



Full wwPDB X-ray Structure Validation Report ⓘ

May 13, 2020 – 11:19 pm BST

PDB ID : 2IIQ
Title : Crystal structure of Pasteurella multocida sialyltransferase in an open conformation with CMP bound
Authors : Ni, L.; Fisher, A.J.
Deposited on : 2006-09-28
Resolution : 2.30 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 ⓘ symbol.

The following versions of software and data (see [references ⓘ](#)) 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 : 2.11
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) : 2.11

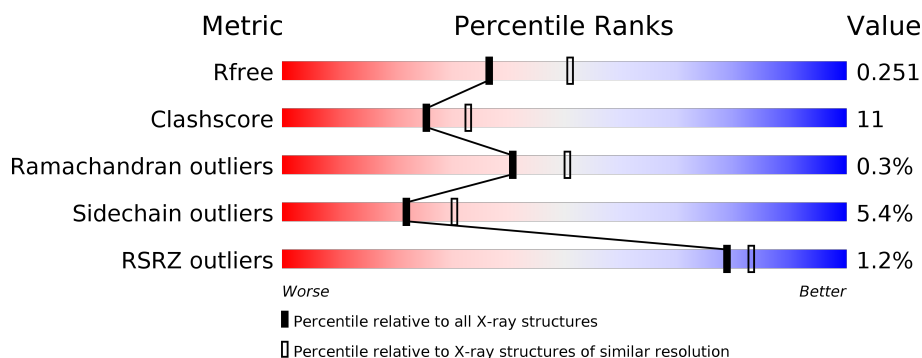
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.30 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	5042 (2.30-2.30)
Clashscore	141614	5643 (2.30-2.30)
Ramachandran outliers	138981	5575 (2.30-2.30)
Sidechain outliers	138945	5575 (2.30-2.30)
RSRZ outliers	127900	4938 (2.30-2.30)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria 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 $\leq 5\%$. 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	399	<div> <div>%</div> <div> <div></div> <div>76%</div> <div>18%</div> <div>• •</div> </div> </div>
1	B	399	<div> <div>%</div> <div> <div></div> <div>81%</div> <div>15%</div> <div>• •</div> </div> </div>

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 6947 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.

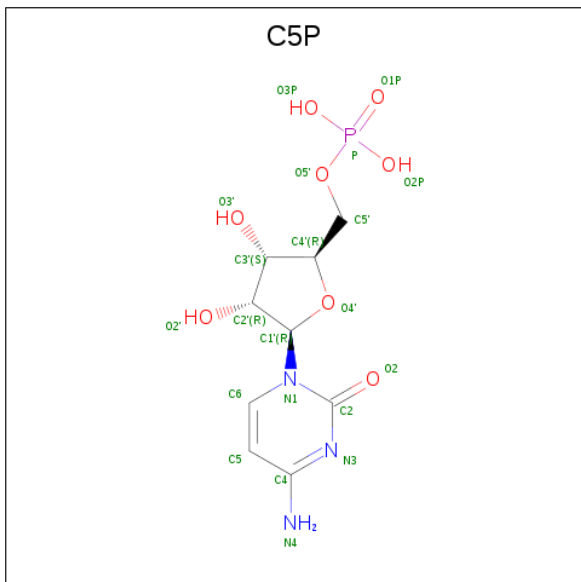
- Molecule 1 is a protein called Alpha-2,3/2,6-sialyltransferase/sialidase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	388	Total	C	N	O	S	0	1	0
			3171	2046	522	596	7			
1	B	388	Total	C	N	O	S	0	0	0
			3165	2042	522	594	7			

There are 24 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	25	MET	-	INITIATING METHIONINE	UNP Q15KI8
A	413	GLY	-	CLONING ARTIFACT	UNP Q15KI8
A	414	GLY	-	CLONING ARTIFACT	UNP Q15KI8
A	415	GLY	-	CLONING ARTIFACT	UNP Q15KI8
A	416	LEU	-	CLONING ARTIFACT	UNP Q15KI8
A	417	GLU	-	CLONING ARTIFACT	UNP Q15KI8
A	418	HIS	-	EXPRESSION TAG	UNP Q15KI8
A	419	HIS	-	EXPRESSION TAG	UNP Q15KI8
A	420	HIS	-	EXPRESSION TAG	UNP Q15KI8
A	421	HIS	-	EXPRESSION TAG	UNP Q15KI8
A	422	HIS	-	EXPRESSION TAG	UNP Q15KI8
A	423	HIS	-	EXPRESSION TAG	UNP Q15KI8
B	25	MET	-	INITIATING METHIONINE	UNP Q15KI8
B	413	GLY	-	CLONING ARTIFACT	UNP Q15KI8
B	414	GLY	-	CLONING ARTIFACT	UNP Q15KI8
B	415	GLY	-	CLONING ARTIFACT	UNP Q15KI8
B	416	LEU	-	CLONING ARTIFACT	UNP Q15KI8
B	417	GLU	-	CLONING ARTIFACT	UNP Q15KI8
B	418	HIS	-	EXPRESSION TAG	UNP Q15KI8
B	419	HIS	-	EXPRESSION TAG	UNP Q15KI8
B	420	HIS	-	EXPRESSION TAG	UNP Q15KI8
B	421	HIS	-	EXPRESSION TAG	UNP Q15KI8
B	422	HIS	-	EXPRESSION TAG	UNP Q15KI8
B	423	HIS	-	EXPRESSION TAG	UNP Q15KI8

