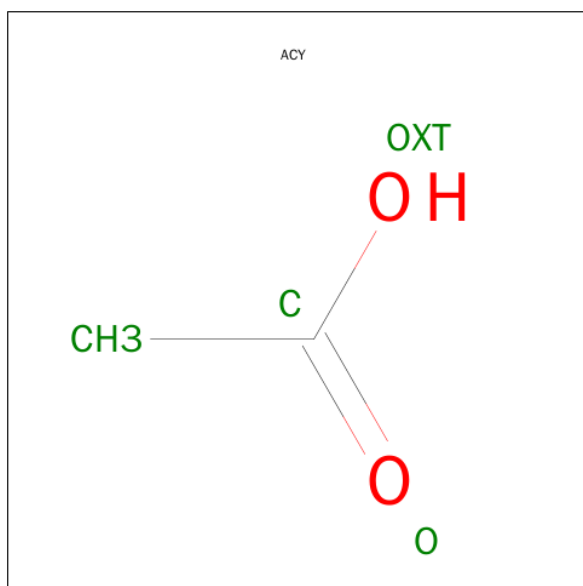
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	Cl	N	O	
			25	18	1	1	5	0
3	A	1	Total	C	Cl	N	O	
			25	18	1	1	5	0
3	A	1	Total	C	Cl	N	O	
			25	18	1	1	5	0
3	A	1	Total	C	Cl	N	O	
			25	18	1	1	5	0
3	B	1	Total	C	Cl	N	O	
			25	18	1	1	5	0

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	B	1	Total	C	Cl	N	O	0	0
			25	18	1	1	5		

- Molecule 4 is ACETIC ACID (three-letter code: ACY) (formula: C₂H₄O₂).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			4	2	2		
4	B	1	Total	C	O	0	0
			4	2	2		

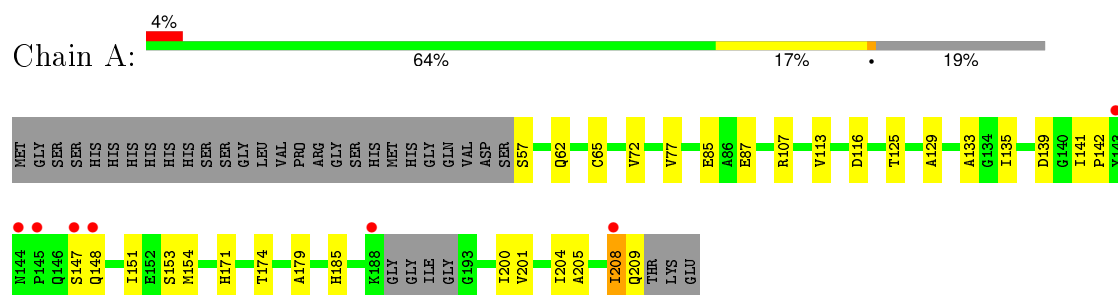
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	51	Total	O	0	0
			51	51		
5	B	51	Total	O	0	0
			51	51		

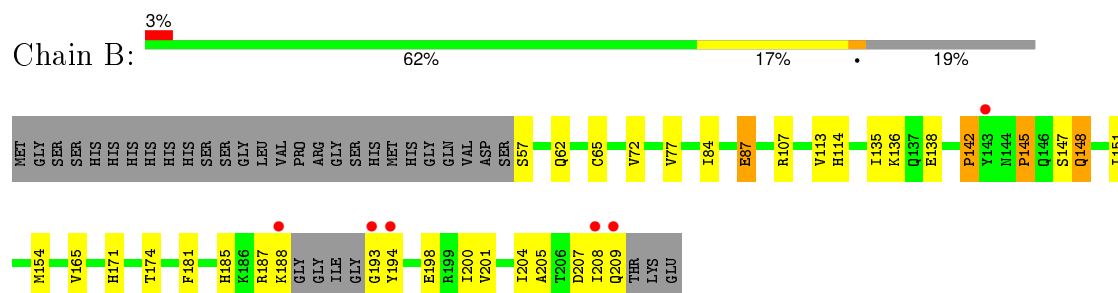
3 Residue-property plots [i](#)

