



Full wwPDB X-ray Structure Validation Report ⓘ

Oct 25, 2017 – 08:31 PM EDT

PDB ID : 3KL3
Title : Crystal structure of Ligand bound XynC
Authors : St John, F.J.; Hurlbert, J.C.; Pozharski, E.
Deposited on : unknown
Resolution : 2.33 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 : 1.7.2 (RC1), CSD as538be (2017)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20030345
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)
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) : rb-20030345

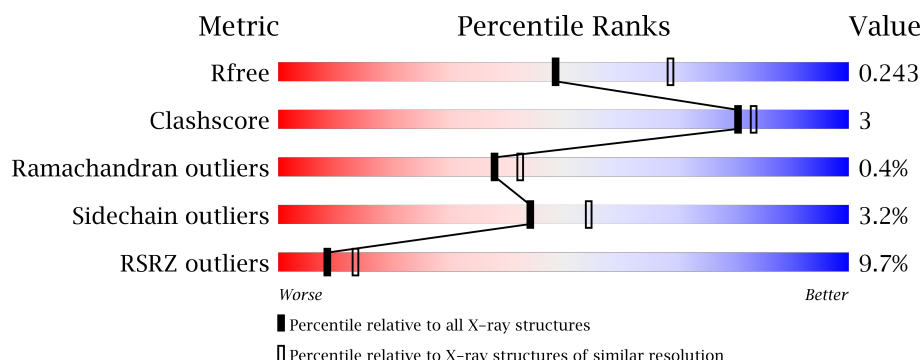
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.33 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}	100719	1570 (2.36-2.32)
Clashscore	112137	1673 (2.36-2.32)
Ramachandran outliers	110173	1654 (2.36-2.32)
Sidechain outliers	110143	1655 (2.36-2.32)
RSRZ outliers	101464	1576 (2.36-2.32)

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	401	<div> <div>2%</div> <div>90%</div> <div>6%</div> <div>• •</div> </div>
1	B	401	<div> <div>90%</div> <div>7%</div> <div>•</div> </div>
1	C	401	<div> <div>2%</div> <div>89%</div> <div>7%</div> <div>•</div> </div>
1	D	401	<div> <div>33%</div> <div>77%</div> <div>13%</div> <div>• 8%</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 crite-

ria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	GCU	B	403	-	-	-	X
3	DHI	A	403	-	-	-	X
3	DHI	B	404	-	-	-	X
4	BDP	B	402	-	-	-	X
5	PG4	B	405	-	-	-	X

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 12822 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 Glucuronoxylanase xynC.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	389	Total	C	N	O	S	0	0	0
			3095	1959	547	580	9			
1	B	390	Total	C	N	O	S	0	1	0
			3112	1970	551	582	9			
1	C	390	Total	C	N	O	S	0	4	0
			3133	1983	556	585	9			
1	D	368	Total	C	N	O	S	0	0	0
			2940	1869	514	548	9			

There are 44 discrepancies between the modelled and reference sequences:

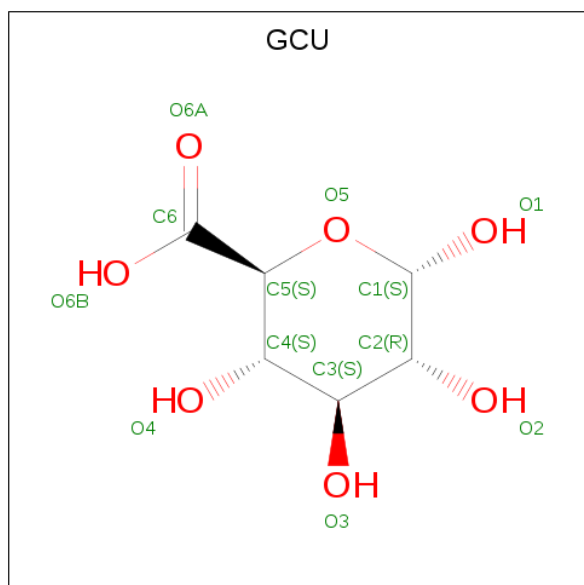
Chain	Residue	Modelled	Actual	Comment	Reference
A	1	MET	-	EXPRESSION TAG	UNP Q45070
A	392	LEU	-	EXPRESSION TAG	UNP Q45070
A	393	GLU	-	EXPRESSION TAG	UNP Q45070
A	394	HIS	-	EXPRESSION TAG	UNP Q45070
A	395	HIS	-	EXPRESSION TAG	UNP Q45070
A	396	HIS	-	EXPRESSION TAG	UNP Q45070
A	397	HIS	-	EXPRESSION TAG	UNP Q45070
A	398	HIS	-	EXPRESSION TAG	UNP Q45070
A	399	HIS	-	EXPRESSION TAG	UNP Q45070
A	400	HIS	-	EXPRESSION TAG	UNP Q45070
A	401	HIS	-	EXPRESSION TAG	UNP Q45070
B	1	MET	-	EXPRESSION TAG	UNP Q45070
B	392	LEU	-	EXPRESSION TAG	UNP Q45070
B	393	GLU	-	EXPRESSION TAG	UNP Q45070
B	394	HIS	-	EXPRESSION TAG	UNP Q45070
B	395	HIS	-	EXPRESSION TAG	UNP Q45070
B	396	HIS	-	EXPRESSION TAG	UNP Q45070
B	397	HIS	-	EXPRESSION TAG	UNP Q45070
B	398	HIS	-	EXPRESSION TAG	UNP Q45070
B	399	HIS	-	EXPRESSION TAG	UNP Q45070
B	400	HIS	-	EXPRESSION TAG	UNP Q45070

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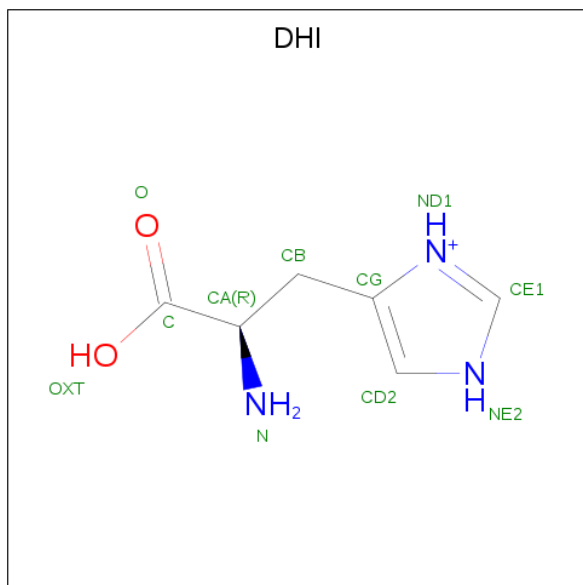
Chain	Residue	Modelled	Actual	Comment	Reference
B	401	HIS	-	EXPRESSION TAG	UNP Q45070
C	1	MET	-	EXPRESSION TAG	UNP Q45070
C	392	LEU	-	EXPRESSION TAG	UNP Q45070
C	393	GLU	-	EXPRESSION TAG	UNP Q45070
C	394	HIS	-	EXPRESSION TAG	UNP Q45070
C	395	HIS	-	EXPRESSION TAG	UNP Q45070
C	396	HIS	-	EXPRESSION TAG	UNP Q45070
C	397	HIS	-	EXPRESSION TAG	UNP Q45070
C	398	HIS	-	EXPRESSION TAG	UNP Q45070
C	399	HIS	-	EXPRESSION TAG	UNP Q45070
C	400	HIS	-	EXPRESSION TAG	UNP Q45070
C	401	HIS	-	EXPRESSION TAG	UNP Q45070
D	1	MET	-	EXPRESSION TAG	UNP Q45070
D	392	LEU	-	EXPRESSION TAG	UNP Q45070
D	393	GLU	-	EXPRESSION TAG	UNP Q45070
D	394	HIS	-	EXPRESSION TAG	UNP Q45070
D	395	HIS	-	EXPRESSION TAG	UNP Q45070
D	396	HIS	-	EXPRESSION TAG	UNP Q45070
D	397	HIS	-	EXPRESSION TAG	UNP Q45070
D	398	HIS	-	EXPRESSION TAG	UNP Q45070
D	399	HIS	-	EXPRESSION TAG	UNP Q45070
D	400	HIS	-	EXPRESSION TAG	UNP Q45070
D	401	HIS	-	EXPRESSION TAG	UNP Q45070

- Molecule 2 is D-GLUCURONIC ACID (three-letter code: GCU) (formula: $C_6H_{10}O_7$).



