



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 1, 2026 – 02:40 AM UTC

PDB ID : 6APL / pdb_00006apl
Title : Crystal Structure of human ST6GALNAC2 in complex with CMP
Authors : Forouhar, F.; Moremen, K.W.; Northeast Structural Genomics Consortium (NESG); Tong, L.
Deposited on : 2017-08-17
Resolution : 2.35 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

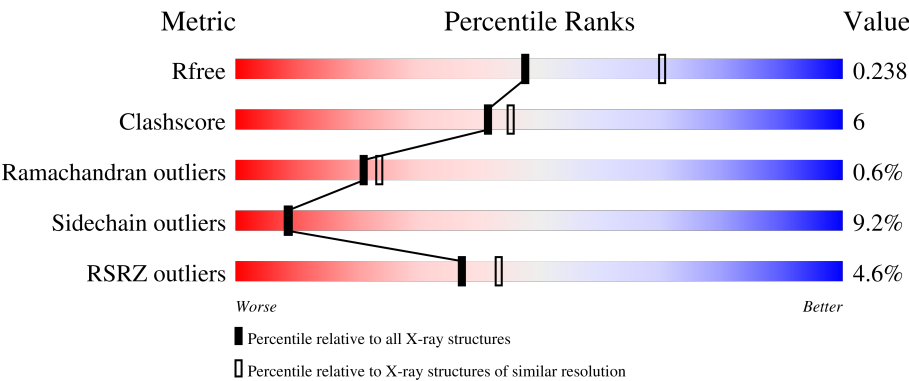
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.35 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	1596 (2.36-2.36)
Clashscore	190562	1663 (2.36-2.36)
Ramachandran outliers	187476	1646 (2.36-2.36)
Sidechain outliers	187428	1646 (2.36-2.36)
RSRZ outliers	180081	1598 (2.36-2.36)

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 $\leq 5\%$. 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	374	4% 64%12%•21%
1	B	374	3% 61%15%•20%
1	C	374	2% 67%12%•18%
1	D	374	3% 64%14%•19%
1	E	374	5% 59%14%•24%

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Mol	Chain	Length	Quality of chain
1	F	374	5% 61% 14% • 24%

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 14650 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.

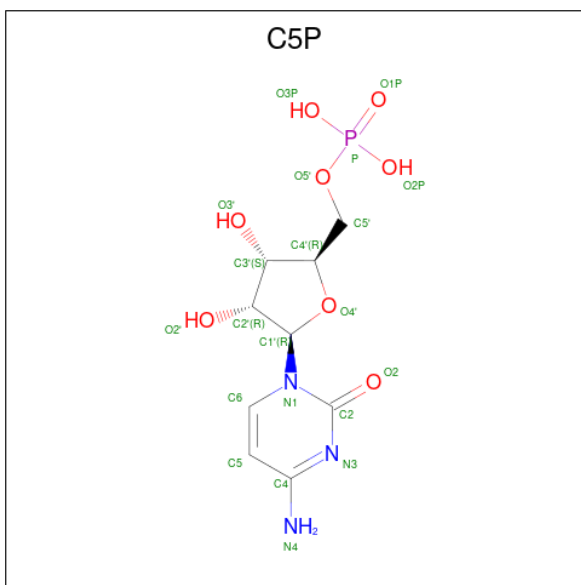
- Molecule 1 is a protein called Alpha-N-acetylgalactosaminide alpha-2,6-sialyltransferase 2.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	294	Total	C	N	O	S	Se	0	0	0
			2349	1523	410	407	4	5			
1	B	300	Total	C	N	O	S	Se	0	0	0
			2399	1553	419	418	4	5			
1	C	306	Total	C	N	O	S	Se	0	0	0
			2450	1591	425	425	4	5			
1	D	302	Total	C	N	O	S	Se	0	0	0
			2420	1571	420	420	4	5			
1	E	285	Total	C	N	O	S	Se	0	0	0
			2279	1476	396	399	4	4			
1	F	285	Total	C	N	O	S	Se	0	0	0
			2272	1472	391	402	3	4			

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	MSE	-	initiating methionine	UNP Q9UJ37
B	1	MSE	-	initiating methionine	UNP Q9UJ37
C	1	MSE	-	initiating methionine	UNP Q9UJ37
D	1	MSE	-	initiating methionine	UNP Q9UJ37
E	1	MSE	-	initiating methionine	UNP Q9UJ37
F	1	MSE	-	initiating methionine	UNP Q9UJ37

- Molecule 2 is CYTIDINE-5'-MONOPHOSPHATE (CCD ID: C5P) (formula: C₉H₁₄N₃O₈P).



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		
2	C	1	Total	C	N	O	P	0	0
			21	9	3	8	1		
2	D	1	Total	C	N	O	P	0	0
			21	9	3	8	1		
2	E	1	Total	C	N	O	P	0	0
			21	9	3	8	1		
2	F	1	Total	C	N	O	P	0	0
			21	9	3	8	1		

- Molecule 3 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: $C_8H_{15}NO_6$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	0	0
			14	8	1	5		
3	A	1	Total	C	N	O	0	0
			14	8	1	5		
3	B	1	Total	C	N	O	0	0
			14	8	1	5		
3	B	1	Total	C	N	O	0	0
			14	8	1	5		
3	C	1	Total	C	N	O	0	0
			14	8	1	5		
3	C	1	Total	C	N	O	0	0
			14	8	1	5		
3	D	1	Total	C	N	O	0	0
			14	8	1	5		
3	D	1	Total	C	N	O	0	0
			14	8	1	5		
3	D	1	Total	C	N	O	0	0
			14	8	1	5		
3	F	1	Total	C	N	O	0	0
			14	8	1	5		

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	48	Total	O	0	0
			48	48		
4	B	52	Total	O	0	0
			52	52		

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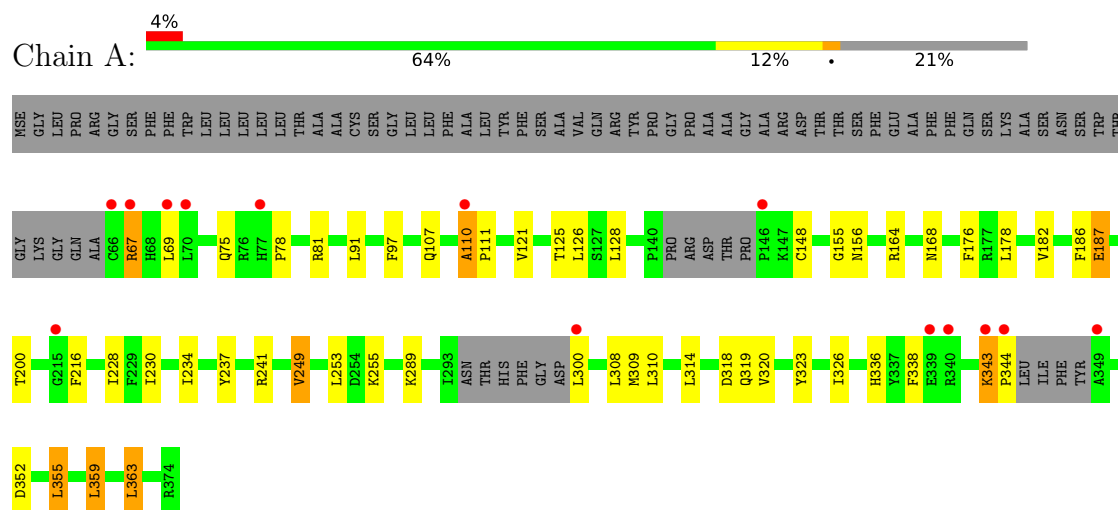
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	C	32	Total 32	O 32	0	0
4	D	38	Total 38	O 38	0	0
4	E	21	Total 21	O 21	0	0
4	F	24	Total 24	O 24	0	0

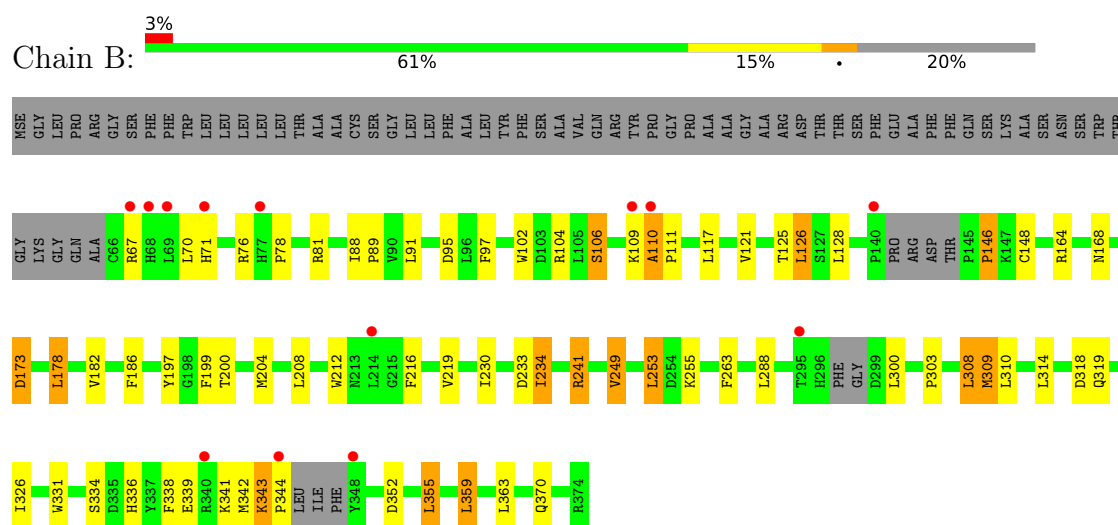
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