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: Integrase



- Molecule 1: Integrase



4 Data and refinement statistics

Property	Value	Source
Space group	P 31	Depositor
Cell constants a, b, c, α , β , γ	71.55Å 71.55Å 67.10Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	45.52 – 1.90 45.52 – 1.90	Depositor EDS
% Data completeness (in resolution range)	100.0 (45.52-1.90) 99.9 (45.52-1.90)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.48 (at 1.89Å)	Xtriage
Refinement program	REFMAC 5.5.0102	Depositor
R, R_{free}	0.169 , 0.198 0.167 , 0.197	Depositor DCC
R_{free} test set	1532 reflections (5.33%)	DCC
Wilson B-factor (Å ²)	28.3	Xtriage
Anisotropy	0.004	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 37.6	EDS
Estimated twinning fraction	0.023 for -h,-k,l 0.487 for h,-h-k,-l 0.023 for -k,-h,-l	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.34$	Xtriage
Outliers	0 of 30264 reflections	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	2737	wwPDB-VP
Average B, all atoms (Å ²)	31.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 8.54% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.375 respectively for untwinned datasets, and 0.333, 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: ACY, SO4, CDQ

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	1.21	5/1273 (0.4%)	1.02	3/1727 (0.2%)
1	B	1.20	3/1269 (0.2%)	1.02	2/1719 (0.1%)
All	All	1.21	8/2542 (0.3%)	1.02	5/3446 (0.1%)

All (8) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	165	VAL	CB-CG1	-6.36	1.39	1.52
1	A	133	ALA	CA-CB	6.08	1.65	1.52
1	A	129	ALA	CA-CB	5.89	1.64	1.52
1	A	179	ALA	CA-CB	5.66	1.64	1.52
1	A	87[A]	GLU	CG-CD	5.36	1.59	1.51
1	A	87[B]	GLU	CG-CD	5.36	1.59	1.51
1	B	87[A]	GLU	CG-CD	5.11	1.59	1.51
1	B	87[B]	GLU	CG-CD	5.11	1.59	1.51

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	116	ASP	CB-CG-OD1	5.46	123.22	118.30
1	A	87[A]	GLU	OE1-CD-OE2	-5.32	116.92	123.30
1	A	87[B]	GLU	OE1-CD-OE2	-5.32	116.92	123.30
1	B	87[A]	GLU	OE1-CD-OE2	-5.23	117.03	123.30
1	B	87[B]	GLU	OE1-CD-OE2	-5.23	117.03	123.30

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	1224	0	1253	33	0
1	B	1223	0	1247	40	0
2	A	15	0	0	4	0
2	B	15	0	0	2	0
3	A	100	0	52	7	0
3	B	50	0	26	2	0
4	A	4	0	3	0	0
4	B	4	0	3	0	0
5	A	51	0	0	2	0
5	B	51	0	0	5	0
All	All	2737	0	2584	66	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 13.

All (66) 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:107:ARG:CD	1:B:107[B]:ARG:HH22	1.15	1.58
1:A:107:ARG:HD3	1:B:107[B]:ARG:NH2	0.92	1.25
1:A:107:ARG:CD	1:B:107[B]:ARG:NH2	1.83	1.23
2:A:5:SO4:O2	5:A:239:HOH:O	1.68	1.12
1:A:107:ARG:HD2	1:B:107[B]:ARG:HH22	1.29	0.95
1:B:62[B]:GLN:NE2	1:B:151:ILE:HD11	1.83	0.93
1:A:107:ARG:HD3	1:B:107[B]:ARG:CZ	2.00	0.91
1:A:107:ARG:HD3	1:B:107[B]:ARG:HH21	1.37	0.88
1:A:62[B]:GLN:NE2	1:A:151:ILE:HD11	1.89	0.87
1:B:194:TYR:CD1	1:B:198:GLU:OE2	2.33	0.81
1:A:204:ILE:HG23	3:A:225:CDQ:H7A	1.69	0.74
1:A:205:ALA:HA	1:A:208:ILE:HG23	1.71	0.72
1:A:62[B]:GLN:HE21	1:A:151:ILE:HD11	1.58	0.68
1:B:171:HIS:HD2	2:B:3:SO4:O1	1.79	0.66
1:B:174:THR:HG21	3:B:235:CDQ:H3	1.79	0.65
1:A:174:THR:HG21	3:A:267:CDQ:H3	1.78	0.64
1:A:204:ILE:CG2	3:A:225:CDQ:H7A	2.26	0.64

