



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 6, 2026 – 06:02 PM UTC

PDB ID : 6AOC / pdb_00006aoc
Title : Crystal Structure of an N-Hydroxythienopyrimidine-2,4-dione RNase H Active Site Inhibitor with Multiple Binding Modes to HIV Reverse Transcriptase
Authors : Kirby, K.A.; Sarafianos, S.G.
Deposited on : 2017-08-15
Resolution : 1.80 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

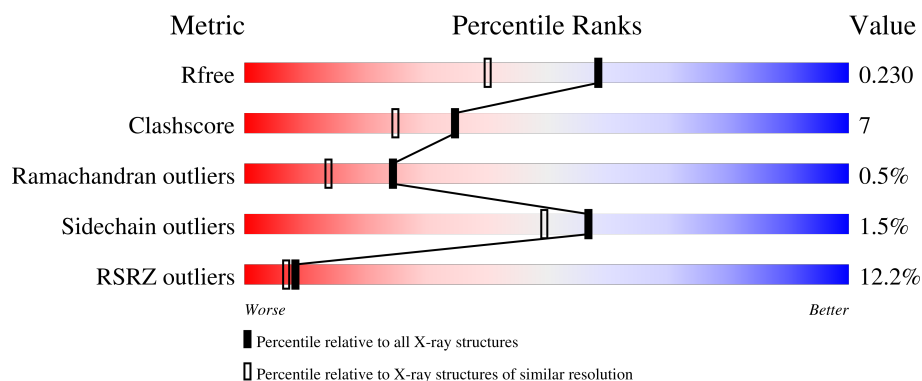
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.80 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	7662 (1.80-1.80)
Clashscore	190562	8479 (1.80-1.80)
Ramachandran outliers	187476	8391 (1.80-1.80)
Sidechain outliers	187428	8390 (1.80-1.80)
RSRZ outliers	180081	7663 (1.80-1.80)

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	557	20% 81%18%
1	C	557	8% 82%17%
2	B	429	9% 86%12%
2	D	429	11% 84%12%

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard

residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
4	ZW2	C	603	-	X	-	-
6	EDO	A	618	-	-	X	-

2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 18190 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 Reverse transcriptase/ribonuclease H.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	555	Total	C	N	O	S	0	16	0
			4607	2985	767	848	7			
1	C	557	Total	C	N	O	S	0	41	0
			4785	3114	791	871	9			

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-1	MET	-	initiating methionine	UNP P03366
A	0	VAL	-	expression tag	UNP P03366
A	280	SER	CYS	engineered mutation	UNP P03366
C	-1	MET	-	initiating methionine	UNP P03366
C	0	VAL	-	expression tag	UNP P03366
C	280	SER	CYS	engineered mutation	UNP P03366

- Molecule 2 is a protein called p51 RT.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	425	Total	C	N	O	S	4	32	0
			3702	2429	607	659	7			
2	D	416	Total	C	N	O	S	11	21	0
			3565	2333	584	640	8			

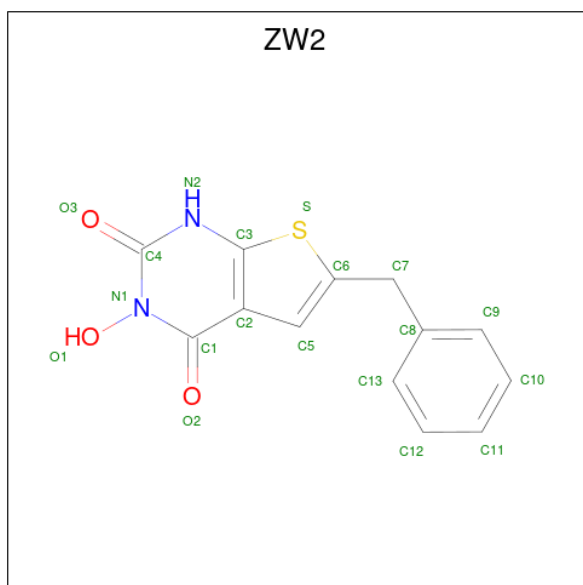
There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	0	GLY	-	expression tag	UNP P03366
B	280	SER	CYS	engineered mutation	UNP P03366
D	0	GLY	-	expression tag	UNP P03366
D	280	SER	CYS	engineered mutation	UNP P03366