- Molecule 1: Alpha-N-acetylgalactosaminide alpha-2,6-sialyltransferase 2

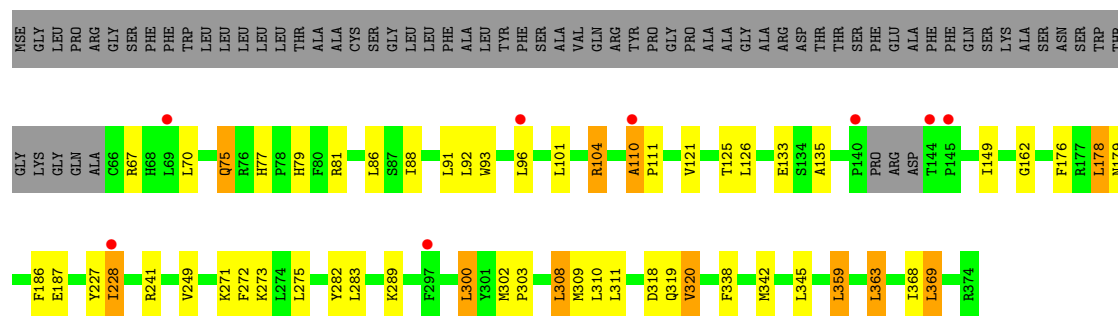


- Molecule 1: Alpha-N-acetylgalactosaminide alpha-2,6-sialyltransferase 2

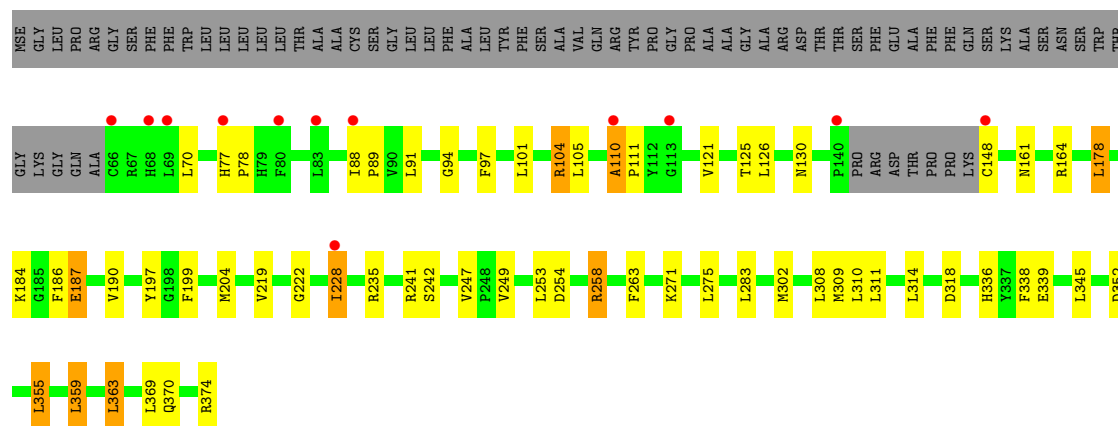


- Molecule 1: Alpha-N-acetylgalactosaminide alpha-2,6-sialyltransferase 2

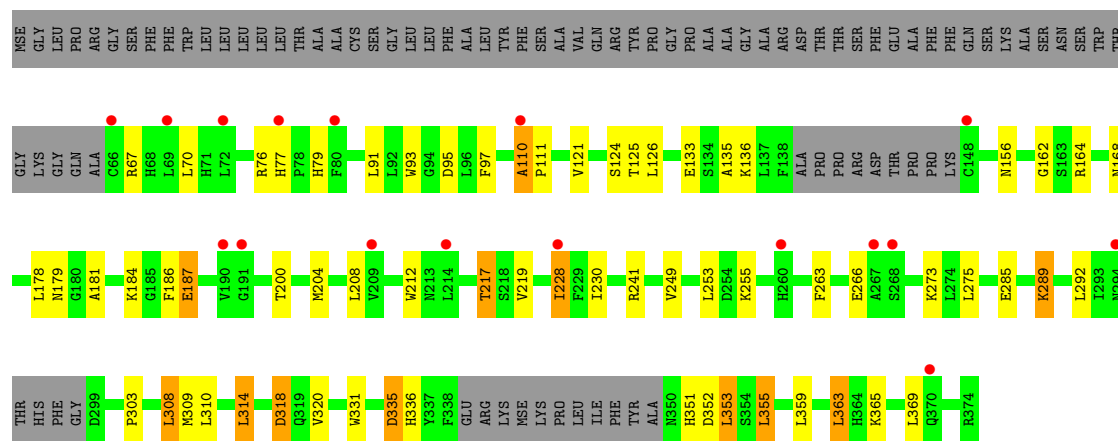




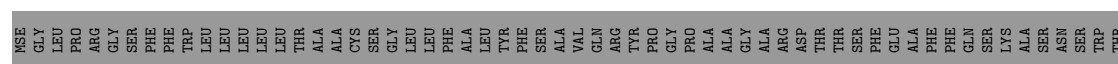
- Molecule 1: Alpha-N-acetylgalactosaminide alpha-2,6-sialyltransferase 2

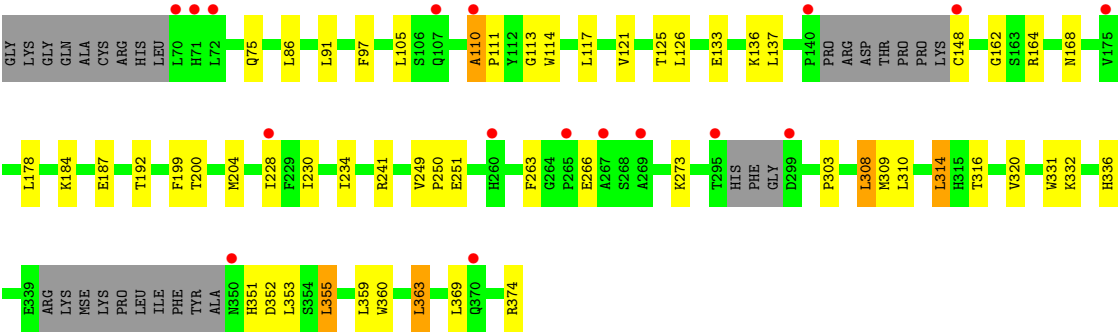


- Molecule 1: Alpha-N-acetylgalactosaminide alpha-2,6-sialyltransferase 2



- Molecule 1: Alpha-N-acetylgalactosaminide alpha-2,6-sialyltransferase 2





4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	71.17Å 71.12Å 138.61Å 103.69° 97.26° 103.03°	Depositor
Resolution (Å)	41.60 – 2.35 41.60 – 2.35	Depositor EDS
% Data completeness (in resolution range)	97.9 (41.60-2.35) 97.9 (41.60-2.35)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.23 (at 2.34Å)	Xtriage
Refinement program	PHENIX (1.12_2829: ???)	Depositor
R, R_{free}	0.196 , 0.236 0.199 , 0.238	Depositor DCC
R_{free} test set	10325 reflections (10.03%)	wwPDB-VP
Wilson B-factor (Å ²)	58.6	Xtriage
Anisotropy	0.281	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 54.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.074 for k,h,-h-k-l	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	14650	wwPDB-VP
Average B, all atoms (Å ²)	79.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.27% 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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: NAG, 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	0.19	0/2411	0.41	0/3257
1	B	0.18	0/2463	0.42	1/3329 (0.0%)
1	C	0.16	0/2519	0.37	0/3410
1	D	0.17	0/2487	0.38	0/3365
1	E	0.17	0/2339	0.38	0/3164
1	F	0.16	0/2332	0.38	0/3157
All	All	0.17	0/14551	0.39	1/19682 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	146	PRO	N-CA-CB	7.35	110.97	103.25

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	2349	0	2328	26	0
1	B	2399	0	2362	38	0
1	C	2450	0	2419	29	0
1	D	2420	0	2384	31	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	E	2279	0	2241	38	0
1	F	2272	0	2231	29	0
2	A	21	0	12	2	0
2	B	21	0	12	2	0
2	C	21	0	12	1	0
2	D	21	0	12	0	0
2	E	21	0	12	2	0
2	F	21	0	12	1	0
3	A	28	0	26	0	0
3	B	28	0	26	0	0
3	C	28	0	26	1	0
3	D	42	0	39	0	0
3	F	14	0	13	0	0
4	A	48	0	0	0	0
4	B	52	0	0	0	0
4	C	32	0	0	0	0
4	D	38	0	0	0	0
4	E	21	0	0	0	0
4	F	24	0	0	0	0
All	All	14650	0	14167	184	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 6.