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:139:ASP:OD1	1:A:141[B]:ILE:HG23	1.98	0.64
1:B:107[B]:ARG:NH1	5:B:251:HOH:O	2.31	0.63
1:B:194:TYR:HD1	1:B:198:GLU:OE2	1.79	0.61
1:B:205:ALA:O	1:B:209:GLN:HB2	2.03	0.59
1:A:77[A]:VAL:HG21	1:A:154:MET:SD	2.43	0.59
1:A:208:ILE:HG13	1:A:209:GLN:N	2.19	0.57
1:A:185:HIS:CE1	3:A:277:CDQ:H22A	2.40	0.57
1:A:113[B]:VAL:HG23	1:A:135:ILE:CG2	2.34	0.57
1:B:107[B]:ARG:NE	5:B:5:HOH:O	2.32	0.55
1:A:85:GLU:OE1	1:B:107[B]:ARG:CZ	2.56	0.54
1:A:205:ALA:HA	1:A:208:ILE:CG2	2.38	0.54
1:A:125[B]:THR:HG23	2:A:5:SO4:O4	2.08	0.53
1:B:142:PRO:HB3	1:B:147:SER:HB2	1.89	0.53
1:B:77[A]:VAL:HG21	1:B:154:MET:SD	2.48	0.53
1:B:145:PRO:O	1:B:148:GLN:NE2	2.38	0.53
1:B:154:MET:HG3	3:B:257:CDQ:C15	2.39	0.52
1:A:113[B]:VAL:HG23	1:A:135:ILE:HG21	1.92	0.52
1:B:107[B]:ARG:NH2	5:B:5:HOH:O	2.29	0.52
1:B:187:ARG:HD2	1:B:193:GLY:O	2.10	0.51
1:A:154:MET:HG3	3:A:247:CDQ:C15	2.42	0.50
1:A:171:HIS:HD2	2:A:4:SO4:O3	1.95	0.49
1:A:65:CYS:SG	1:A:72:VAL:HG13	2.51	0.49
1:B:65:CYS:SG	1:B:72:VAL:HG13	2.53	0.49
1:B:181:PHE:O	1:B:185:HIS:HD2	1.95	0.49
1:A:125[A]:THR:OG1	2:A:5:SO4:O4	2.20	0.49
1:B:113[A]:VAL:HG23	1:B:135:ILE:CG2	2.45	0.47
1:B:187:ARG:CG	1:B:193:GLY:O	2.63	0.47
1:A:201:VAL:HG12	1:B:205:ALA:HB2	1.98	0.46
1:B:142:PRO:HG3	1:B:148:GLN:HG3	1.98	0.45
3:A:277:CDQ:H7A	1:B:204:ILE:HG23	1.98	0.45
1:B:87[B]:GLU:OE1	5:B:213:HOH:O	2.21	0.44
1:B:200:ILE:HG12	1:B:204:ILE:HD12	1.99	0.44
1:B:113[A]:VAL:HG23	1:B:135:ILE:HG21	2.00	0.44
1:A:200:ILE:HG12	1:A:204:ILE:HD12	2.00	0.43
1:B:114[A]:HIS:CE1	1:B:138:GLU:OE2	2.72	0.43
1:A:205:ALA:CA	1:A:208:ILE:HG23	2.46	0.43
1:B:142:PRO:HG3	1:B:148:GLN:CG	2.49	0.42
1:A:205:ALA:HB2	1:B:201:VAL:HG12	2.01	0.42
1:A:142:PRO:HG3	1:A:148:GLN:CG	2.49	0.42
1:B:77[A]:VAL:HG22	1:B:84:ILE:HG22	2.01	0.42
1:B:57:SER:N	5:B:242:HOH:O	2.52	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:62[B]:GLN:HE21	1:B:151:ILE:HD11	1.77	0.41
1:A:77[A]:VAL:CG2	1:A:154:MET:SD	3.08	0.41
1:B:171:HIS:CD2	2:B:3:SO4:O1	2.67	0.41
1:A:141[B]:ILE:HA	1:A:142:PRO:HD2	1.79	0.41
1:B:187:ARG:CD	1:B:193:GLY:O	2.70	0.40
3:A:247:CDQ:H11A	5:A:237:HOH:O	2.22	0.40
1:A:113[B]:VAL:CG2	1:A:135:ILE:HG21	2.50	0.40
1:B:136[B]:LYS:HE2	1:B:136[B]:LYS:HB3	1.79	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	156/183 (85%)	152 (97%)	4 (3%)	0	100	100
1	B	155/183 (85%)	150 (97%)	1 (1%)	4 (3%)	7	1
All	All	311/366 (85%)	302 (97%)	5 (2%)	4 (1%)	14	4