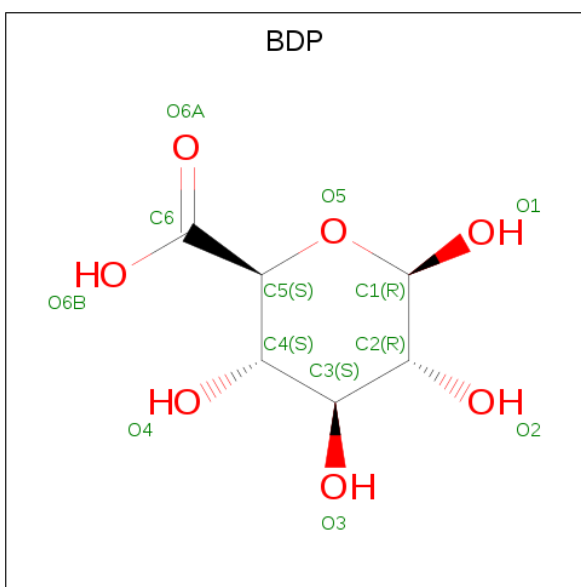
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	C	O	0	0
			13	6	7		
2	B	1	Total	C	O	0	0
			13	6	7		

- Molecule 3 is D-HISTIDINE (three-letter code: DHI) (formula: $C_6H_{10}N_3O_2$).



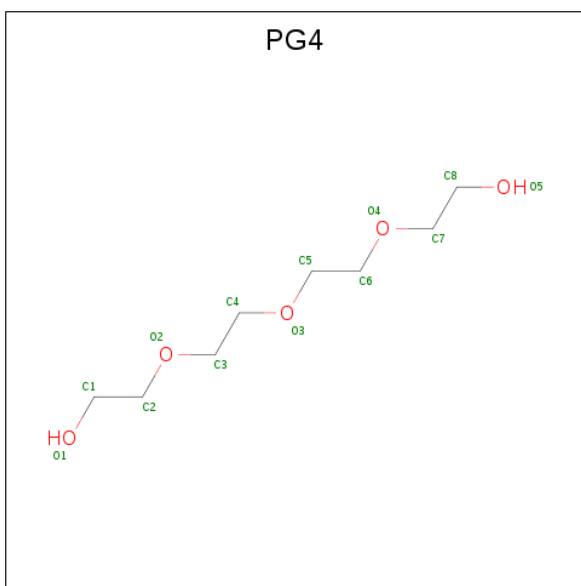
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	0	0
			11	6	3	2		
3	B	1	Total	C	N	O	0	0
			11	6	3	2		

- Molecule 4 is BETA-D-GLUCOPYRANURONIC ACID (three-letter code: BDP) (formula: $C_6H_{10}O_7$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	B	1	Total	C	O	0	0
			13	6	7		

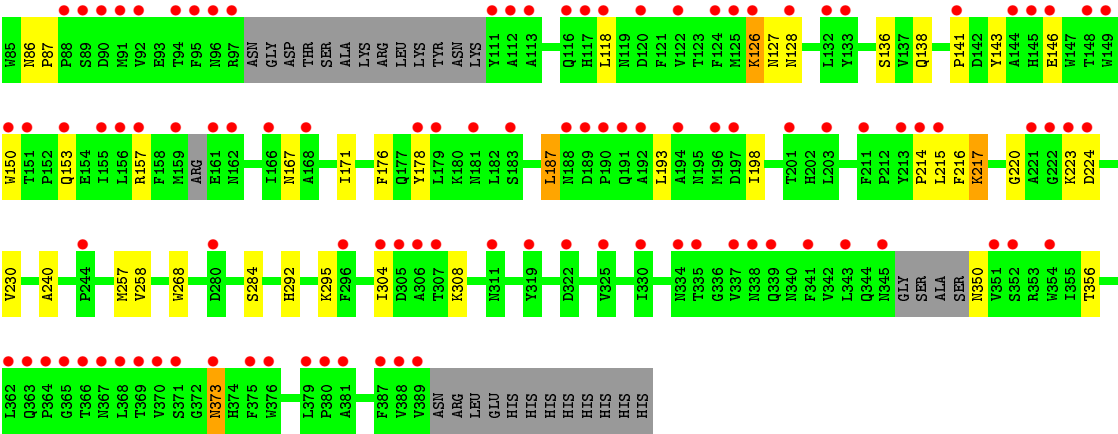
- Molecule 5 is TETRAETHYLENE GLYCOL (three-letter code: PG4) (formula: $C_8H_{18}O_5$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	B	1	Total	C	O	0	0
			13	8	5		
5	C	1	Total	C	O	0	0
			10	6	4		

- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	112	Total 112	O 112	0	0
6	B	189	Total 189	O 189	0	0
6	C	156	Total 157	O 157	0	1



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α , β , γ	137.87Å 192.73Å 65.55Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	50.00 – 2.33 38.20 – 2.33	Depositor EDS
% Data completeness (in resolution range)	99.7 (50.00-2.33) 99.8 (38.20-2.33)	Depositor EDS
R_{merge}	0.14	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.49 (at 2.34Å)	Xtriage
Refinement program	REFMAC 5.5.0102	Depositor
R, R_{free}	0.195 , 0.248 0.193 , 0.243	Depositor DCC
R_{free} test set	3791 reflections (5.30%)	DCC
Wilson B-factor (Å ²)	36.2	Xtriage
Anisotropy	0.097	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 52.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	12822	wwPDB-VP
Average B, all atoms (Å ²)	42.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.98% 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, 0.333 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: PG4, GCU, BDP, DHI

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	0.52	0/3182	0.59	0/4335
1	B	0.57	0/3202	0.64	1/4361 (0.0%)
1	C	0.54	0/3229	0.62	0/4397
1	D	0.40	0/3023	0.51	1/4119 (0.0%)
All	All	0.51	0/12636	0.59	2/17212 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	187	LEU	CA-CB-CG	5.62	128.23	115.30
1	B	368	LEU	CA-CB-CG	5.20	127.27	115.30

There are no chirality outliers.

There are no planarity outliers.

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	3095	0	2950	13	0
1	B	3112	0	2974	23	0
1	C	3133	0	2999	17	0
1	D	2940	0	2792	25	0
2	A	13	0	9	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	B	13	0	9	1	0
3	A	11	0	9	2	0
3	B	11	0	9	0	0
4	B	13	0	9	0	0
5	B	13	0	18	6	0
5	C	10	0	13	1	0
6	A	112	0	0	0	0
6	B	189	0	0	1	0
6	C	157	0	0	0	0
All	All	12822	0	11791	75	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 3.