All (184) 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:E:125:THR:HG22	1:E:241:ARG:HB2	1.54	0.89
1:D:125:THR:HG22	1:D:241:ARG:HB2	1.56	0.85
1:F:125:THR:HG22	1:F:241:ARG:HB2	1.59	0.83
1:A:125:THR:HG22	1:A:241:ARG:HB2	1.59	0.82
1:C:125:THR:HG22	1:C:241:ARG:HB2	1.60	0.82
1:E:110:ALA:HB1	1:E:111:PRO:HD2	1.64	0.79
1:F:110:ALA:HB1	1:F:111:PRO:HD2	1.68	0.75
1:B:125:THR:HG22	1:B:241:ARG:HB2	1.68	0.75
1:D:110:ALA:HB1	1:D:111:PRO:HD2	1.69	0.74
1:A:110:ALA:HB1	1:A:111:PRO:HD2	1.72	0.71
1:C:179:ASN:ND2	2:C:401:C5P:O2P	2.20	0.70
1:D:101:LEU:HD12	1:D:104:ARG:HH22	1.54	0.70
1:C:110:ALA:HB1	1:C:111:PRO:HD2	1.73	0.69
1:D:94:GLY:HA3	1:D:130:ASN:HB3	1.74	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:110:ALA:HB1	1:B:111:PRO:HD2	1.75	0.68
1:B:336:HIS:HB2	1:B:339:GLU:HG2	1.74	0.68
1:C:176:PHE:HD2	1:C:309:MSE:HE3	1.58	0.68
1:F:200:THR:HG22	1:F:230:ILE:HB	1.79	0.65
1:E:228:ILE:HD11	1:E:275:LEU:HB2	1.77	0.65
1:A:187:GLU:HG3	1:F:331:TRP:CE2	2.32	0.65
1:B:117:LEU:HG	1:B:234:ILE:HG23	1.78	0.65
1:D:204:MSE:HE2	1:D:219:VAL:HG11	1.79	0.64
1:F:314:LEU:HD22	1:F:320:VAL:HG21	1.82	0.62
1:E:303:PRO:HB2	1:E:308:LEU:HD13	1.82	0.61
1:A:228:ILE:HD12	1:A:309:MSE:HE1	1.83	0.61
1:F:363:LEU:HB3	1:F:369:LEU:HB3	1.82	0.60
1:B:67:ARG:HD3	1:B:71:HIS:HB2	1.83	0.60
1:B:331:TRP:CE2	1:D:187:GLU:HG3	2.36	0.60
1:A:121:VAL:O	1:A:125:THR:HG23	2.02	0.60
1:F:97:PHE:HB2	1:F:126:LEU:HD23	1.84	0.60
1:A:97:PHE:HB2	1:A:126:LEU:HD23	1.85	0.58
1:D:97:PHE:HB2	1:D:126:LEU:HD23	1.84	0.58
1:C:111:PRO:HG3	1:C:302:MSE:SE	2.54	0.58
1:F:121:VAL:O	1:F:125:THR:HG23	2.03	0.58
1:E:200:THR:HG22	1:E:230:ILE:HB	1.86	0.57
1:E:124:SER:OG	1:E:241:ARG:NH2	2.37	0.56
1:E:121:VAL:O	1:E:125:THR:HG23	2.06	0.56
1:B:182:VAL:HG22	1:B:216:PHE:HB2	1.88	0.55
1:D:359:LEU:HD22	1:D:363:LEU:HD22	1.88	0.55
1:E:162:GLY:HA2	1:E:164:ARG:HH11	1.70	0.55
1:C:75:GLN:HG3	1:C:81:ARG:HD3	1.87	0.55
1:D:70:LEU:HB2	1:D:318:ASP:O	2.07	0.55
1:F:303:PRO:HB2	1:F:308:LEU:HD13	1.88	0.55
1:D:88:ILE:HG13	1:D:89:PRO:HD2	1.88	0.54
1:C:359:LEU:HD22	1:C:363:LEU:HD22	1.88	0.54
1:A:343:LYS:HD2	1:A:344:PRO:HD2	1.90	0.54
1:B:173:ASP:OD1	1:B:173:ASP:N	2.28	0.54
1:C:228:ILE:HD11	1:C:275:LEU:HD13	1.89	0.54
1:D:204:MSE:HE1	1:D:263:PHE:HE1	1.72	0.54
1:D:283:LEU:HD22	1:D:311:LEU:HD13	1.89	0.54
1:E:212:TRP:HZ3	1:E:217:THR:HA	1.73	0.53
1:B:102:TRP:O	1:B:106:SER:HB2	2.08	0.53
1:B:121:VAL:O	1:B:125:THR:HG23	2.08	0.53
1:B:204:MSE:HE2	1:B:219:VAL:HG11	1.91	0.52
1:D:111:PRO:HG3	1:D:302:MSE:SE	2.58	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:363:LEU:HB3	1:E:369:LEU:HB3	1.90	0.52
1:B:303:PRO:HB2	1:B:308:LEU:HD13	1.91	0.52
1:F:352:ASP:OD1	1:F:355:LEU:HB2	2.09	0.52
1:C:93:TRP:CE2	1:C:135:ALA:HB2	2.45	0.52
1:E:336:HIS:NE2	2:E:401:C5P:O3P	2.38	0.52
1:A:249:VAL:HG22	1:A:255:LYS:HA	1.91	0.52
1:A:168:ASN:HD21	1:F:352:ASP:HB2	1.74	0.51
1:C:227:TYR:HE2	1:C:271:LYS:HE3	1.76	0.51
1:B:109:LYS:HG2	1:B:110:ALA:H	1.76	0.51
1:E:67:ARG:HD3	1:E:318:ASP:OD2	2.10	0.51
1:A:336:HIS:NE2	2:A:401:C5P:O2P	2.43	0.51
1:A:182:VAL:HG22	1:A:216:PHE:HB2	1.94	0.50
1:E:335:ASP:N	1:E:335:ASP:OD1	2.44	0.50
1:D:199:PHE:CG	1:D:204:MSE:HE3	2.47	0.50
1:B:204:MSE:HE1	1:B:263:PHE:HE1	1.78	0.49
1:B:331:TRP:CD2	1:D:187:GLU:HG3	2.48	0.49
1:F:310:LEU:HD23	1:F:314:LEU:HD23	1.94	0.49
1:B:168:ASN:HD21	1:E:352:ASP:HB2	1.77	0.49
1:B:200:THR:HG22	1:B:230:ILE:HB	1.94	0.49
1:E:310:LEU:HD23	1:E:314:LEU:HD23	1.93	0.49
1:E:208:LEU:O	1:E:212:TRP:HB2	2.11	0.49
1:B:70:LEU:HB2	1:B:318:ASP:O	2.12	0.49
1:B:197:TYR:HE1	1:B:204:MSE:HE2	1.78	0.49
1:D:363:LEU:HB3	1:D:369:LEU:HB3	1.94	0.49
1:B:199:PHE:CG	1:B:204:MSE:HE3	2.49	0.48
1:A:168:ASN:ND2	1:F:352:ASP:HB2	2.28	0.48
1:C:178:LEU:HD12	1:C:309:MSE:HG3	1.96	0.48
1:C:110:ALA:HB2	1:C:300:LEU:HD13	1.95	0.48
1:F:136:LYS:O	1:F:273:LYS:NZ	2.45	0.48
1:B:249:VAL:HG22	1:B:255:LYS:HA	1.95	0.48
1:C:104:ARG:HH21	1:C:104:ARG:HB3	1.78	0.48
1:C:70:LEU:HB2	1:C:318:ASP:O	2.13	0.48
1:E:204:MSE:HE1	1:E:263:PHE:HE1	1.79	0.48
1:C:149:ILE:N	1:C:318:ASP:OD1	2.43	0.48
1:B:186:PHE:CZ	1:B:338:PHE:HA	2.49	0.47
1:B:309:MSE:HE3	1:B:309:MSE:HA	1.96	0.47
1:F:310:LEU:HD22	1:F:360:TRP:CZ3	2.49	0.47
1:C:121:VAL:O	1:C:125:THR:HG23	2.14	0.47
1:C:186:PHE:CZ	1:C:338:PHE:HA	2.50	0.47
1:B:352:ASP:CG	1:B:355:LEU:HB2	2.40	0.47
1:F:230:ILE:HD11	1:F:309:MSE:HE3	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:336:HIS:HB2	1:D:339:GLU:HG2	1.96	0.47
1:A:228:ILE:HD12	1:A:309:MSE:CE	2.45	0.47
1:D:228:ILE:HD11	1:D:275:LEU:HB2	1.96	0.46
1:C:67:ARG:NH2	1:C:86:LEU:HD21	2.31	0.46
1:E:314:LEU:HD22	1:E:320:VAL:HG21	1.96	0.46
1:B:343:LYS:HB3	1:B:343:LYS:NZ	2.30	0.46
1:D:222:GLY:O	1:D:271:LYS:NZ	2.48	0.46
1:F:336:HIS:NE2	2:F:401:C5P:O2P	2.48	0.46
1:B:331:TRP:H	1:B:331:TRP:CD1	2.34	0.46
1:D:104:ARG:HB3	1:D:104:ARG:NH2	2.31	0.46
1:F:110:ALA:HB1	1:F:111:PRO:CD	2.40	0.46
1:C:162:GLY:HA3	3:C:403:NAG:H82	1.98	0.46
1:C:101:LEU:HD12	1:C:104:ARG:HH22	1.80	0.46
1:B:97:PHE:CD1	1:B:126:LEU:HD23	2.51	0.45
1:D:235:ARG:HB3	1:D:254:ASP:OD2	2.17	0.45
1:E:70:LEU:HB2	1:E:318:ASP:O	2.16	0.45
1:E:162:GLY:HA2	1:E:164:ARG:NH1	2.31	0.45
1:A:125:THR:HG21	1:A:237:TYR:HB3	1.99	0.45
1:A:352:ASP:CG	1:A:355:LEU:HB2	2.42	0.45
1:F:162:GLY:HA2	1:F:164:ARG:HH11	1.82	0.45
1:C:67:ARG:HD2	1:C:318:ASP:HA	1.97	0.45
1:E:352:ASP:OD1	1:E:355:LEU:HB2	2.17	0.45
1:E:156:ASN:ND2	2:E:401:C5P:O1P	2.48	0.45
1:E:156:ASN:O	1:E:336:HIS:HA	2.17	0.45
1:D:242:SER:HB3	1:D:247:VAL:O	2.17	0.44
1:F:204:MSE:HE1	1:F:263:PHE:CE1	2.52	0.44
1:B:253:LEU:HD22	1:B:253:LEU:HA	1.86	0.44
1:E:204:MSE:HE2	1:E:219:VAL:HG11	1.99	0.44
1:E:353:LEU:HD22	1:E:353:LEU:H	1.81	0.44
1:F:204:MSE:HE1	1:F:263:PHE:HE1	1.83	0.44
1:E:93:TRP:CH2	1:E:95:ASP:HB2	2.52	0.44
1:A:78:PRO:HB3	1:A:81:ARG:HH11	1.82	0.44
1:E:67:ARG:HA	1:E:318:ASP:HB3	1.99	0.44
1:E:230:ILE:HD11	1:E:309:MSE:HE1	2.00	0.44
1:A:187:GLU:HG3	1:F:331:TRP:CD2	2.53	0.44
1:C:92:LEU:HG	1:C:126:LEU:HD11	2.00	0.44
1:D:186:PHE:O	1:D:190:VAL:HG22	2.18	0.44
1:E:292:LEU:HD11	1:E:352:ASP:HB3	1.99	0.44
1:A:343:LYS:NZ	1:A:343:LYS:HB3	2.33	0.44
1:A:359:LEU:HD22	1:A:363:LEU:HD22	2.00	0.43
1:B:343:LYS:HD2	1:B:344:PRO:HD2	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:250:PRO:HG2	1:F:251:GLU:HG2	2.00	0.43
1:E:77:HIS:CD2	1:E:79:HIS:HB3	2.52	0.43
1:A:156:ASN:ND2	2:A:401:C5P:H5'1	2.33	0.43
1:E:93:TRP:CE2	1:E:135:ALA:HB2	2.54	0.43
1:C:303:PRO:HB2	1:C:308:LEU:HD13	2.00	0.43
1:A:155:GLY:N	1:A:323:TYR:O	2.46	0.43
1:B:88:ILE:HG13	1:B:89:PRO:HD2	1.99	0.43
1:C:70:LEU:HD11	1:C:368:ILE:HG23	2.00	0.43
1:C:77:HIS:CD2	1:C:79:HIS:HB3	2.54	0.43
1:D:178:LEU:HD12	1:D:309:MSE:HG3	2.01	0.43
1:D:352:ASP:OD1	1:D:355:LEU:HB2	2.19	0.43
1:A:200:THR:HG22	1:A:230:ILE:HB	2.01	0.43
1:B:78:PRO:HA	1:B:81:ARG:HB2	2.01	0.43
1:F:105:LEU:HG	1:F:113:GLY:HA2	2.01	0.43
1:D:186:PHE:CZ	1:D:338:PHE:HA	2.53	0.43
1:B:178:LEU:HD21	2:B:401:C5P:H4'	2.01	0.43
1:D:77:HIS:CG	1:D:78:PRO:HD2	2.54	0.43
1:F:331:TRP:CZ2	1:F:332:LYS:HE3	2.54	0.43
1:D:197:TYR:HE1	1:D:204:MSE:HE2	1.84	0.43
1:F:199:PHE:O	1:F:230:ILE:HG12	2.18	0.43
1:E:136:LYS:O	1:E:273:LYS:NZ	2.52	0.42
1:A:67:ARG:HB2	1:A:318:ASP:OD2	2.19	0.42
1:B:234:ILE:H	1:B:234:ILE:HG13	1.52	0.42
1:E:179:ASN:O	1:E:181:ALA:N	2.51	0.42
1:E:186:PHE:N	1:E:187:GLU:OE1	2.52	0.42
1:A:186:PHE:CZ	1:A:338:PHE:HA	2.55	0.42
1:A:67:ARG:C	1:A:69:LEU:H	2.27	0.42
1:E:331:TRP:CD1	1:E:331:TRP:H	2.37	0.42
1:C:272:PHE:C	1:C:273:LYS:HD2	2.45	0.41
1:C:283:LEU:HD22	1:C:311:LEU:HD13	2.02	0.41
1:D:121:VAL:O	1:D:125:THR:HG23	2.21	0.41
1:D:258:ARG:H	1:D:258:ARG:HG2	1.69	0.41
1:F:114:TRP:HB2	1:F:117:LEU:HB2	2.02	0.41
1:B:197:TYR:HE1	1:B:204:MSE:CE	2.33	0.41
1:B:288:LEU:HD21	1:B:359:LEU:HD12	2.02	0.41
1:B:336:HIS:NE2	2:B:401:C5P:O3P	2.54	0.41
1:E:285:GLU:O	1:E:289:LYS:HD2	2.21	0.41
1:C:363:LEU:HD12	1:C:363:LEU:HA	1.89	0.41
1:E:110:ALA:HB1	1:E:111:PRO:CD	2.43	0.41
1:F:331:TRP:CD1	1:F:331:TRP:H	2.37	0.41
1:B:208:LEU:O	1:B:212:TRP:HB2	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:161:ASN:O	1:D:374:ARG:NH1	2.54	0.40
1:A:176:PHE:HD2	1:A:309:MSE:HE3	1.86	0.40
1:C:320:VAL:HG23	1:C:369:LEU:HD13	2.03	0.40
1:B:197:TYR:CE1	1:B:204:MSE:HE2	2.57	0.40
1:E:97:PHE:HB2	1:E:126:LEU:HD23	2.02	0.40
1:F:137:LEU:HD12	1:F:316:THR:HG21	2.03	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	286/374 (76%)	271 (95%)	14 (5%)	1 (0%)	36	43
1	B	292/374 (78%)	273 (94%)	16 (6%)	3 (1%)	12	12
1	C	302/374 (81%)	286 (95%)	14 (5%)	2 (1%)	18	20
1	D	298/374 (80%)	277 (93%)	20 (7%)	1 (0%)	36	43
1	E	277/374 (74%)	261 (94%)	14 (5%)	2 (1%)	18	20
1	F	277/374 (74%)	266 (96%)	9 (3%)	2 (1%)	18	20
All	All	1732/2244 (77%)	1634 (94%)	87 (5%)	11 (1%)	21	24