- Molecule 3 is MANGANESE (II) ION (CCD ID: MN) (formula: Mn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	2	Total	Mn	0	0
			2	2		
3	C	2	Total	Mn	0	0
			2	2		

- Molecule 4 is 6-benzyl-3-hydroxythieno[2,3-d]pyrimidine-2,4(1H,3H)-dione (CCD ID: ZW2) (formula: C₁₃H₁₀N₂O₃S).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	A	1	Total	C	N	O	S	0	0
			19	13	2	3	1		
4	C	1	Total	C	N	O	S	0	0
			19	13	2	3	1		

- Molecule 5 is TRIETHYLENE GLYCOL (CCD ID: PGE) (formula: C₆H₁₄O₄).



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

- Molecule 6 is 1,2-ETHANEDIOL (CCD ID: EDO) (formula: C₂H₆O₂).



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

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

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

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	D	1	Total C O 4 2 2	0	0
6	D	1	Total C O 4 2 2	0	0
6	D	1	Total C O 4 2 2	0	0
6	D	1	Total C O 4 2 2	0	0
6	D	1	Total C O 4 2 2	0	0
6	D	1	Total C O 4 2 2	0	0
6	D	1	Total C O 4 2 2	0	0
6	D	1	Total C O 4 2 2	0	0
6	D	1	Total C O 4 2 2	0	0
6	D	1	Total C O 4 2 2	0	0
6	D	1	Total C O 4 2 2	0	0
6	D	1	Total C O 4 2 2	0	0

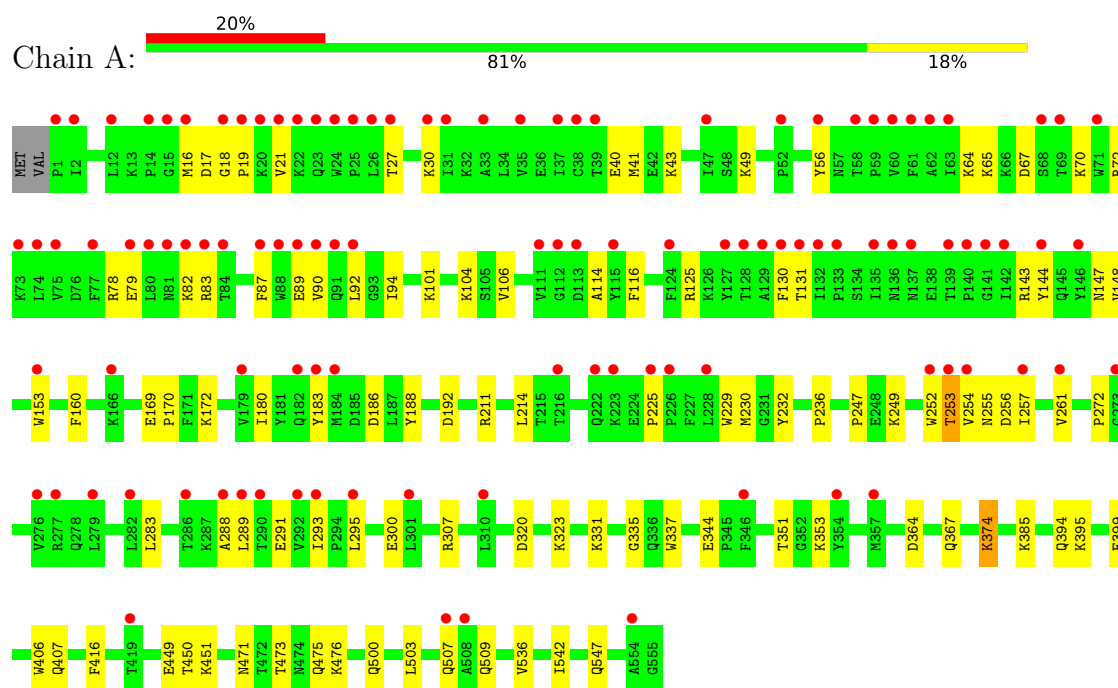
- Molecule 7 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	A	262	Total O 262 262	0	0
7	B	282	Total O 282 282	0	0
7	C	338	Total O 338 338	0	0
7	D	265	Total O 265 265	0	0