- Molecule 2 is CYTIDINE-5'-MONOPHOSPHATE (three-letter code: C5P) (formula: $C_9H_{14}N_3O_8P$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	P	0	0
			21	9	3	8	1		
2	B	1	Total	C	N	O	P	0	0
			21	9	3	8	1		

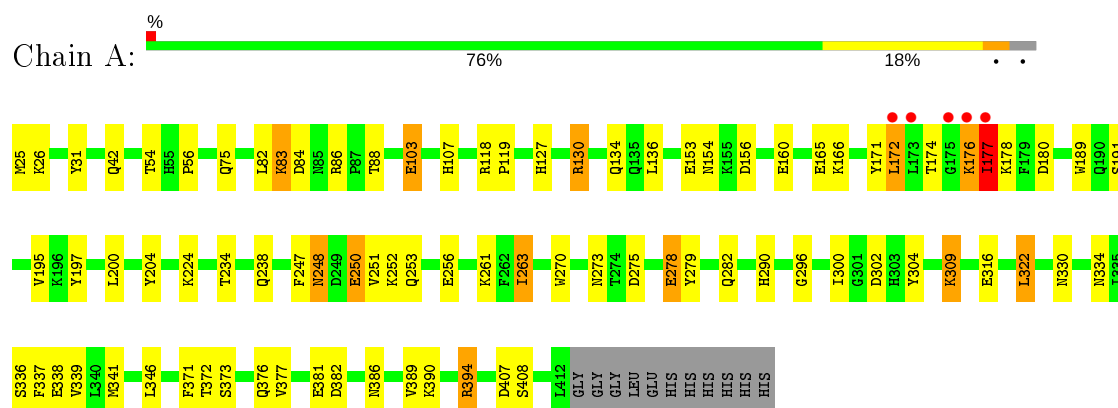
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	303	Total	O	0	0
			303	303		
3	B	266	Total	O	0	0
			266	266		

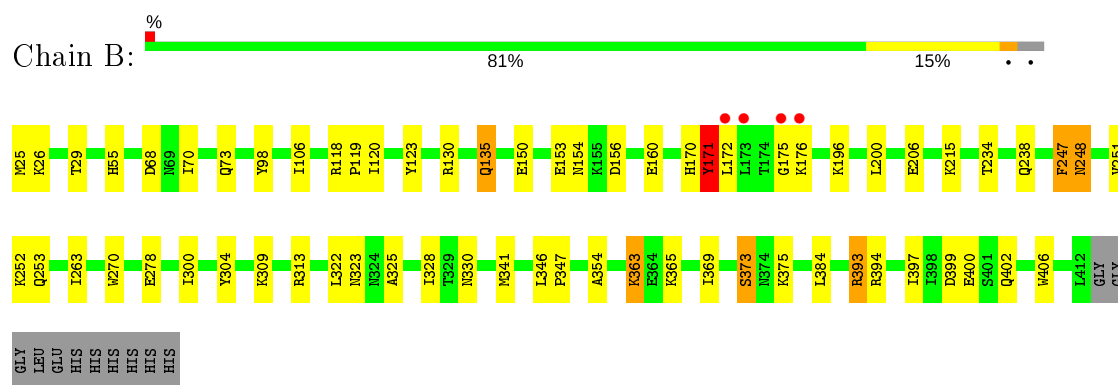
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of 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: Alpha-2,3/2,6-sialyltransferase/sialidase



- Molecule 1: Alpha-2,3/2,6-sialyltransferase/sialidase



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	52.53Å 61.57Å 119.55Å 90.00° 94.77° 90.00°	Depositor
Resolution (Å)	59.55 – 2.30 59.57 – 2.20	Depositor EDS
% Data completeness (in resolution range)	100.0 (59.55-2.30) 99.6 (59.57-2.20)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.10	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.63 (at 2.20Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.208 , 0.256 0.203 , 0.251	Depositor DCC
R_{free} test set	1957 reflections (5.03%)	wwPDB-VP
Wilson B-factor (Å ²)	16.4	Xtriage
Anisotropy	0.355	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 26.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.52$, $\langle L^2 \rangle = 0.35$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	6947	wwPDB-VP
Average B, all atoms (Å ²)	5.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 46.67 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 1.1072e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: C5P