All (11) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	F	110	ALA
1	A	110	ALA
1	B	110	ALA
1	B	342	MSE
1	C	110	ALA
1	C	133	GLU

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Mol	Chain	Res	Type
1	D	110	ALA
1	E	110	ALA
1	E	255	LYS
1	F	184	LYS
1	B	146	PRO

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	251/307 (82%)	227 (90%)	24 (10%)	8	7
1	B	256/307 (83%)	226 (88%)	30 (12%)	5	5
1	C	262/307 (85%)	241 (92%)	21 (8%)	11	12
1	D	258/307 (84%)	238 (92%)	20 (8%)	11	12
1	E	244/307 (80%)	221 (91%)	23 (9%)	8	8
1	F	243/307 (79%)	222 (91%)	21 (9%)	10	10
All	All	1514/1842 (82%)	1375 (91%)	139 (9%)	8	9

All (139) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	67	ARG
1	A	75	GLN
1	A	91	LEU
1	A	107	GLN
1	A	128	LEU
1	A	148	CYS
1	A	164	ARG
1	A	178	LEU
1	A	187	GLU
1	A	234	ILE
1	A	249	VAL
1	A	253	LEU
1	A	289	LYS

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Mol	Chain	Res	Type
1	A	300	LEU
1	A	308	LEU
1	A	310	LEU
1	A	314	LEU
1	A	319	GLN
1	A	320	VAL
1	A	326	ILE
1	A	343	LYS
1	A	355	LEU
1	A	359	LEU
1	A	363	LEU
1	B	76	ARG
1	B	91	LEU
1	B	95	ASP
1	B	104	ARG
1	B	106	SER
1	B	126	LEU
1	B	128	LEU
1	B	148	CYS
1	B	164	ARG
1	B	173	ASP
1	B	178	LEU
1	B	233	ASP
1	B	234	ILE
1	B	241	ARG
1	B	249	VAL
1	B	253	LEU
1	B	300	LEU
1	B	308	LEU
1	B	309	MSE
1	B	310	LEU
1	B	314	LEU
1	B	319	GLN
1	B	326	ILE
1	B	334	SER
1	B	341	LYS
1	B	343	LYS
1	B	355	LEU
1	B	359	LEU
1	B	363	LEU
1	B	370	GLN
1	C	75	GLN

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Mol	Chain	Res	Type
1	C	88	ILE
1	C	91	LEU
1	C	96	LEU
1	C	104	ARG
1	C	178	LEU
1	C	187	GLU
1	C	228	ILE
1	C	249	VAL
1	C	282	TYR
1	C	289	LYS
1	C	300	LEU
1	C	308	LEU
1	C	310	LEU
1	C	319	GLN
1	C	320	VAL
1	C	342	MSE
1	C	345	LEU
1	C	359	LEU
1	C	363	LEU
1	C	369	LEU
1	D	91	LEU
1	D	104	ARG
1	D	105	LEU
1	D	148	CYS
1	D	164	ARG
1	D	178	LEU
1	D	184	LYS
1	D	187	GLU
1	D	228	ILE
1	D	249	VAL
1	D	253	LEU
1	D	258	ARG
1	D	308	LEU
1	D	310	LEU
1	D	314	LEU
1	D	345	LEU
1	D	355	LEU
1	D	359	LEU
1	D	363	LEU
1	D	370	GLN
1	E	76	ARG
1	E	91	LEU

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Mol	Chain	Res	Type
1	E	133	GLU
1	E	168	ASN
1	E	178	LEU
1	E	184	LYS
1	E	187	GLU
1	E	217	THR
1	E	228	ILE
1	E	249	VAL
1	E	253	LEU
1	E	266	GLU
1	E	289	LYS
1	E	308	LEU
1	E	314	LEU
1	E	318	ASP
1	E	335	ASP
1	E	351	HIS
1	E	353	LEU
1	E	355	LEU
1	E	359	LEU
1	E	363	LEU
1	E	365	LYS
1	F	75	GLN
1	F	86	LEU
1	F	91	LEU
1	F	133	GLU
1	F	148	CYS
1	F	168	ASN
1	F	178	LEU
1	F	187	GLU
1	F	192	THR
1	F	228	ILE
1	F	234	ILE
1	F	249	VAL
1	F	266	GLU
1	F	308	LEU
1	F	314	LEU
1	F	351	HIS
1	F	353	LEU
1	F	355	LEU
1	F	359	LEU
1	F	363	LEU
1	F	374	ARG

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

Mol	Chain	Res	Type
1	A	75	GLN
1	A	79	HIS
1	A	156	ASN
1	B	68	HIS
1	B	79	HIS
1	B	202	ASN
1	B	319	GLN
1	C	294	ASN
1	C	319	GLN
1	D	68	HIS
1	D	213	ASN
1	E	168	ASN
1	F	108	HIS
1	F	156	ASN
1	F	226	GLN
1	F	319	GLN
1	F	370	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

16 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	$\# Z > 2$
3	NAG	B	402	1	14,14,15	0.18	0	17,19,21	0.56	0
3	NAG	C	402	1	14,14,15	0.25	0	17,19,21	0.39	0
3	NAG	D	402	1	14,14,15	0.25	0	17,19,21	0.42	0
3	NAG	A	402	1	14,14,15	0.32	0	17,19,21	0.49	0
3	NAG	D	403	1	14,14,15	0.54	0	17,19,21	0.40	0
3	NAG	F	402	1	14,14,15	0.18	0	17,19,21	0.50	0
2	C5P	D	401	-	22,22,22	1.29	3 (13%)	32,33,33	1.03	2 (6%)
2	C5P	A	401	-	22,22,22	1.23	3 (13%)	32,33,33	0.92	2 (6%)
2	C5P	B	401	-	22,22,22	1.26	2 (9%)	32,33,33	1.05	2 (6%)
3	NAG	D	404	1	14,14,15	0.28	0	17,19,21	0.69	1 (5%)
3	NAG	A	403	1	14,14,15	0.76	1 (7%)	17,19,21	0.79	1 (5%)
2	C5P	F	401	-	22,22,22	1.21	2 (9%)	32,33,33	0.83	1 (3%)
2	C5P	E	401	-	22,22,22	1.18	3 (13%)	32,33,33	0.94	1 (3%)
3	NAG	C	403	1	14,14,15	0.67	0	17,19,21	0.49	0
2	C5P	C	401	-	22,22,22	1.19	2 (9%)	32,33,33	0.82	1 (3%)
3	NAG	B	403	1	14,14,15	0.50	0	17,19,21	1.13	1 (5%)

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
3	NAG	B	402	1	-	2/6/23/26	0/1/1/1
3	NAG	C	402	1	-	2/6/23/26	0/1/1/1
3	NAG	D	402	1	-	2/6/23/26	0/1/1/1
3	NAG	A	402	1	-	1/6/23/26	0/1/1/1
3	NAG	D	403	1	-	4/6/23/26	0/1/1/1
3	NAG	F	402	1	-	0/6/23/26	0/1/1/1
2	C5P	D	401	-	-	2/10/26/26	0/2/2/2
2	C5P	A	401	-	-	0/10/26/26	0/2/2/2
2	C5P	B	401	-	-	0/10/26/26	0/2/2/2
3	NAG	D	404	1	-	4/6/23/26	0/1/1/1
3	NAG	A	403	1	-	4/6/23/26	0/1/1/1
2	C5P	F	401	-	-	0/10/26/26	0/2/2/2
2	C5P	E	401	-	-	0/10/26/26	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	NAG	C	403	1	-	1/6/23/26	0/1/1/1
2	C5P	C	401	-	-	1/10/26/26	0/2/2/2
3	NAG	B	403	1	-	4/6/23/26	0/1/1/1