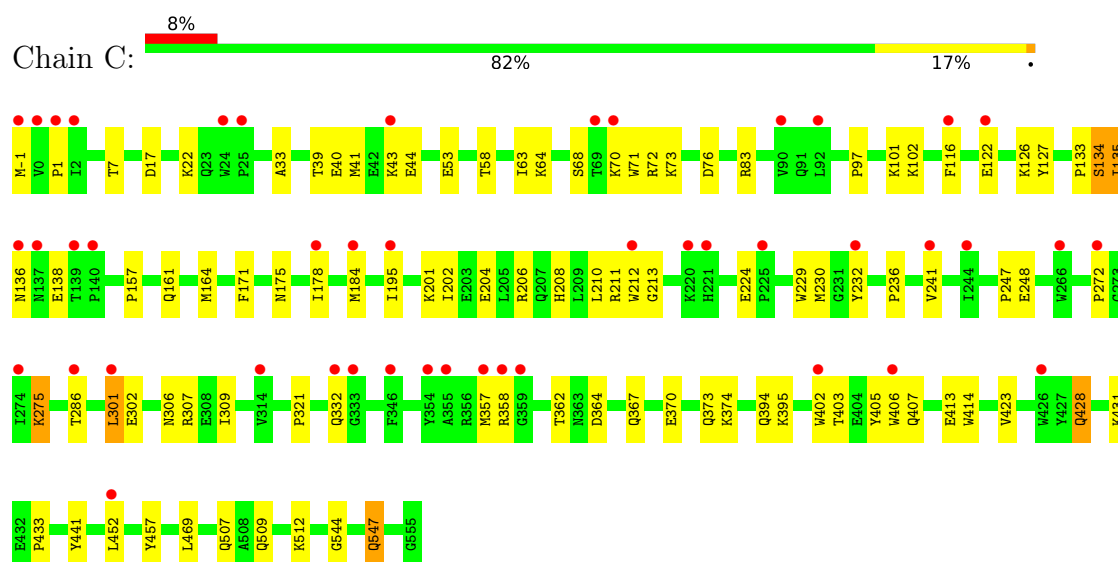
3 Residue-property plots

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.

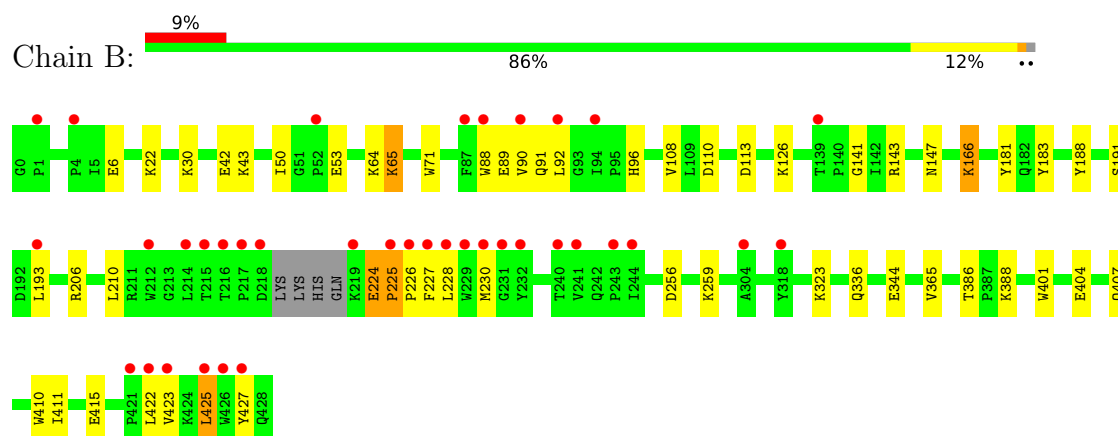
• Molecule 1: Reverse transcriptase/ribonuclease H