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	0.57	1/3249 (0.0%)	0.67	3/4407 (0.1%)
1	B	0.55	0/3241	0.64	0/4398
All	All	0.56	1/6490 (0.0%)	0.66	3/8805 (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	2

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	83	LYS	C-N	-6.89	1.18	1.34

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	82	LEU	C-N-CA	6.79	138.68	121.70
1	A	82	LEU	O-C-N	-5.66	113.65	122.70
1	A	177	ILE	N-CA-C	-5.03	97.42	111.00

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	172	LEU	Peptide

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Mol	Chain	Res	Type	Group
1	A	176	LYS	Peptide

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	3171	0	3112	74	0
1	B	3165	0	3093	60	1
2	A	21	0	12	0	0
2	B	21	0	12	0	0
3	A	303	0	0	14	1
3	B	266	0	0	9	0
All	All	6947	0	6229	134	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 11.

All (134) 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:70:ILE:HD13	3:B:1693:HOH:O	1.34	1.27
1:B:206:GLU:HG2	1:B:215:LYS:HZ1	1.15	1.12
1:B:263:ILE:HD13	1:B:347:PRO:HG2	1.22	1.12
1:B:263:ILE:CD1	1:B:347:PRO:HG2	1.78	1.11
1:B:251:VAL:HB	3:B:1631:HOH:O	1.54	1.07
1:A:322:LEU:HD21	1:A:330:ASN:HB2	1.38	1.04
1:A:263:ILE:HD11	1:A:309:LYS:HB3	1.39	1.03
1:B:206:GLU:HG2	1:B:215:LYS:NZ	1.71	1.03
1:B:263:ILE:HD13	1:B:347:PRO:CG	1.89	1.01
1:A:177:ILE:HG21	3:A:1689:HOH:O	1.63	0.97
1:B:341:MET:HG2	1:B:346:LEU:HD22	1.47	0.96
1:B:393:ARG:HG2	1:B:393:ARG:HH11	1.34	0.90
1:A:83:LYS:HG3	3:A:1630:HOH:O	1.70	0.89
1:A:252:LYS:HE3	3:A:1597:HOH:O	1.74	0.87
1:A:263:ILE:HD12	1:A:337:PHE:HZ	1.40	0.86
1:B:384:LEU:HD21	1:B:400:GLU:HB2	1.59	0.83