All (16) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	401	C5P	C4-N4	4.11	1.43	1.33
2	A	401	C5P	C4-N4	4.10	1.43	1.33
2	F	401	C5P	C4-N4	4.02	1.43	1.33
2	D	401	C5P	C4-N4	3.92	1.43	1.33
2	E	401	C5P	C4-N4	3.80	1.43	1.33
2	C	401	C5P	C4-N4	3.61	1.42	1.33
2	B	401	C5P	C2-N1	-3.10	1.33	1.40
2	D	401	C5P	C2-N1	-3.07	1.33	1.40
2	E	401	C5P	C2-N1	-2.66	1.34	1.40
2	C	401	C5P	C2-N1	-2.65	1.34	1.40
2	A	401	C5P	C2-N1	-2.60	1.34	1.40
2	F	401	C5P	C2-N1	-2.57	1.34	1.40
2	D	401	C5P	C6-C5	2.28	1.40	1.35
2	E	401	C5P	C6-C5	2.14	1.40	1.35
3	A	403	NAG	O5-C1	-2.12	1.40	1.43
2	A	401	C5P	C6-C5	2.10	1.40	1.35

All (12) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	403	NAG	C1-O5-C5	4.00	117.55	112.19
2	D	401	C5P	O2P-P-O3P	3.72	121.73	107.80
2	B	401	C5P	O2P-P-O3P	3.40	120.57	107.80
2	E	401	C5P	O2P-P-O3P	3.13	119.54	107.80
2	A	401	C5P	O2P-P-O1P	2.47	120.47	110.83
3	A	403	NAG	C1-O5-C5	2.46	115.49	112.19
2	A	401	C5P	N4-C4-N3	2.24	121.92	117.91
2	B	401	C5P	N4-C4-N3	2.23	121.90	117.91
2	F	401	C5P	O2P-P-O1P	2.19	119.37	110.83
2	D	401	C5P	C5-C6-N1	-2.17	118.31	121.84
3	D	404	NAG	C1-O5-C5	2.15	115.06	112.19
2	C	401	C5P	O2P-P-O1P	2.03	118.75	110.83

There are no chirality outliers.

All (27) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	403	NAG	O5-C5-C6-O6
3	B	403	NAG	O5-C5-C6-O6
3	A	403	NAG	C4-C5-C6-O6
3	C	402	NAG	C4-C5-C6-O6
3	C	402	NAG	O5-C5-C6-O6
3	B	403	NAG	C4-C5-C6-O6
3	A	403	NAG	C8-C7-N2-C2
3	A	403	NAG	O7-C7-N2-C2
3	D	403	NAG	C8-C7-N2-C2
3	D	403	NAG	O7-C7-N2-C2
3	D	403	NAG	C4-C5-C6-O6
3	D	403	NAG	O5-C5-C6-O6
3	D	404	NAG	C4-C5-C6-O6
3	D	404	NAG	O5-C5-C6-O6
2	D	401	C5P	C5'-O5'-P-O1P
3	D	402	NAG	C4-C5-C6-O6
3	B	402	NAG	C1-C2-N2-C7
3	D	404	NAG	C1-C2-N2-C7
3	B	403	NAG	C3-C2-N2-C7
3	C	403	NAG	C3-C2-N2-C7
3	D	404	NAG	C3-C2-N2-C7
3	A	402	NAG	C1-C2-N2-C7
3	B	403	NAG	C1-C2-N2-C7
3	D	402	NAG	O5-C5-C6-O6
3	B	402	NAG	C3-C2-N2-C7
2	C	401	C5P	C5'-O5'-P-O2P
2	D	401	C5P	C5'-O5'-P-O2P

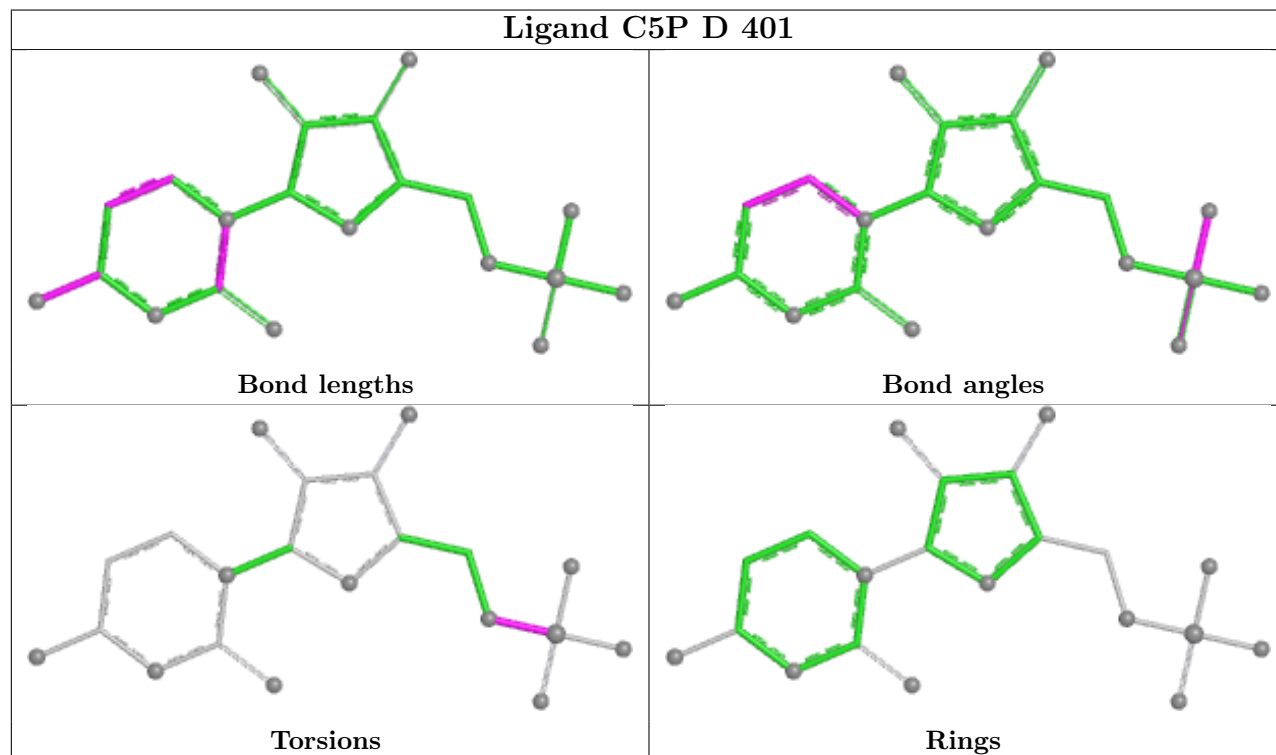
There are no ring outliers.

6 monomers are involved in 9 short contacts:

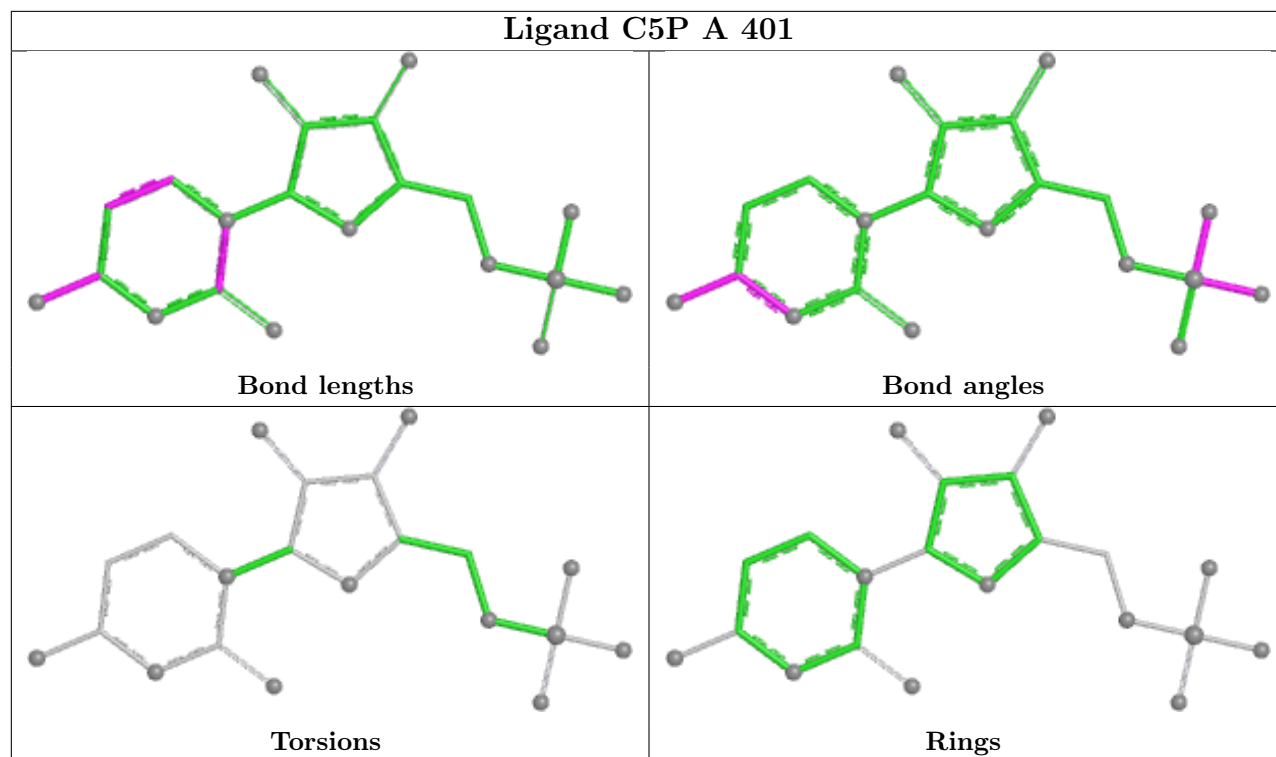
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	401	C5P	2	0
2	B	401	C5P	2	0
2	F	401	C5P	1	0
2	E	401	C5P	2	0
3	C	403	NAG	1	0
2	C	401	C5P	1	0