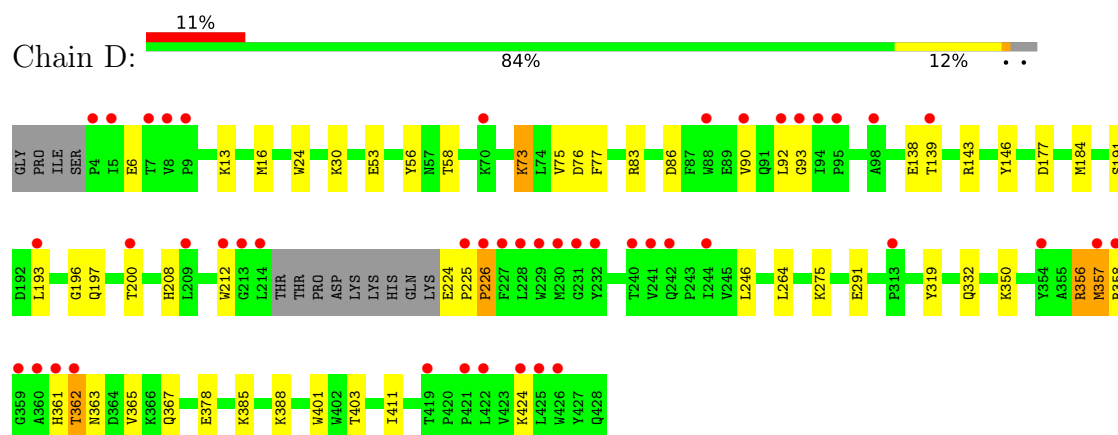
• Molecule 1: Reverse transcriptase/ribonuclease H



- Molecule 2: p51 RT



- Molecule 2: p51 RT



4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	70.37Å 89.12Å 112.73Å 105.72° 95.03° 110.72°	Depositor
Resolution (Å)	55.32 – 1.80 55.32 – 1.80	Depositor EDS
% Data completeness (in resolution range)	97.0 (55.32-1.80) 97.0 (55.32-1.80)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.15 (at 1.80Å)	Xtriage
Refinement program	PHENIX (1.11.1_2575)	Depositor
R, R_{free}	0.186 , 0.226 0.193 , 0.230	Depositor DCC
R_{free} test set	10776 reflections (4.82%)	wwPDB-VP
Wilson B-factor (Å ²)	35.7	Xtriage
Anisotropy	0.194	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 56.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	18190	wwPDB-VP
Average B, all atoms (Å ²)	61.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.28% 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: PGE, ZW2, EDO, MN

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	0.42	0/4767	0.56	0/6467
1	C	0.39	0/5010	0.54	0/6789
2	B	0.48	0/3892	0.57	0/5277
2	D	0.43	0/3722	0.57	0/5049
All	All	0.43	0/17391	0.56	0/23582

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	1
2	D	0	1
All	All	0	2

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	67	ASP	Peptide
2	D	357	MET	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	4607	0	4711	83	1
1	C	4785	0	4966	81	0
2	B	3702	0	3851	53	0
2	D	3565	0	3651	45	0
3	A	2	0	0	0	0
3	C	2	0	0	0	0
4	A	19	0	0	0	0
4	C	19	0	0	0	0
5	A	10	0	14	4	0
5	B	40	0	56	11	0
5	D	20	0	28	6	0
6	A	56	0	84	6	0
6	B	76	0	114	3	0
6	C	92	0	138	4	0
6	D	48	0	72	2	0
7	A	262	0	0	14	1
7	B	282	0	0	14	0
7	C	338	0	0	19	0
7	D	265	0	0	6	2
All	All	18190	0	17685	259	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 7.