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:263:ILE:HD11	1:A:309:LYS:CB	2.08	0.82
1:A:25:MET:SD	1:A:103:GLU:HG2	2.19	0.82
1:B:253:GLN:HB2	3:B:1586:HOH:O	1.79	0.82
1:A:273:ASN:HB3	3:A:1721:HOH:O	1.79	0.82
1:B:399:ASP:H	1:B:402:GLN:HE21	1.27	0.81
1:A:86:ARG:HH11	1:A:118:ARG:NH1	1.77	0.81
1:B:118:ARG:HB3	1:B:119:PRO:HD3	1.64	0.80
1:A:248:ASN:C	1:A:248:ASN:HD22	1.86	0.78
1:A:279:TYR:HA	1:A:282:GLN:NE2	1.99	0.78
1:B:206:GLU:HA	1:B:215:LYS:HE2	1.66	0.78
1:A:130:ARG:NH2	3:A:1634:HOH:O	2.15	0.77
1:A:176:LYS:O	1:A:177:ILE:HG12	1.85	0.77
1:B:341:MET:CG	1:B:346:LEU:HD22	2.15	0.76
1:A:309:LYS:HG2	1:A:337:PHE:CE2	2.23	0.73
1:B:263:ILE:CD1	1:B:347:PRO:CG	2.60	0.73
1:B:73:GLN:NE2	3:B:1693:HOH:O	2.22	0.72
1:A:86:ARG:HH11	1:A:118:ARG:HH12	1.34	0.72
1:A:263:ILE:HD12	1:A:337:PHE:CZ	2.25	0.72
1:B:206:GLU:HA	1:B:215:LYS:CE	2.21	0.70
1:B:325:ALA:HB3	1:B:328:ILE:HD13	1.72	0.69
1:A:118:ARG:HB3	1:A:119:PRO:HD3	1.73	0.69
1:B:175:GLY:O	3:B:1662:HOH:O	2.09	0.69
1:B:263:ILE:HD13	1:B:347:PRO:CB	2.22	0.68
1:B:118:ARG:HA	1:B:171:TYR:OH	1.96	0.66
1:A:84:ASP:HB2	1:A:86:ARG:HH21	1.62	0.65
1:B:384:LEU:CD2	1:B:400:GLU:HB2	2.28	0.64
1:A:174:THR:C	1:A:176:LYS:H	2.01	0.64
1:A:83:LYS:HG2	1:A:88:THR:HG22	1.81	0.62
1:A:136:LEU:HB2	1:A:195:VAL:HG12	1.81	0.62
1:A:263:ILE:HD13	1:A:263:ILE:C	2.19	0.62
1:A:224:LYS:HE2	3:A:1653:HOH:O	2.00	0.60
1:B:123:TYR:OH	1:B:130:ARG:NH2	2.35	0.60
1:A:279:TYR:HA	1:A:282:GLN:HE21	1.67	0.60
1:B:393:ARG:HH11	1:B:393:ARG:CG	2.11	0.60
1:B:150:GLU:OE2	1:B:394:ARG:NH2	2.35	0.60
1:A:336:SER:O	1:A:339:VAL:HG12	2.03	0.59
1:B:234:THR:O	1:B:238:GLN:HG3	2.03	0.59
1:A:180:ASP:OD2	3:A:1727:HOH:O	2.17	0.59
1:B:399:ASP:H	1:B:402:GLN:NE2	1.99	0.59
1:A:341:MET:HG2	1:A:346:LEU:HD22	1.85	0.59
1:A:261:LYS:NZ	3:A:1664:HOH:O	2.38	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:171:TYR:CB	1:A:176:LYS:HB2	2.34	0.57
1:A:177:ILE:HD12	3:A:1689:HOH:O	2.05	0.57
1:A:278:GLU:O	1:A:282:GLN:HG3	2.06	0.55
1:A:234:THR:O	1:A:238:GLN:HG3	2.07	0.55
3:A:1524:HOH:O	1:B:26:LYS:HE2	2.05	0.55
1:A:263:ILE:CD1	1:A:337:PHE:HZ	2.16	0.55
1:B:29:THR:OG1	1:B:55:HIS:NE2	2.28	0.55
1:A:322:LEU:HD21	1:A:330:ASN:CB	2.26	0.54
1:B:156:ASP:O	1:B:160:GLU:HG2	2.08	0.54
1:A:86:ARG:NH1	1:A:118:ARG:HH12	2.03	0.54
1:A:377:VAL:HA	1:A:382:ASP:HB3	1.90	0.53
1:A:300:ILE:HD12	1:A:304:TYR:CB	2.38	0.52
1:A:174:THR:C	1:A:176:LYS:N	2.63	0.52
1:B:206:GLU:HG2	1:B:215:LYS:HZ3	1.67	0.51
1:A:248:ASN:ND2	1:A:251:VAL:H	2.09	0.51
1:B:248:ASN:C	1:B:248:ASN:OD1	2.50	0.51
1:A:103:GLU:OE2	1:A:134:GLN:NE2	2.42	0.51
1:B:98:TYR:O	1:B:130:ARG:NH1	2.43	0.51
1:B:270:TRP:HB2	1:B:373:SER:O	2.11	0.51
1:A:83:LYS:HE3	3:A:1630:HOH:O	2.11	0.51
1:B:322:LEU:HD11	1:B:330:ASN:CG	2.31	0.50
1:B:325:ALA:HB3	1:B:328:ILE:CD1	2.41	0.50
1:A:176:LYS:HD3	1:A:178:LYS:H	1.77	0.50
1:B:171:TYR:HA	1:B:176:LYS:O	2.12	0.50
1:B:354:ALA:HB2	1:B:369:ILE:HG22	1.94	0.50
1:A:341:MET:CG	1:A:346:LEU:HD22	2.42	0.49
1:A:248:ASN:C	1:A:248:ASN:ND2	2.60	0.49
1:B:347:PRO:O	1:B:365:LYS:HE3	2.13	0.49
1:B:263:ILE:HD11	1:B:347:PRO:HG2	1.83	0.48
1:A:156:ASP:O	1:A:160:GLU:HG2	2.13	0.48
1:A:189:TRP:HD1	1:A:197:TYR:HH	1.60	0.48
1:A:252:LYS:HE2	1:A:256:GLU:OE2	2.13	0.48
1:B:170:HIS:C	1:B:172:LEU:N	2.65	0.48
1:A:386:ASN:O	1:A:390:LYS:HG3	2.14	0.48
1:A:83:LYS:CD	1:A:88:THR:HG22	2.44	0.47
1:A:153:GLU:O	1:A:154:ASN:HB2	2.13	0.47
1:B:325:ALA:CB	1:B:328:ILE:HD13	2.44	0.47
1:B:170:HIS:O	1:B:172:LEU:N	2.48	0.47
1:B:170:HIS:O	1:B:171:TYR:C	2.53	0.47
1:B:252:LYS:HE3	3:B:1632:HOH:O	2.14	0.47
1:A:204:TYR:CE1	1:A:394:ARG:NH2	2.83	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:54:THR:HG22	1:A:75:GLN:HG2	1.96	0.47
1:A:127:HIS:HE1	3:A:1576:HOH:O	1.97	0.46
1:A:171:TYR:C	1:A:174:THR:H	2.18	0.46
1:A:83:LYS:CG	1:A:88:THR:HG22	2.44	0.46
1:B:363:LYS:HB2	1:B:397:ILE:O	2.16	0.46
1:B:247:PHE:CE2	1:B:251:VAL:HG13	2.51	0.46
1:B:26:LYS:NZ	3:B:1488:HOH:O	2.48	0.46
1:A:83:LYS:HE2	1:A:88:THR:HA	1.97	0.46
1:B:206:GLU:CG	1:B:215:LYS:HZ1	2.05	0.45
1:B:153:GLU:O	1:B:154:ASN:HB2	2.16	0.45
1:A:248:ASN:ND2	1:A:250:GLU:H	2.15	0.45
1:A:26:LYS:HD3	1:A:56:PRO:HG2	1.99	0.45
1:A:290:HIS:HA	1:A:296:GLY:HA3	1.98	0.44
1:B:373:SER:HB2	1:B:406:TRP:HE1	1.82	0.44
1:A:300:ILE:HD12	1:A:304:TYR:CG	2.53	0.44
1:A:270:TRP:CG	1:A:372:THR:HB	2.53	0.44
1:B:322:LEU:HA	1:B:328:ILE:HD11	1.99	0.44
1:A:31:TYR:CD1	1:A:42:GLN:HB3	2.52	0.44
1:A:171:TYR:O	1:A:174:THR:N	2.43	0.43
1:A:371:PHE:CZ	1:A:389:VAL:HG21	2.53	0.43
1:B:135:GLN:HG3	3:B:1522:HOH:O	2.19	0.43
1:A:42:GLN:HG2	1:A:107:HIS:HB3	2.00	0.42
1:B:323:ASN:ND2	1:B:323:ASN:O	2.52	0.42
1:A:176:LYS:C	1:A:177:ILE:HG12	2.40	0.42
1:B:170:HIS:C	1:B:172:LEU:H	2.21	0.42
1:A:103:GLU:HB2	1:A:134:GLN:HB2	2.02	0.42
1:B:106:ILE:HD13	1:B:120:ILE:HD13	2.02	0.42
1:A:407[B]:ASP:OD1	1:A:408:SER:N	2.52	0.42
1:B:393:ARG:HD3	3:B:1653:HOH:O	2.18	0.42
1:A:178:LYS:HD2	3:A:1694:HOH:O	2.20	0.41
1:A:165:GLU:HG2	1:A:191:SER:CB	2.51	0.41
1:B:300:ILE:HD12	1:B:304:TYR:CG	2.56	0.41
1:A:178:LYS:CD	3:A:1694:HOH:O	2.69	0.40
1:B:206:GLU:CG	1:B:215:LYS:NZ	2.62	0.40
1:A:165:GLU:HG2	1:A:191:SER:HB3	2.04	0.40
1:A:336:SER:HB2	1:A:338:GLU:OE1	2.21	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)
3:A:1694:HOH:O	3:A:1730:HOH:O[2_545]	2.07	0.13
1:B:118:ARG:NH2	1:B:399:ASP:OD2[2_444]	2.18	0.02