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

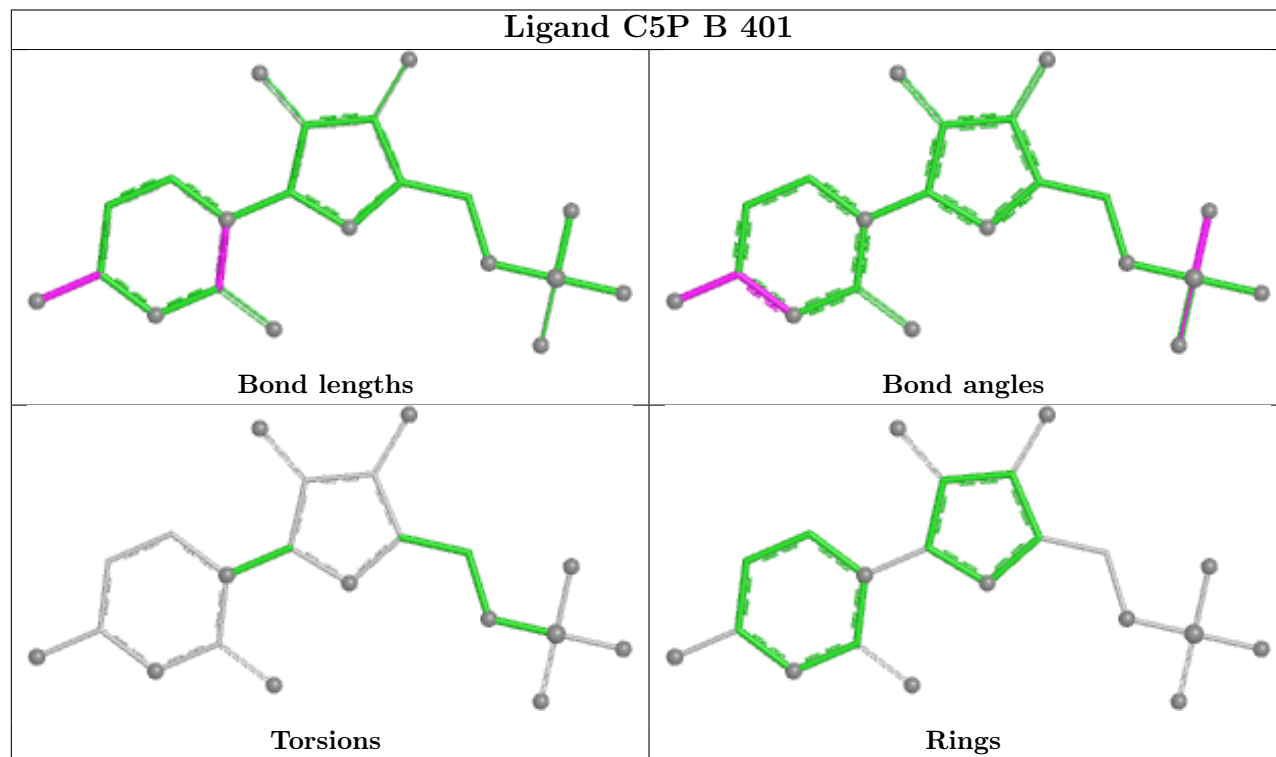
addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. 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.