All (75) 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:103:ALA:HA	2:B:403:GCU:H1	1.42	1.01
1:A:141:PRO:HG2	1:A:182:LEU:HD21	1.71	0.72
1:B:282:THR:HB	5:B:405:PG4:H11	1.71	0.72
1:B:363:GLN:NE2	6:B:481:HOH:O	2.00	0.72
1:B:283:ILE:H	5:B:405:PG4:H32	1.57	0.70
1:C:331:ASN:ND2	1:C:337:VAL:HG12	2.11	0.66
1:C:96:ASN:HD21	5:C:402:PG4:H52	1.59	0.66
1:B:353:ARG:HE	1:B:368:LEU:HD21	1.62	0.65
1:B:335:THR:HG23	1:C:168:ALA:HA	1.81	0.63
1:D:240:ALA:HB1	1:D:284:SER:HB2	1.80	0.62
1:C:363[A]:GLN:HE21	1:C:363[A]:GLN:HA	1.64	0.62
1:D:46:GLN:O	1:D:295:LYS:HE2	2.01	0.61
1:C:240:ALA:HB1	1:C:284:SER:HB2	1.83	0.61
1:D:171:ILE:HG12	1:D:198:ILE:HB	1.82	0.61
1:B:283:ILE:H	5:B:405:PG4:C3	2.12	0.61
1:D:138:GLN:HE21	1:D:150:TRP:HE1	1.49	0.60
1:C:38:THR:HA	1:C:46:GLN:HG2	1.85	0.59
1:C:240:ALA:HB1	1:C:284:SER:CB	2.32	0.59
1:D:258:VAL:HG11	1:D:308:LYS:HG2	1.86	0.58
1:B:141:PRO:HG2	1:B:182:LEU:HD21	1.86	0.58
1:D:8:ASN:O	1:D:304:ILE:HB	2.06	0.56
1:D:138:GLN:HG2	1:D:141:PRO:HB3	1.88	0.55
1:B:282:THR:HB	5:B:405:PG4:C1	2.36	0.55
1:B:324:LYS:HZ2	1:B:324:LYS:HB2	1.70	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:240:ALA:HB1	1:D:284:SER:CB	2.39	0.53
1:A:119:ASN:ND2	1:A:166:ILE:HA	2.24	0.53
1:A:22:MET:SD	1:A:53:ARG:HD3	2.49	0.52
1:A:322:ASP:H	3:A:403:DHI:HB2	1.74	0.52
1:B:207:GLN:HG3	1:C:218[B]:GLN:HA	1.90	0.52
1:B:353:ARG:NE	1:B:368:LEU:HD21	2.24	0.52
1:A:140:GLU:OE2	1:A:202:HIS:HD2	1.93	0.52
1:D:43:GLY:H	1:D:46:GLN:HE21	1.59	0.50
1:D:84:PRO:HG3	1:D:118:LEU:HD21	1.94	0.49
1:D:198:ILE:HG12	1:D:224:ASP:HB2	1.94	0.49
1:D:193:LEU:HD22	1:D:223:LYS:HE3	1.95	0.48
1:A:366:THR:HG22	1:A:367:ASN:O	2.14	0.47
1:B:207:GLN:HG3	1:C:218[A]:GLN:HA	1.94	0.47
1:D:143:TYR:HB2	1:D:176:PHE:CD1	2.50	0.47
1:D:292:HIS:HE1	1:D:356:THR:OG1	1.98	0.47
1:B:351:VAL:HB	1:B:368:LEU:HB2	1.97	0.47
1:A:353:ARG:HD2	1:A:355:ILE:HD11	1.97	0.46
1:B:282:THR:HG22	5:B:405:PG4:H61	1.98	0.46
1:A:40:PHE:HZ	1:A:52:LEU:HD13	1.81	0.46
1:C:83:SER:HA	1:C:136:SER:HB3	1.96	0.46
1:D:214:PRO:O	1:D:217:LYS:HG3	2.16	0.45
1:C:138:GLN:HG2	1:C:150:TRP:CD1	2.52	0.45
1:B:240:ALA:HB1	1:B:284:SER:HB2	1.98	0.45
1:C:141:PRO:HG2	1:C:182:LEU:HD21	1.99	0.45
1:A:322:ASP:HB2	3:A:403:DHI:HD2	1.99	0.45
1:D:126:LYS:HD2	1:D:127:ASN:HD22	1.81	0.44
1:A:119:ASN:HD21	1:A:166:ILE:HA	1.82	0.44
1:C:363[A]:GLN:NE2	1:C:363[A]:GLN:HA	2.31	0.44
1:D:86:ASN:HA	1:D:87:PRO:HD2	1.80	0.44
1:B:240:ALA:HB1	1:B:284:SER:CB	2.48	0.43
1:B:309:ASN:HB3	1:C:15:VAL:HG21	2.00	0.43
1:C:6:THR:O	1:C:306:ALA:HA	2.18	0.43
1:D:373:ASN:H	1:D:373:ASN:HD22	1.67	0.42
1:B:291:ALA:HA	1:B:294:SER:OG	2.19	0.42
1:D:67:VAL:HG21	1:D:128:ASN:HD22	1.84	0.42
1:D:40:PHE:CZ	1:D:52:LEU:HG	2.55	0.42
1:B:332:LYS:HE2	1:B:332:LYS:HB3	1.93	0.41
1:A:141:PRO:HB2	1:A:150:TRP:HB2	2.02	0.41
1:C:211:PHE:N	1:C:212:PRO:CD	2.83	0.41
1:D:83:SER:HA	1:D:136:SER:HB3	2.01	0.41
5:B:405:PG4:H11	5:B:405:PG4:H31	1.78	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:301:TYR:OH	1:B:324:LYS:NZ	2.52	0.41
1:B:6:THR:O	1:B:306:ALA:HA	2.21	0.41
1:C:296:PHE:CG	1:C:386:THR:HG21	2.56	0.41
1:A:125:MET:HB2	1:A:132:LEU:HD22	2.03	0.40
1:D:24:HIS:HA	1:D:25:PRO:HD3	1.92	0.40
1:D:373:ASN:HD22	1:D:373:ASN:N	2.19	0.40
1:A:361:ASN:O	1:A:362:LEU:C	2.58	0.40
1:D:216:PHE:O	1:D:220:GLY:N	2.52	0.40
1:B:138:GLN:HG2	1:B:150:TRP:CD1	2.57	0.40
1:D:36:ARG:HD3	1:D:69:THR:HA	2.02	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	387/401 (96%)	370 (96%)	15 (4%)	2 (0%)	32	35
1	B	389/401 (97%)	377 (97%)	11 (3%)	1 (0%)	44	51
1	C	392/401 (98%)	381 (97%)	10 (3%)	1 (0%)	44	51
1	D	360/401 (90%)	338 (94%)	20 (6%)	2 (1%)	28	30
All	All	1528/1604 (95%)	1466 (96%)	56 (4%)	6 (0%)	38	42