All (259) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:56:TYR:O	1:A:143:ARG:NH2	1.88	1.06
1:C:122:GLU:OE2	7:C:701:HOH:O	1.82	0.96
1:A:131:THR:OG1	1:A:143:ARG:NH1	2.03	0.91
1:C:373:GLN:NE2	7:C:703:HOH:O	2.13	0.81
1:A:323:LYS:NZ	1:A:344:GLU:OE2	2.16	0.79
1:C:247:PRO:O	1:C:307[B]:ARG:NH2	2.15	0.79
1:A:64:LYS:NZ	1:A:70:LYS:O	2.14	0.79
1:A:509[B]:GLN:NE2	7:A:705:HOH:O	2.16	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:500:GLN:OE1	7:A:701:HOH:O	2.00	0.78
1:C:102:LYS:HE3	1:C:236:PRO:O	1.84	0.76
1:C:370:GLU:O	1:C:374:LYS:HD2	1.86	0.76
2:B:423:VAL:N	1:C:138:GLU:OE1	2.17	0.76
2:B:415:GLU:OE2	7:B:601:HOH:O	2.03	0.75
1:C:374:LYS:NZ	7:C:703:HOH:O	2.19	0.75
1:C:208:HIS:ND1	7:C:707:HOH:O	2.22	0.73
2:D:75:VAL:O	5:D:501:PGE:O4	2.06	0.72
1:A:475:GLN:OE1	7:A:703:HOH:O	2.08	0.71
2:B:404:GLU:OE2	7:B:602:HOH:O	2.09	0.71
1:C:428[A]:GLN:OE1	1:C:509:GLN:NE2	2.23	0.71
1:C:452:LEU:HD12	1:C:469:LEU:O	1.91	0.70
1:C:102:LYS:NZ	1:C:236:PRO:O	2.24	0.70
1:C:102:LYS:CE	1:C:236:PRO:O	2.41	0.69
1:A:337:TRP:HE1	1:A:367:GLN:HE21	1.42	0.68
1:A:249:LYS:O	7:A:704:HOH:O	2.12	0.68
2:B:336[B]:GLN:NE2	7:B:609:HOH:O	2.27	0.68
1:C:275:LYS:NZ	7:C:712:HOH:O	2.26	0.66
2:D:177:ASP:OD1	7:D:602:HOH:O	2.14	0.66
1:C:364:ASP:OD2	7:C:702:HOH:O	2.13	0.66
2:B:42:GLU:OE1	7:B:603:HOH:O	2.13	0.66
1:C:211:ARG:NH1	6:C:625:EDO:O1	2.30	0.65
1:C:374:LYS:HE3	7:C:966:HOH:O	1.97	0.65
2:D:30[A]:LYS:NZ	7:D:601:HOH:O	2.10	0.65
1:A:253:THR:HG23	1:A:289:LEU:O	1.97	0.64
2:D:358:ARG:CZ	2:D:363:ASN:H	2.10	0.64
1:A:254:VAL:HG22	1:A:293:ILE:HD11	1.80	0.64
1:A:394:GLN:HB3	5:A:604:PGE:H12	1.79	0.63
5:B:501:PGE:H12	7:B:739:HOH:O	1.98	0.63
2:D:388[B]:LYS:NZ	7:D:604:HOH:O	2.32	0.63
1:A:257:ILE:O	1:A:261:VAL:HG23	1.98	0.62
2:B:423:VAL:HG23	1:C:138:GLU:OE1	1.97	0.62
1:A:395:LYS:CG	5:A:604:PGE:H32	2.29	0.62
1:A:247:PRO:O	1:A:307[A]:ARG:NH1	2.24	0.62
2:B:230:MET:O	7:B:604:HOH:O	2.16	0.61
2:B:181:TYR:HA	5:B:504:PGE:H32	1.83	0.61
2:D:358:ARG:NH1	2:D:363:ASN:H	1.97	0.61
2:D:358:ARG:HD2	2:D:361:HIS:HB2	1.82	0.61
1:A:153:TRP:O	7:A:706:HOH:O	2.16	0.60
1:C:41:MET:HE3	1:C:116:PHE:HZ	1.66	0.60
2:D:356:ARG:NH2	7:D:606:HOH:O	2.35	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:65:LYS:HB3	1:A:72:ARG:HH21	1.68	0.58
1:A:114:ALA:HB1	1:A:214:LEU:HD22	1.84	0.58
1:C:7:THR:OG1	7:C:701:HOH:O	1.82	0.58
1:A:92:LEU:HD11	2:B:22[A]:LYS:HD3	1.85	0.57
2:B:96:HIS:HD2	7:B:835:HOH:O	1.88	0.57