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	387/399 (97%)	364 (94%)	22 (6%)	1 (0%)	41	50
1	B	386/399 (97%)	369 (96%)	16 (4%)	1 (0%)	41	50
All	All	773/798 (97%)	733 (95%)	38 (5%)	2 (0%)	41	50

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	171	TYR
1	A	177	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	347/360 (96%)	325 (94%)	22 (6%)	18	24
1	B	344/360 (96%)	329 (96%)	15 (4%)	28	39
All	All	691/720 (96%)	654 (95%)	37 (5%)	22	30

All (37) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	103	GLU
1	A	130	ARG
1	A	166	LYS
1	A	172	LEU
1	A	177	ILE
1	A	200	LEU
1	A	247	PHE
1	A	248	ASN
1	A	250	GLU
1	A	253	GLN
1	A	263	ILE
1	A	275	ASP
1	A	278	GLU
1	A	302	ASP
1	A	309	LYS
1	A	316	GLU
1	A	322	LEU
1	A	334	ASN
1	A	373	SER
1	A	376	GLN
1	A	381	GLU
1	A	394	ARG
1	B	25	MET
1	B	68	ASP
1	B	135	GLN
1	B	171	TYR
1	B	196	LYS
1	B	200	LEU
1	B	247	PHE
1	B	248	ASN
1	B	278	GLU
1	B	309	LYS
1	B	313	ARG
1	B	363	LYS
1	B	373	SER
1	B	375	LYS
1	B	393	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (17) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	48	GLN
1	A	101	ASN