All (6) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	268	TRP
1	D	268	TRP
1	C	268	TRP
1	D	64	TYR
1	A	147	TRP

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Mol	Chain	Res	Type
1	A	268	TRP

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	329/341 (96%)	321 (98%)	8 (2%)	54	66
1	B	332/341 (97%)	326 (98%)	6 (2%)	64	76
1	C	334/341 (98%)	323 (97%)	11 (3%)	43	53
1	D	313/341 (92%)	295 (94%)	18 (6%)	23	27
All	All	1308/1364 (96%)	1265 (97%)	43 (3%)	44	53

All (43) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	44	GLN
1	A	132	LEU
1	A	178	TYR
1	A	202	HIS
1	A	213	TYR
1	A	230	VAL
1	A	343	LEU
1	A	362	LEU
1	B	58	GLU
1	B	178	TYR
1	B	187	LEU
1	B	230	VAL
1	B	251	GLN
1	B	368	LEU
1	C	178	TYR
1	C	209	SER
1	C	210	GLN
1	C	213	TYR
1	C	230	VAL
1	C	337	VAL

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Mol	Chain	Res	Type
1	C	343	LEU
1	C	350	ASN
1	C	363[A]	GLN
1	C	363[B]	GLN
1	C	382	GLN
1	D	13	LYS
1	D	17	ARG
1	D	52	LEU
1	D	54	ILE
1	D	56	VAL
1	D	126	LYS
1	D	146	GLU
1	D	153	GLN
1	D	157	ARG
1	D	167	ASN
1	D	178	TYR
1	D	187	LEU
1	D	215	LEU
1	D	217	LYS
1	D	230	VAL
1	D	257	MET
1	D	350	ASN
1	D	373	ASN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (12) such sidechains are listed below:

Mol	Chain	Res	Type
1	D	24	HIS
1	D	46	GLN
1	D	55	HIS
1	D	127	ASN
1	D	138	GLN
1	D	167	ASN
1	D	181	ASN
1	D	195	ASN
1	D	251	GLN
1	D	292	HIS
1	D	339	GLN
1	D	373	ASN