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	207	ASP
1	B	208	ILE
1	B	142	PRO
1	B	145	PRO

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	134/150 (89%)	130 (97%)	4 (3%)	48	38
1	B	133/150 (89%)	131 (98%)	2 (2%)	72	69
All	All	267/300 (89%)	261 (98%)	6 (2%)	57	53

All (6) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	57	SER
1	A	147	SER
1	A	153	SER
1	A	208	ILE
1	B	148	GLN
1	B	188	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	171	HIS
1	A	209	GLN
1	B	137	GLN
1	B	171	HIS
1	B	185	HIS

5.3.3 RNA ⓘ

There are no RNA molecules 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

14 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
4	ACY	A	1	-	1,3,3	3.41	1 (100%)	0,3,3	0.00	-
2	SO4	A	2	-	4,4,4	0.74	0	6,6,6	0.66	0
3	CDQ	A	225	-	24,28,28	1.01	2 (8%)	31,41,41	1.61	3 (9%)
3	CDQ	A	247	-	24,28,28	1.00	1 (4%)	31,41,41	2.18	10 (32%)
3	CDQ	A	267	-	24,28,28	1.00	2 (8%)	31,41,41	1.73	7 (22%)
3	CDQ	A	277	-	24,28,28	1.30	2 (8%)	31,41,41	2.52	9 (29%)
2	SO4	A	4	-	4,4,4	0.36	0	6,6,6	0.43	0
2	SO4	A	5	-	4,4,4	0.71	0	6,6,6	0.36	0
2	SO4	B	1	-	4,4,4	0.76	0	6,6,6	0.39	0
4	ACY	B	2	-	1,3,3	2.98	1 (100%)	0,3,3	0.00	-
3	CDQ	B	235	-	24,28,28	1.06	2 (8%)	31,41,41	1.76	9 (29%)
3	CDQ	B	257	-	24,28,28	1.17	2 (8%)	31,41,41	2.40	13 (41%)
2	SO4	B	3	-	4,4,4	0.18	0	6,6,6	0.30	0
2	SO4	B	6	-	4,4,4	0.35	0	6,6,6	0.85	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	ACY	A	1	-	-	0/0/0/0	0/0/0/0
2	SO4	A	2	-	-	0/0/0/0	0/0/0/0
3	CDQ	A	225	-	-	0/4/27/27	0/4/4/4
3	CDQ	A	247	-	-	0/4/27/27	0/4/4/4
3	CDQ	A	267	-	-	0/4/27/27	0/4/4/4
3	CDQ	A	277	-	-	0/4/27/27	0/4/4/4
2	SO4	A	4	-	-	0/0/0/0	0/0/0/0
2	SO4	A	5	-	-	0/0/0/0	0/0/0/0
2	SO4	B	1	-	-	0/0/0/0	0/0/0/0