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Mol	Chain	Res	Type
1	A	127	HIS
1	A	154	ASN
1	A	248	ASN
1	A	282	GLN
1	A	293	GLN
1	A	323	ASN
1	A	334	ASN
1	B	73	GLN
1	B	105	ASN
1	B	232	GLN
1	B	282	GLN
1	B	323	ASN
1	B	330	ASN
1	B	385	ASN
1	B	402	GLN

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 ⓘ

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	C5P	A	1427	-	19,22,22	1.21	2 (10%)	24,33,33	1.53	3 (12%)
2	C5P	B	1427	-	19,22,22	1.11	2 (10%)	24,33,33	1.46	4 (16%)

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	C5P	A	1427	-	-	1/8/26/26	0/2/2/2
2	C5P	B	1427	-	-	3/8/26/26	0/2/2/2

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	1427	C5P	P-O1P	3.01	1.60	1.50
2	B	1427	C5P	P-O1P	2.95	1.60	1.50
2	A	1427	C5P	O4'-C1'	2.51	1.44	1.41
2	B	1427	C5P	O4'-C1'	2.26	1.44	1.41

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	1427	C5P	C2-N3-C4	5.02	121.43	116.34
2	B	1427	C5P	C2-N3-C4	4.20	120.60	116.34
2	B	1427	C5P	C3'-C2'-C1'	3.13	105.69	100.98
2	A	1427	C5P	C2'-C3'-C4'	2.83	108.14	102.64
2	A	1427	C5P	C3'-C2'-C1'	2.63	104.94	100.98
2	B	1427	C5P	C2'-C3'-C4'	2.32	107.16	102.64
2	B	1427	C5P	N4-C4-N3	2.02	119.68	116.49

There are no chirality outliers.

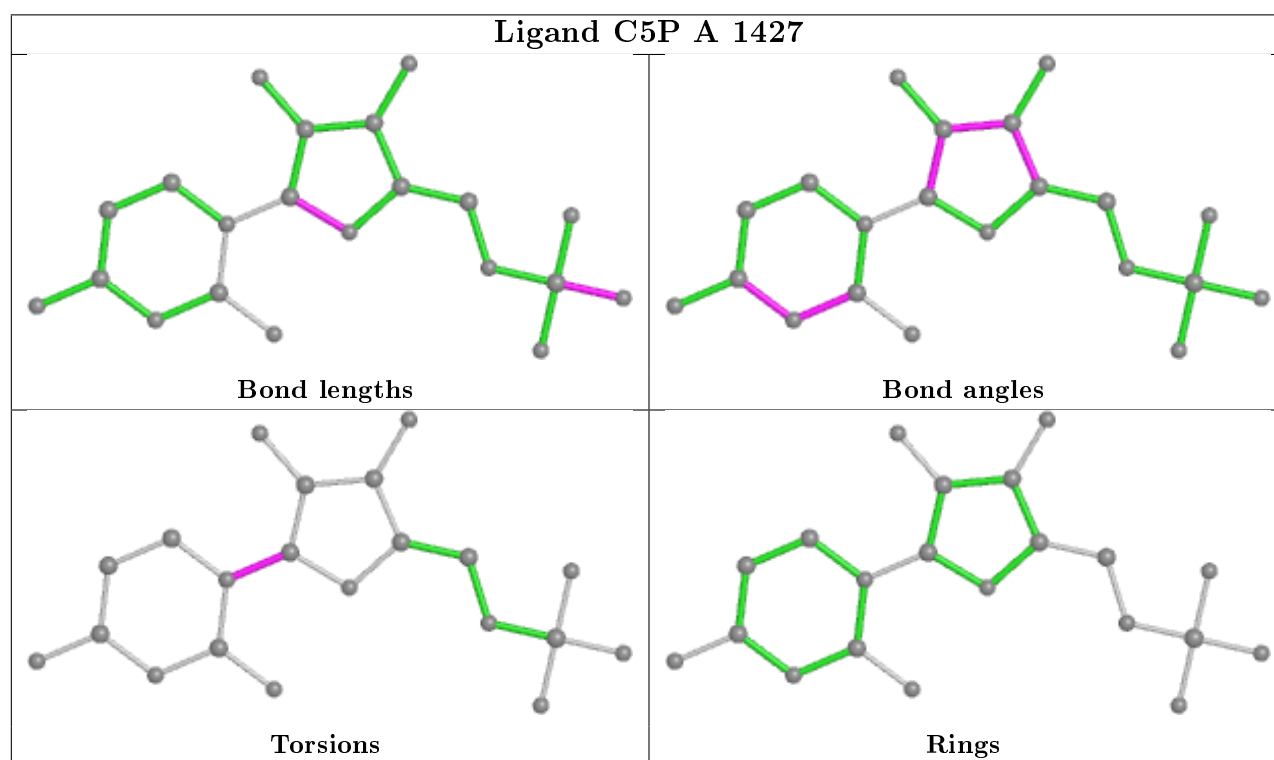
All (4) torsion outliers are listed below:

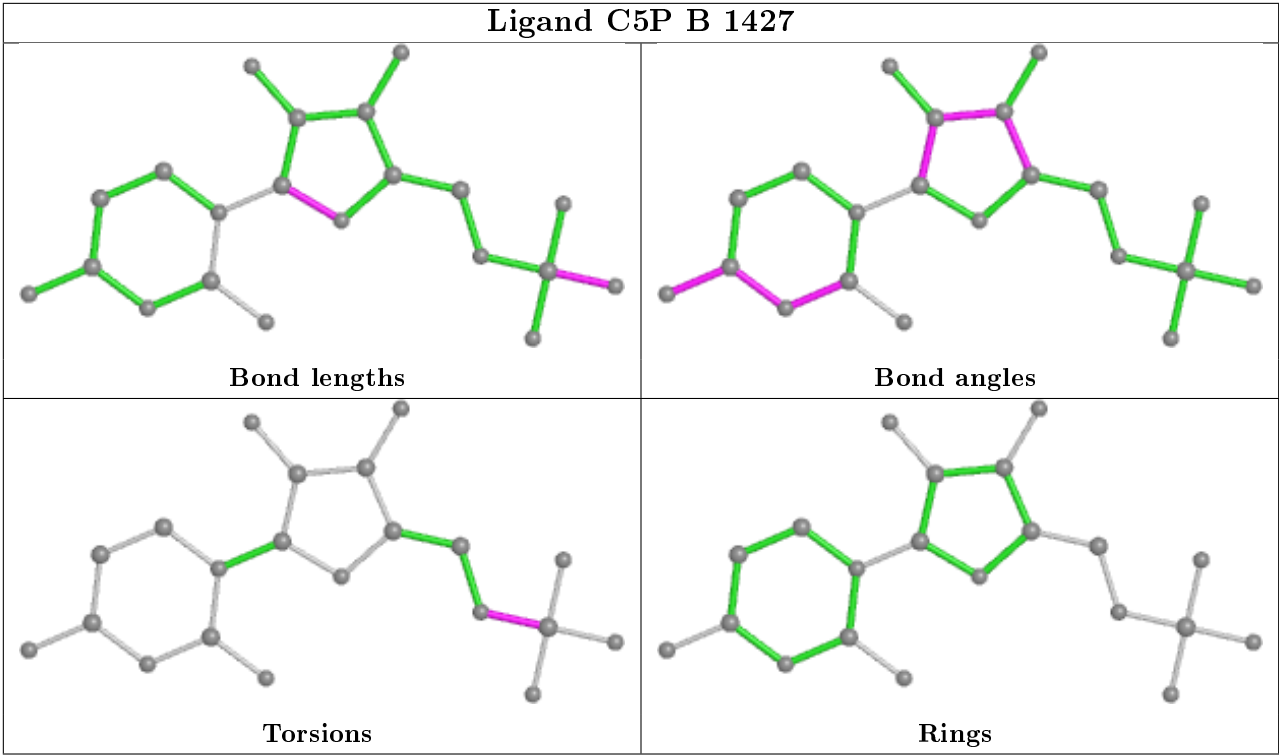
Mol	Chain	Res	Type	Atoms
2	A	1427	C5P	O4'-C1'-N1-C6
2	B	1427	C5P	C5'-O5'-P-O3P
2	B	1427	C5P	C5'-O5'-P-O1P
2	B	1427	C5P	C5'-O5'-P-O2P

There are no ring outliers.

No monomer is involved in short contacts.

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 than 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.