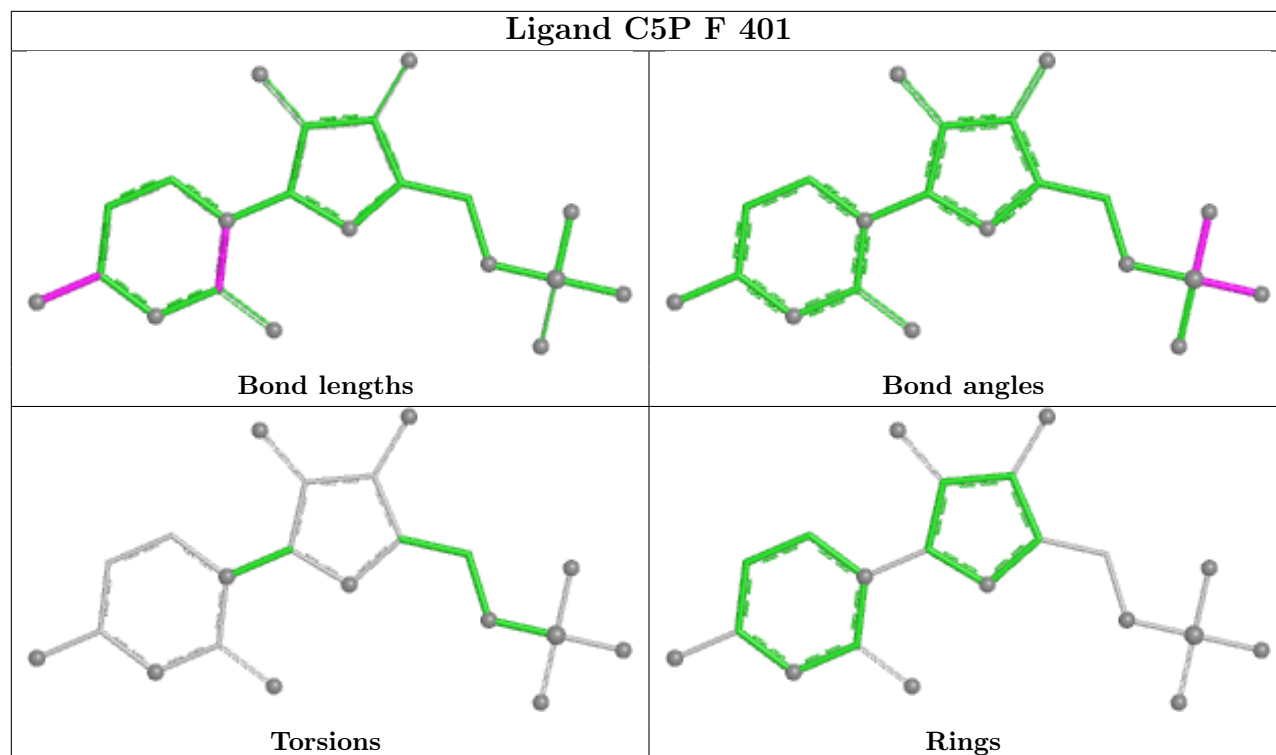
Ligand C5P A 401



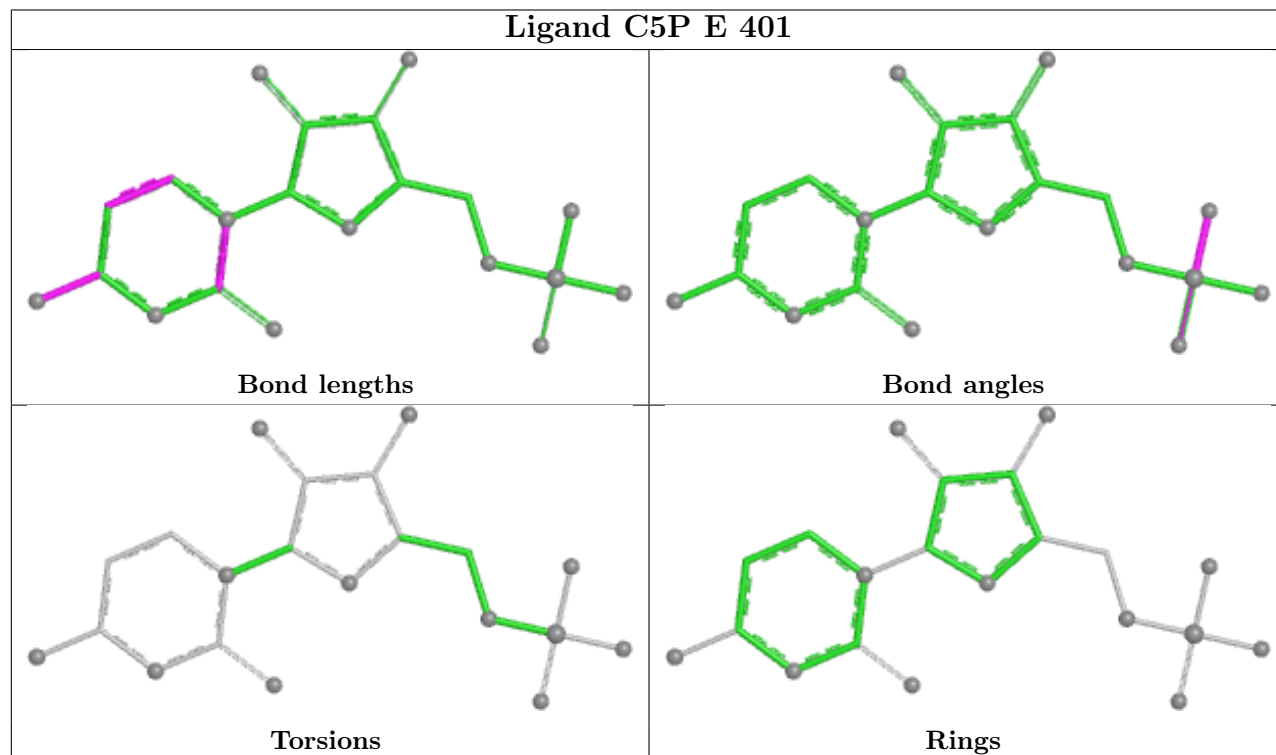
Ligand C5P B 401

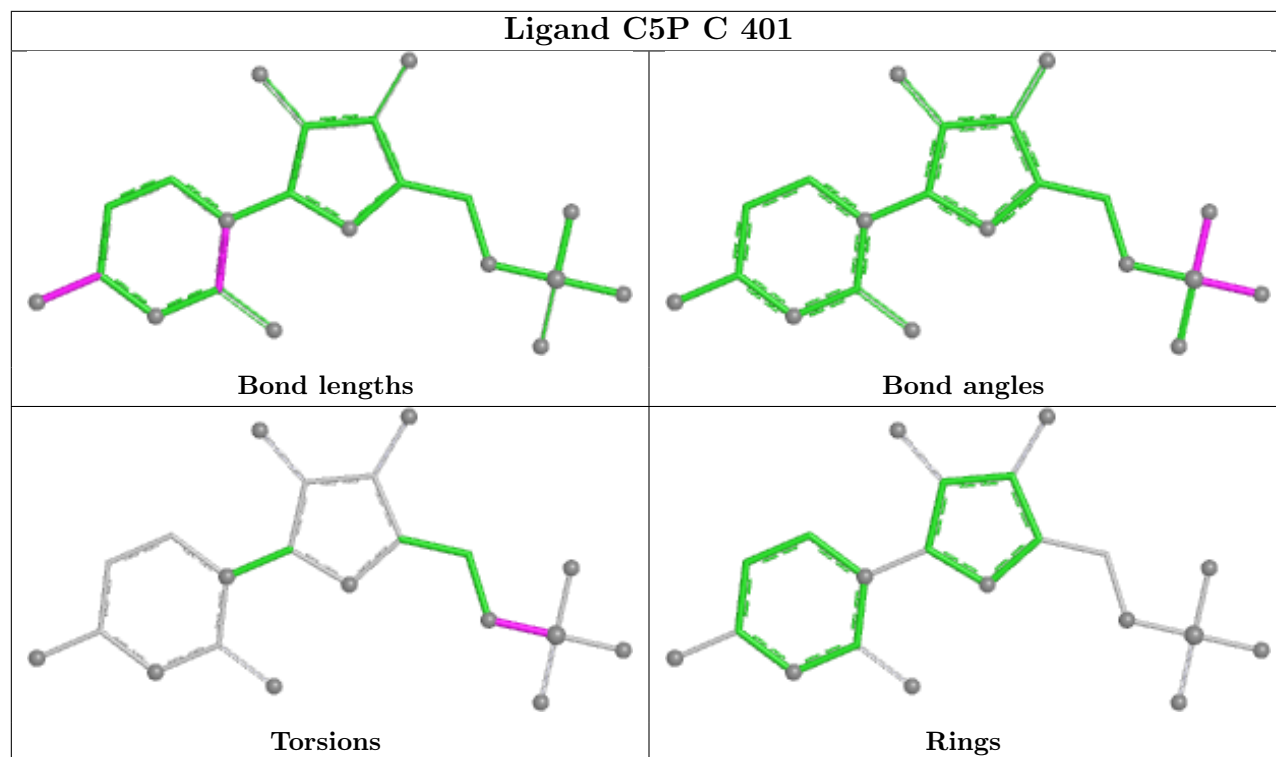


Ligand C5P F 401



Ligand C5P E 401





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	289/374 (77%)	0.15	14 (4%) 35 41	41, 60, 114, 156	0
1	B	295/374 (78%)	0.19	13 (4%) 39 45	41, 61, 130, 183	0
1	C	301/374 (80%)	0.27	8 (2%) 56 63	46, 73, 123, 187	0
1	D	297/374 (79%)	0.32	12 (4%) 42 48	44, 76, 129, 181	0
1	E	281/374 (75%)	0.59	17 (6%) 27 31	46, 84, 142, 193	0
1	F	281/374 (75%)	0.53	17 (6%) 27 31	45, 84, 134, 172	0
All	All	1744/2244 (77%)	0.34	81 (4%) 37 43	41, 72, 132, 193	0

All (81) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	110	ALA	4.8
1	A	344	PRO	4.6
1	D	228	ILE	4.2
1	C	110	ALA	4.1
1	B	110	ALA	4.0
1	B	69	LEU	3.9
1	F	110	ALA	3.8
1	F	260	HIS	3.7
1	C	140	PRO	3.6
1	B	348	TYR	3.5
1	B	340	ARG	3.5
1	E	69	LEU	3.5
1	A	69	LEU	3.3
1	F	228	ILE	3.3
1	E	110	ALA	3.3
1	A	339	GLU	3.3
1	E	267	ALA	3.2
1	F	72	LEU	3.2
1	A	146	PRO	3.2

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Mol	Chain	Res	Type	RSRZ
1	B	344	PRO	3.2
1	F	71	HIS	3.1
1	C	96	LEU	3.1
1	A	343	LYS	3.1
1	C	297	PHE	3.1
1	D	110	ALA	2.9
1	D	113	GLY	2.9
1	F	148	CYS	2.8
1	F	370	GLN	2.8
1	F	265	PRO	2.8
1	A	340	ARG	2.8
1	F	70	LEU	2.7
1	F	295	THR	2.7
1	E	72	LEU	2.7
1	E	260	HIS	2.6
1	D	148	CYS	2.6
1	E	148	CYS	2.6
1	A	349	ALA	2.6
1	C	144	THR	2.5
1	D	68	HIS	2.5
1	C	69	LEU	2.5
1	E	214	LEU	2.5
1	F	267	ALA	2.5
1	E	190	VAL	2.4
1	E	294	ASN	2.4
1	F	175	VAL	2.4
1	B	67	ARG	2.4
1	B	140	PRO	2.4
1	C	145	PRO	2.4
1	D	69	LEU	2.4
1	D	66	CYS	2.3
1	A	67	ARG	2.3
1	E	228	ILE	2.3
1	E	66	CYS	2.3
1	B	68	HIS	2.3
1	D	80	PHE	2.2
1	E	370	GLN	2.2
1	A	300	LEU	2.2
1	B	214	LEU	2.2
1	E	209	VAL	2.2
1	D	83	LEU	2.2
1	D	88	ILE	2.2

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Mol	Chain	Res	Type	RSRZ
1	F	299	ASP	2.2
1	B	71	HIS	2.2
1	F	350	ASN	2.1
1	D	140	PRO	2.1
1	F	140	PRO	2.1
1	A	77	HIS	2.1
1	B	295	THR	2.1
1	F	269	ALA	2.1
1	E	77	HIS	2.1
1	C	228	ILE	2.1
1	D	77	HIS	2.1
1	F	107	GLN	2.1
1	A	215	GLY	2.1
1	E	191	GLY	2.1
1	A	66	CYS	2.1
1	E	80	PHE	2.1
1	B	77	HIS	2.0
1	B	109	LYS	2.0
1	E	268	SER	2.0
1	A	70	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 oligosaccharides in this entry.

6.4 Ligands [i](#)

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
3	NAG	B	403	14/15	0.63	0.18	113,125,136,137	0
3	NAG	D	403	14/15	0.66	0.14	123,149,155,159	0
3	NAG	A	403	14/15	0.68	0.17	88,117,130,133	0

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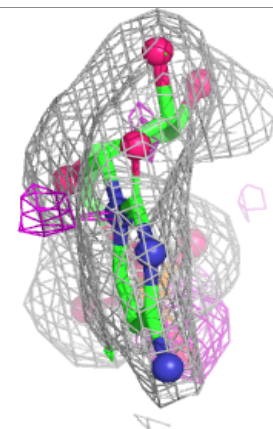
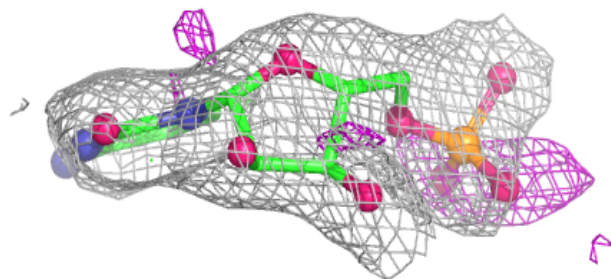
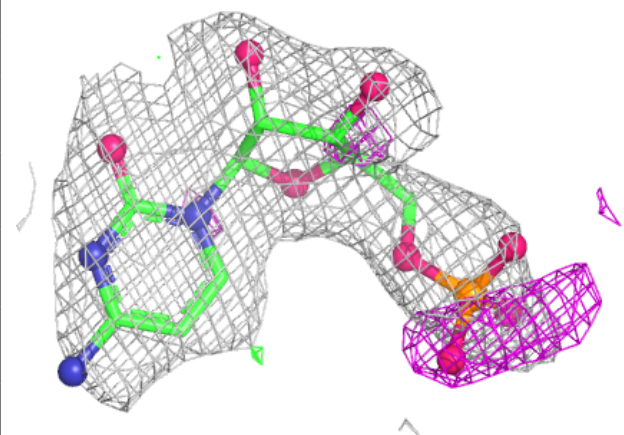
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
3	NAG	C	402	14/15	0.69	0.12	127,133,138,144	0
3	NAG	D	404	14/15	0.71	0.13	78,95,102,103	0
3	NAG	C	403	14/15	0.74	0.15	102,122,124,130	0
3	NAG	B	402	14/15	0.75	0.12	98,106,116,122	0
3	NAG	D	402	14/15	0.77	0.11	129,135,143,148	0
3	NAG	F	402	14/15	0.77	0.12	111,130,141,142	0
3	NAG	A	402	14/15	0.78	0.12	102,115,122,123	0
2	C5P	F	401	21/21	0.82	0.15	66,99,126,139	0
2	C5P	B	401	21/21	0.85	0.14	63,79,97,100	0
2	C5P	A	401	21/21	0.87	0.13	62,79,91,97	0
2	C5P	E	401	21/21	0.88	0.12	68,93,118,127	0
2	C5P	D	401	21/21	0.96	0.07	52,63,68,70	0
2	C5P	C	401	21/21	0.97	0.07	51,58,63,70	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.