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	ACY	B	2	-	-	0/0/0/0	0/0/0/0
3	CDQ	B	235	-	-	0/4/27/27	0/4/4/4
3	CDQ	B	257	-	-	0/4/27/27	0/4/4/4
2	SO4	B	3	-	-	0/0/0/0	0/0/0/0
2	SO4	B	6	-	-	0/0/0/0	0/0/0/0

All (13) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	235	CDQ	O24-C15	-2.85	1.34	1.37
3	A	267	CDQ	C4-C5	-2.82	1.35	1.39
3	A	267	CDQ	O24-C15	-2.39	1.35	1.37
3	B	235	CDQ	C4-C5	-2.38	1.36	1.39
3	B	257	CDQ	O24-C23	2.03	1.48	1.43
3	A	225	CDQ	C8-N10	2.17	1.39	1.36
3	A	225	CDQ	O24-C23	2.23	1.49	1.43
3	B	257	CDQ	C8-N10	2.43	1.39	1.36
3	A	247	CDQ	C8-N10	2.43	1.39	1.36
3	A	277	CDQ	O24-C23	2.44	1.49	1.43
4	B	2	ACY	CH3-C	2.98	1.52	1.48
4	A	1	ACY	CH3-C	3.41	1.53	1.48
3	A	277	CDQ	C8-N10	4.33	1.42	1.36

All (51) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	257	CDQ	C4-N10-C8	-4.87	108.50	111.13
3	A	277	CDQ	C4-N10-C8	-4.79	108.55	111.13
3	A	247	CDQ	C4-N10-C8	-4.72	108.58	111.13
3	A	247	CDQ	C2-C1-CL25	-3.81	113.11	119.35
3	B	257	CDQ	C1-C6-C5	-3.76	114.49	119.97
3	B	257	CDQ	C2-C1-CL25	-3.46	113.68	119.35
3	A	267	CDQ	C11-N10-C4	-3.31	118.56	124.88
3	A	247	CDQ	C11-C12-C13	-3.29	113.73	120.16
3	B	235	CDQ	C11-N10-C4	-3.19	118.79	124.88
3	A	277	CDQ	C1-C6-C5	-3.05	115.53	119.97
3	A	277	CDQ	C7-C5-C6	-2.90	124.86	129.61
3	A	247	CDQ	C1-C6-C5	-2.90	115.75	119.97
3	B	235	CDQ	C13-C14-C15	-2.76	114.69	120.03
3	A	247	CDQ	O21-C16-C15	-2.70	118.14	121.62
3	A	267	CDQ	C3-C4-N10	-2.45	125.63	130.79
3	A	267	CDQ	C1-C6-C5	-2.30	116.61	119.97