5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	A	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	A	83:LYS	C	84:ASP	N	1.18

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	388/399 (97%)	-0.15	5 (1%) 77 81	2, 4, 12, 25	0
1	B	388/399 (97%)	-0.14	4 (1%) 82 86	2, 5, 14, 23	0
All	All	776/798 (97%)	-0.15	9 (1%) 79 83	2, 4, 13, 25	0

All (9) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	176	LYS	4.4
1	A	172	LEU	4.1
1	A	173	LEU	3.5
1	B	173	LEU	3.1
1	B	175	GLY	2.6
1	A	177	ILE	2.5
1	B	176	LYS	2.3
1	A	175	GLY	2.1
1	B	172	LEU	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. The B-factors column lists the minimum,

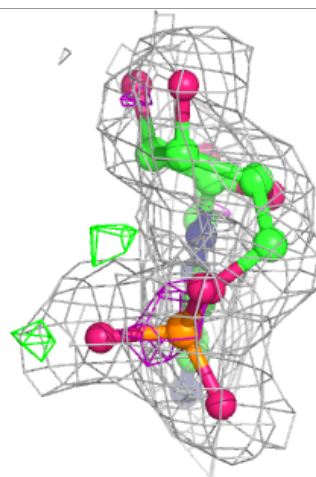
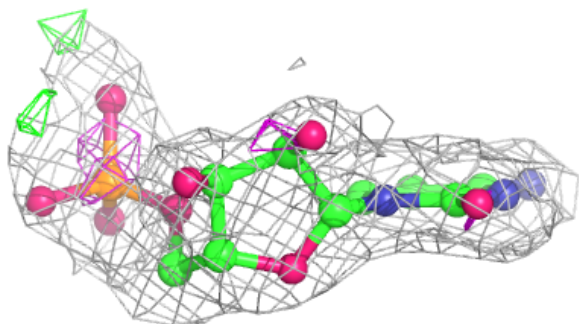
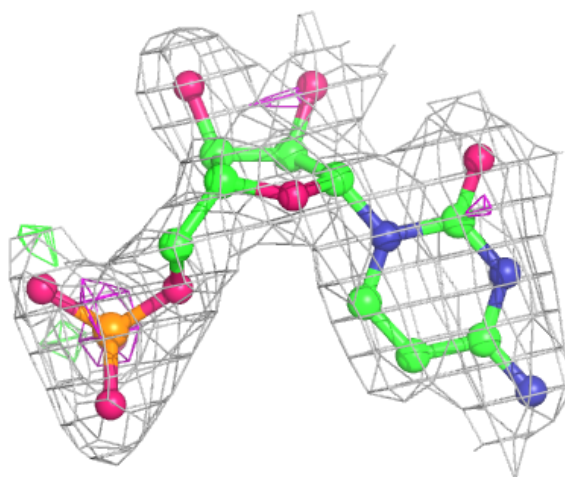
median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q<0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
2	C5P	B	1427	21/21	0.89	0.17	4,10,21,22	0
2	C5P	A	1427	21/21	0.94	0.15	3,9,15,17	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.

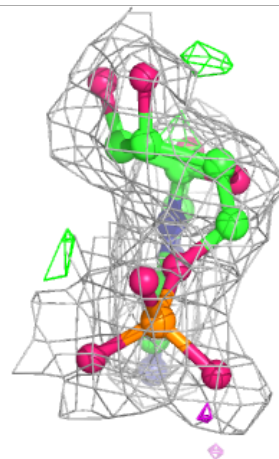
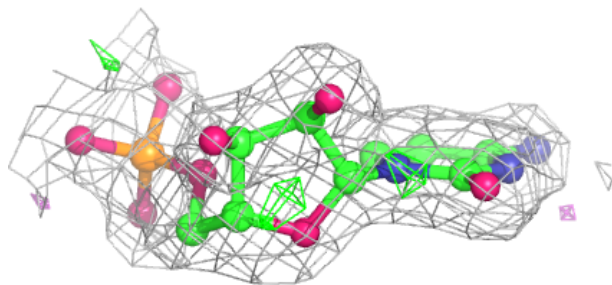
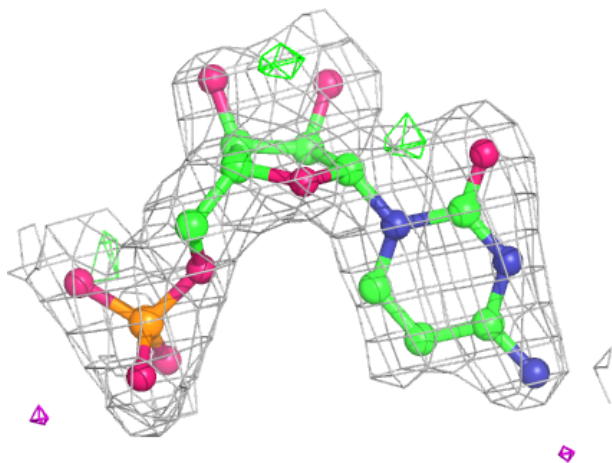
Electron density around C5P B 1427:

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 C5P A 1427:

$2mF_o-DF_c$ (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.