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 ⓘ

7 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	GCU	A	402	-	10,13,13	0.62	0	15,19,19	2.23	3 (20%)
3	DHI	A	403	-	3,11,11	0.55	0	3,14,14	0.74	0
4	BDP	B	402	-	10,13,13	0.47	0	15,19,19	1.14	2 (13%)
2	GCU	B	403	-	10,13,13	0.57	0	15,19,19	2.25	4 (26%)
3	DHI	B	404	-	3,11,11	0.70	0	3,14,14	1.02	0
5	PG4	B	405	-	12,12,12	0.50	0	11,11,11	0.37	0
5	PG4	C	402	-	9,9,12	0.47	0	8,8,11	0.37	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	GCU	A	402	-	-	0/0/24/24	0/1/1/1
3	DHI	A	403	-	-	0/4/8/8	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	BDP	B	402	-	-	0/0/24/24	0/1/1/1
2	GCU	B	403	-	-	0/0/24/24	0/1/1/1
3	DHI	B	404	-	-	0/4/8/8	0/1/1/1
5	PG4	B	405	-	-	0/10/10/10	0/0/0/0
5	PG4	C	402	-	-	0/7/7/10	0/0/0/0

There are no bond length outliers.

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	B	402	BDP	C1-C2-C3	-2.07	106.91	110.65
2	B	403	GCU	C1-C2-C3	2.08	114.41	110.65
4	B	402	BDP	O5-C5-C4	2.12	112.50	108.91
2	A	402	GCU	O5-C5-C4	2.65	113.38	108.91
2	B	403	GCU	O5-C5-C4	3.31	114.50	108.91
2	A	402	GCU	O5-C1-C2	3.44	115.75	110.04
2	B	403	GCU	O5-C1-C2	4.69	117.83	110.04
2	B	403	GCU	C1-O5-C5	6.01	121.07	112.22
2	A	402	GCU	C1-O5-C5	6.97	122.47	112.22

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

4 monomers are involved in 10 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	403	DHI	2	0
2	B	403	GCU	1	0
5	B	405	PG4	6	0
5	C	402	PG4	1	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 ⓘ

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	389/401 (97%)	0.10	10 (2%) 56 65	20, 36, 54, 72	0
1	B	390/401 (97%)	-0.25	0 100 100	17, 27, 42, 50	0
1	C	390/401 (97%)	-0.15	7 (1%) 69 77	20, 31, 49, 57	1 (0%)
1	D	368/401 (91%)	1.78	132 (35%) 0 0	39, 76, 107, 143	366 (99%)
All	All	1537/1604 (95%)	0.35	149 (9%) 8 13	17, 36, 93, 143	367 (23%)

All (149) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	96	ASN	10.1
1	D	95	PHE	9.7
1	D	64	TYR	7.8
1	D	112	ALA	7.7
1	D	192	ALA	5.9
1	D	156	LEU	5.8
1	D	369	THR	5.7
1	D	341	PHE	5.5
1	D	88	PRO	5.4
1	D	111	TYR	5.4
1	D	145	HIS	5.4
1	D	325	VAL	5.3
1	D	183	SER	5.3
1	D	367	ASN	5.3
1	D	97	ARG	5.0
1	D	120	ASP	4.9
1	D	366	THR	4.9
1	D	149	TRP	4.8
1	D	157	ARG	4.8
1	D	113	ALA	4.7
1	D	351	VAL	4.6

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Mol	Chain	Res	Type	RSRZ
1	D	44	GLN	4.6
1	D	188	ASN	4.6
1	D	94	THR	4.5
1	D	89	SER	4.4
1	D	45	ASN	4.4
1	D	373	ASN	4.4
1	D	222	GLY	4.4
1	A	98	ASN	4.4
1	D	33	ALA	4.4
1	D	92	VAL	4.3
1	D	12	GLU	4.3
1	C	346	GLY	4.2
1	D	307	THR	4.2
1	D	4	ASP	4.2
1	D	352	SER	4.1
1	D	76	HIS	4.1
1	D	339	GLN	4.1
1	C	347	SER	4.1
1	D	178	TYR	4.0
1	D	133	TYR	4.0
1	D	161	GLU	4.0
1	D	211	PHE	4.0
1	D	90	ASP	3.9
1	D	10	SER	3.9
1	D	368	LEU	3.9
1	D	335	THR	3.9
1	D	75	LYS	3.8
1	D	61	ASN	3.8
1	D	117	HIS	3.8
1	D	311	ASN	3.7
1	D	190	PRO	3.7
1	D	345	ASN	3.7
1	D	151	THR	3.7
1	D	196	MET	3.7
1	D	203	LEU	3.6
1	A	345	ASN	3.6
1	D	148	THR	3.5
1	D	296	PHE	3.4
1	D	11	ALA	3.4
1	D	179	LEU	3.4
1	D	194	ALA	3.4
1	D	387	PHE	3.4