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	235	CDQ	C1-C6-C5	-2.30	116.62	119.97
3	B	235	CDQ	C3-C4-N10	-2.27	126.00	130.79
3	B	235	CDQ	C4-N10-C8	-2.26	109.91	111.13
3	A	225	CDQ	C1-C6-C5	-2.19	116.78	119.97
3	B	257	CDQ	C2-C3-C4	-2.15	114.58	119.29
3	A	247	CDQ	C3-C4-N10	-2.14	126.29	130.79
3	A	277	CDQ	C13-C14-C15	-2.10	115.96	120.03
3	A	277	CDQ	O24-C15-C16	-2.04	120.34	121.90
3	A	267	CDQ	C13-C14-C15	-2.03	116.10	120.03
3	A	277	CDQ	C22-O21-C16	-2.02	108.43	113.90
3	B	257	CDQ	C22-O21-C16	2.01	119.33	113.90
3	B	235	CDQ	C3-C4-C5	2.06	123.65	121.54
3	B	235	CDQ	C14-C15-C16	2.14	124.08	120.33
3	A	267	CDQ	C3-C4-C5	2.33	123.92	121.54
3	B	257	CDQ	O24-C15-C14	2.35	120.60	116.73
3	B	257	CDQ	O21-C22-C23	2.36	120.65	112.00
3	A	247	CDQ	C3-C2-C1	2.67	122.20	119.23
3	B	235	CDQ	C11-N10-C8	2.70	127.43	122.94
3	A	267	CDQ	C11-N10-C8	2.90	127.75	122.94
3	B	257	CDQ	C7-C8-N10	3.06	109.31	107.87
3	B	257	CDQ	C3-C2-C1	3.26	122.86	119.23
3	A	277	CDQ	C12-C11-N10	3.37	117.86	113.17
3	A	247	CDQ	C23-O24-C15	3.47	120.06	113.90
3	B	257	CDQ	C23-O24-C15	3.63	120.34	113.90
3	A	247	CDQ	C7-C8-N10	3.65	109.58	107.87
3	B	257	CDQ	C6-C1-CL25	3.78	123.84	119.14
3	A	225	CDQ	O9-C8-N10	3.92	128.49	125.47
3	B	257	CDQ	O9-C8-N10	4.23	128.73	125.47
3	A	225	CDQ	C6-C5-C4	4.32	122.47	120.33
3	A	247	CDQ	C6-C1-CL25	4.44	124.65	119.14
3	B	257	CDQ	C6-C5-C4	4.49	122.56	120.33
3	B	235	CDQ	C12-C11-N10	4.50	119.44	113.17
3	A	267	CDQ	C12-C11-N10	5.28	120.53	113.17
3	A	277	CDQ	C6-C5-C4	6.91	123.76	120.33
3	A	277	CDQ	O9-C8-N10	7.92	131.57	125.47

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

9 monomers are involved in 15 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	225	CDQ	2	0
3	A	247	CDQ	2	0
3	A	267	CDQ	1	0
3	A	277	CDQ	2	0
2	A	4	SO4	1	0
2	A	5	SO4	3	0
3	B	235	CDQ	1	0
3	B	257	CDQ	1	0
2	B	3	SO4	2	0

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data [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	149/183 (81%)	-0.24	7 (4%) 35 38	17, 26, 62, 76	21 (14%)
1	B	149/183 (81%)	-0.19	6 (4%) 42 46	17, 26, 65, 75	22 (14%)
All	All	298/366 (81%)	-0.21	13 (4%) 38 41	17, 26, 65, 76	43 (14%)

All (13) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	143	TYR	6.0
1	B	143	TYR	5.9
1	B	193	GLY	5.9
1	A	188	LYS	5.7
1	B	208	ILE	4.9
1	B	194	TYR	3.1
1	A	144	ASN	2.6
1	A	148	GLN	2.4
1	A	145	PRO	2.4
1	A	147	SER	2.4
1	B	209	GLN	2.3
1	B	188	LYS	2.0
1	A	208	ILE	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 carbohydrates in this entry.

6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(Å ²)	Q<0.9
3	CDQ	A	225	25/25	0.84	0.17	2.07	27,35,48,55	25
3	CDQ	A	277	25/25	0.80	0.18	1.29	26,35,48,56	25
3	CDQ	B	257	25/25	0.88	0.15	0.93	27,36,40,45	25
2	SO4	B	1	5/5	0.98	0.12	0.49	32,33,40,40	5
3	CDQ	A	267	25/25	0.95	0.10	0.32	21,30,33,37	25
2	SO4	B	6	5/5	0.98	0.10	0.30	39,46,48,49	5
3	CDQ	B	235	25/25	0.95	0.09	0.23	21,30,32,34	25
3	CDQ	A	247	25/25	0.88	0.14	0.23	27,34,43,45	25
4	ACY	B	2	4/4	0.97	0.10	0.21	44,45,46,46	0
2	SO4	A	2	5/5	0.98	0.10	0.16	31,35,39,40	5
2	SO4	A	4	5/5	0.97	0.08	-0.74	28,37,41,44	5
4	ACY	A	1	4/4	0.94	0.08	-0.79	40,41,42,43	0
2	SO4	B	3	5/5	0.98	0.07	-0.96	30,42,45,45	5
2	SO4	A	5	5/5	0.98	0.08	-1.25	39,46,49,50	5

6.5 Other polymers [i](#)

There are no such residues in this entry.