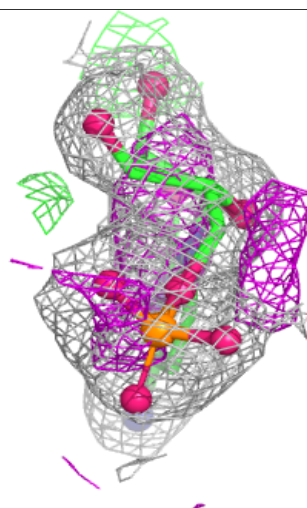
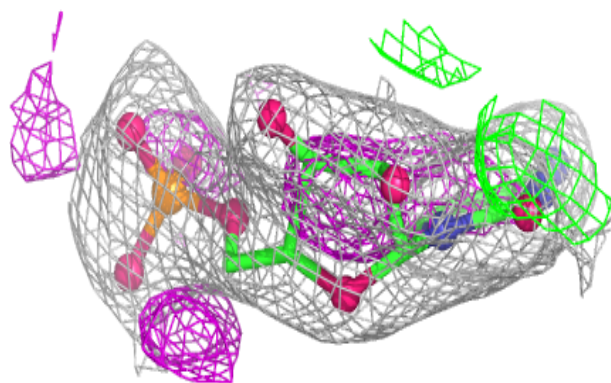
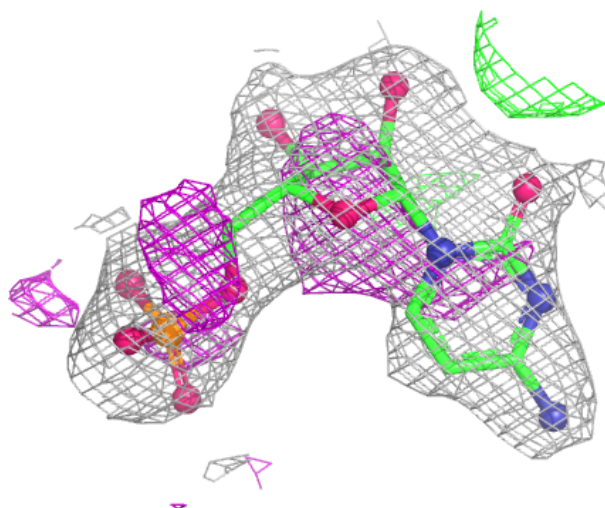
Electron density around C5P F 401:

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



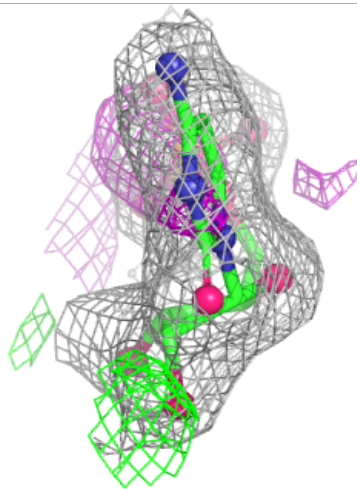
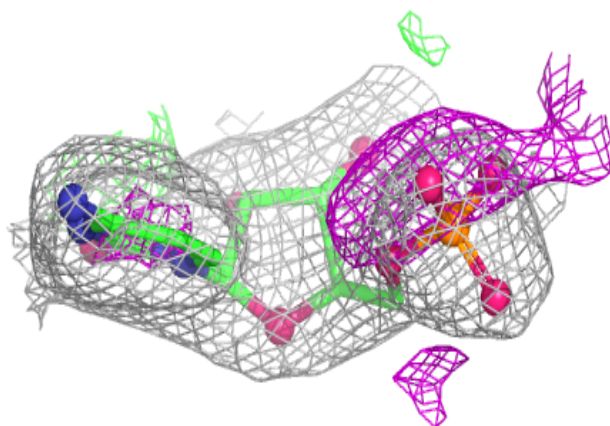
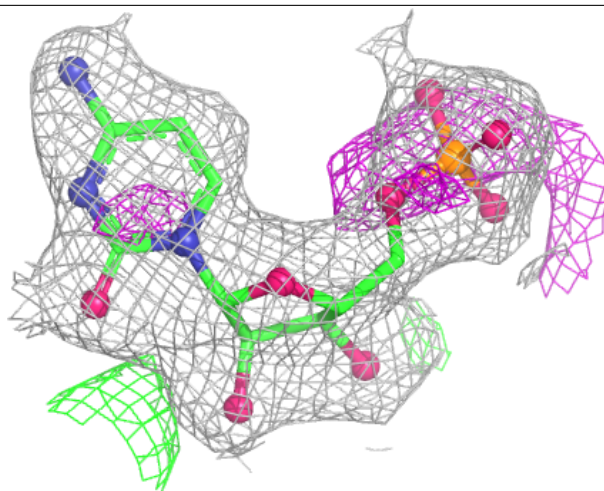
Electron density around C5P B 401:

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



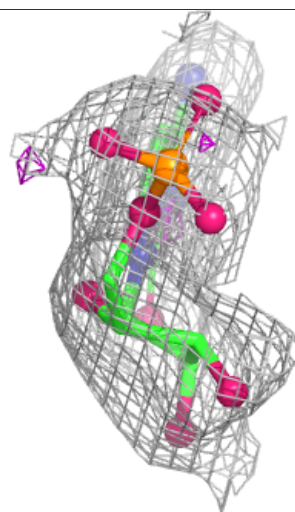
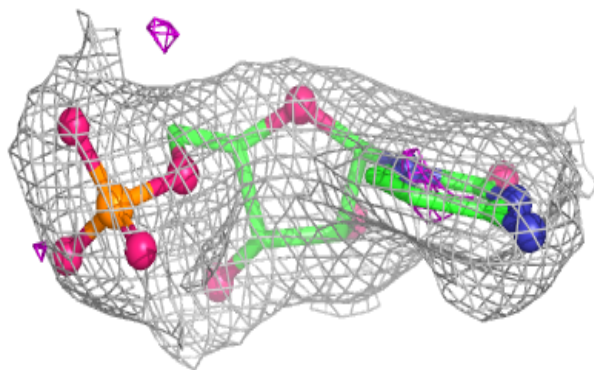
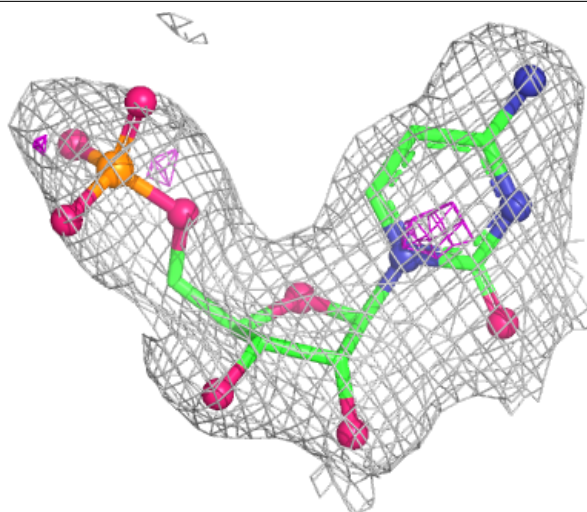
Electron density around C5P A 401:

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



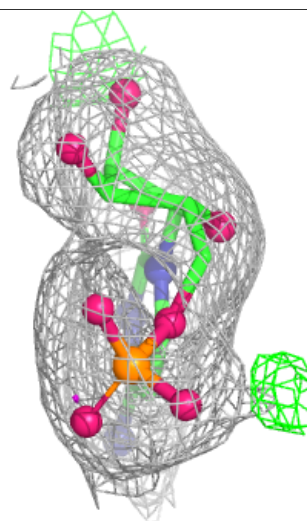
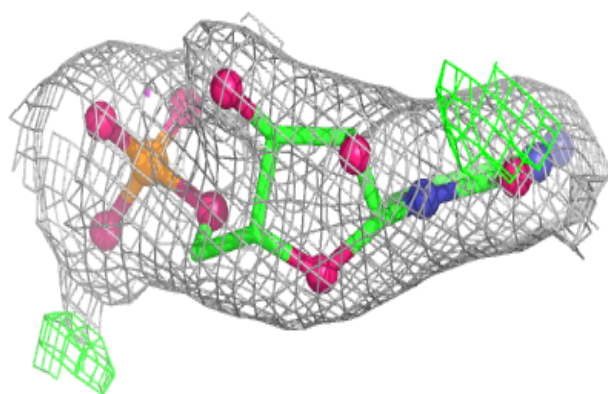
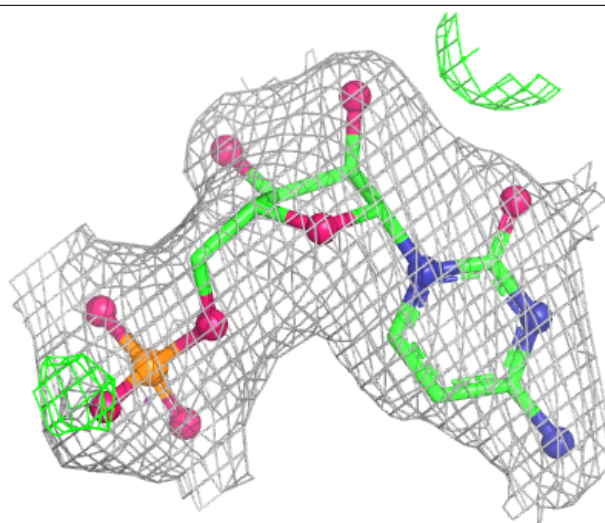
Electron density around C5P E 401:

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



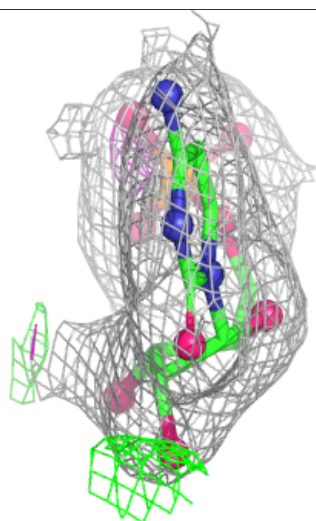
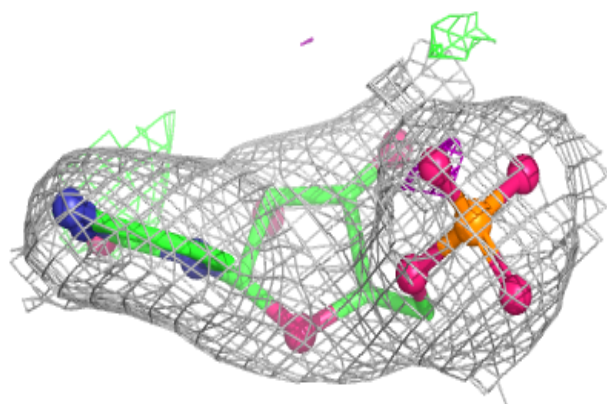
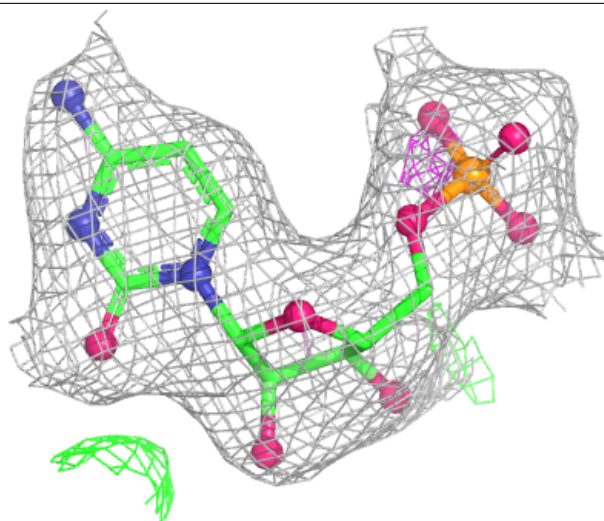
Electron density around C5P D 401:

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



Electron density around C5P C 401:

$2mF_o-DF_c$ (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.