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Mol	Chain	Res	Type	RSRZ
1	D	370	VAL	3.3
1	A	100	ASP	3.3
1	D	116	GLN	3.3
1	A	347	SER	3.2
1	D	191	GLN	3.2
1	D	304	ILE	3.2
1	D	9	VAL	3.1
1	D	162	ASN	3.1
1	D	166	ILE	3.1
1	D	141	PRO	3.1
1	D	364	PRO	3.1
1	D	51	ILE	3.1
1	D	91	MET	3.0
1	D	375	PHE	3.0
1	D	52	LEU	3.0
1	A	346	GLY	3.0
1	D	337	VAL	3.0
1	D	221	ALA	3.0
1	D	41	GLY	2.9
1	D	354	TRP	2.9
1	D	305	ASP	2.9
1	A	2	ALA	2.9
1	A	101	THR	2.9
1	D	40	PHE	2.9
1	C	345	ASN	2.8
1	D	37	GLU	2.8
1	D	68	GLU	2.8
1	D	376	TRP	2.8
1	A	145	HIS	2.8
1	D	389	VAL	2.8
1	D	322	ASP	2.7
1	D	343	LEU	2.7
1	D	8	ASN	2.7
1	D	223	LYS	2.7
1	D	122	VAL	2.7
1	D	146	GLU	2.7
1	D	153	GLN	2.7
1	D	181	ASN	2.6
1	D	201	THR	2.6
1	D	381	ALA	2.6
1	D	380	PRO	2.6
1	D	150	TRP	2.6

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Mol	Chain	Res	Type	RSRZ
1	D	189	ASP	2.6
1	D	244	PRO	2.6
1	D	67	VAL	2.5
1	D	371	SER	2.5
1	D	144	ALA	2.4
1	D	365	GLY	2.4
1	D	168	ALA	2.4
1	D	197	ASP	2.4
1	D	132	LEU	2.4
1	D	5	VAL	2.4
1	D	280	ASP	2.4
1	D	213	TYR	2.3
1	D	15	VAL	2.3
1	C	372	GLY	2.3
1	D	338	ASN	2.3
1	D	77	GLY	2.3
1	D	379	LEU	2.2
1	D	38	THR	2.2
1	D	30	ASP	2.2
1	D	32	THR	2.2
1	D	20	GLY	2.2
1	D	362	LEU	2.2
1	D	159	MET	2.2
1	D	306	ALA	2.2
1	D	319	TYR	2.2
1	D	128	ASN	2.2
1	D	334	ASN	2.2
1	D	215	LEU	2.2
1	D	214	PRO	2.2
1	A	373	ASN	2.1
1	D	126	LYS	2.1
1	C	61	ASN	2.1
1	D	124	PHE	2.1
1	D	388	VAL	2.1
1	A	372	GLY	2.1
1	D	125	MET	2.1
1	C	238	ASN	2.1
1	C	21	GLY	2.1
1	D	46	GLN	2.0
1	D	155	ILE	2.0
1	D	363	GLN	2.0
1	D	118	LEU	2.0

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Mol	Chain	Res	Type	RSRZ
1	D	330	ILE	2.0
1	D	224	ASP	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	DHI	B	404	11/11	0.77	0.23	8.05	75,76,77,77	0
4	BDP	B	402	13/13	0.87	0.20	6.70	58,61,63,64	0
2	GCU	B	403	13/13	0.84	0.33	6.04	50,54,54,55	0
3	DHI	A	403	11/11	0.70	0.33	5.58	88,89,89,89	0
5	PG4	B	405	13/13	0.94	0.19	2.67	34,37,46,47	0
5	PG4	C	402	10/13	0.97	0.12	0.72	36,37,40,41	0
2	GCU	A	402	13/13	0.95	0.09	-5.69	44,47,48,48	0

6.5 Other polymers [i](#)

There are no such residues in this entry.