2:B:422:LEU:N	1:C:138:GLU:OE1	2.37	0.57
2:B:224:GLU:N	2:B:225:PRO:HD3	2.20	0.56
1:A:374:LYS:NZ	7:A:702:HOH:O	2.16	0.56
1:C:275:LYS:HE2	1:C:302:GLU:HG3	1.88	0.55
1:A:87:PHE:HB2	1:A:89:GLU:OE2	2.06	0.54
2:B:411:ILE:O	5:B:501:PGE:H1	2.07	0.54
1:C:507:GLN:NE2	7:C:721:HOH:O	2.39	0.54
1:C:171:PHE:HE2	1:C:178:ILE:CD1	2.20	0.54
2:D:358:ARG:NH1	2:D:367:GLN:NE2	2.54	0.54
1:A:104:LYS:HB2	1:A:192:ASP:HA	1.89	0.54
2:D:77:PHE:H	5:D:501:PGE:H62	1.71	0.54
1:C:201:LYS:NZ	1:C:204:GLU:OE2	2.37	0.54
1:C:362:THR:HG21	1:C:367[A]:GLN:HE21	1.73	0.53
2:B:224:GLU:H	2:B:225:PRO:HD3	1.71	0.53
2:D:196:GLY:O	2:D:200:THR:HG23	2.08	0.53
1:A:16:MET:HB3	1:A:83:ARG:HH11	1.74	0.53
1:A:320:ASP:OD2	1:A:323:LYS:HE3	2.09	0.53
2:D:53:GLU:OE2	2:D:53:GLU:N	2.37	0.53
1:A:272:PRO:HB2	1:A:353[B]:LYS:HG3	1.90	0.53
2:B:64:LYS:H	5:B:502:PGE:H5	1.73	0.53
2:B:64:LYS:HB2	5:B:502:PGE:H4	1.90	0.53
1:A:230:MET:HE3	1:A:232:TYR:CE2	2.44	0.52
2:B:91:GLN:C	2:B:92:LEU:HD12	2.35	0.52
1:A:406:TRP:CE2	1:A:407:GLN:HG3	2.45	0.52
1:A:473:THR:OG1	1:A:476[B]:LYS:HD3	2.10	0.52
1:C:136:ASN:C	1:C:138:GLU:H	2.17	0.51
2:D:275:LYS:NZ	7:D:611:HOH:O	2.43	0.51
2:D:358:ARG:NH1	2:D:362:THR:HA	2.25	0.51
2:D:332:GLN:OE1	2:D:424:LYS:HE2	2.09	0.51
2:D:184[A]:MET:HE2	5:D:501:PGE:H4	1.93	0.51
1:C:134[B]:SER:O	7:C:705:HOH:O	2.18	0.51
2:D:208:HIS:O	2:D:212:TRP:HD1	1.94	0.51
1:A:125:ARG:HD3	1:A:147:ASN:HA	1.91	0.51
1:A:254:VAL:HA	1:A:257:ILE:HG22	1.92	0.51
1:A:335:GLY:N	6:A:618:EDO:O2	2.40	0.51
1:A:367:GLN:NE2	6:A:618:EDO:O1	2.43	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:210:LEU:HD21	2:B:225:PRO:HB3	1.93	0.50
1:A:79:GLU:HA	1:A:82:LYS:HE3	1.93	0.50
2:B:92:LEU:HD23	7:B:743:HOH:O	2.11	0.50
2:B:191:SER:HB2	2:B:193:LEU:HD13	1.93	0.50
1:A:78:ARG:HH22	1:A:288:ALA:HA	1.77	0.50
1:C:406:TRP:CE3	1:C:407[B]:GLN:HG2	2.46	0.50
1:C:134[B]:SER:O	1:C:135[B]:ILE:HB	2.11	0.50
1:A:19:PRO:HD2	1:A:56:TYR:HB3	1.93	0.50
2:B:64:LYS:H	5:B:502:PGE:C5	2.25	0.50
2:D:224:GLU:C	2:D:226:PRO:HD3	2.36	0.50
2:D:13:LYS:HD2	2:D:16:MET:CE	2.41	0.50
1:A:351:THR:O	7:A:708:HOH:O	2.20	0.49
2:B:65[B]:LYS:HZ2	2:B:227:PHE:HB3	1.77	0.49
1:C:406:TRP:CD1	1:C:406:TRP:H	2.29	0.49
6:A:608:EDO:O2	1:C:70:LYS:HE2	2.13	0.49
2:B:65[B]:LYS:NZ	2:B:110:ASP:OD2	2.25	0.49
2:B:422:LEU:H	1:C:138:GLU:CD	2.20	0.49
5:B:504:PGE:H4	7:B:847:HOH:O	2.12	0.49
1:C:210:LEU:HD23	1:C:210:LEU:O	2.13	0.49
1:A:90:VAL:CG1	2:B:141:GLY:H	2.25	0.49
1:A:106:VAL:HG21	6:A:606:EDO:H11	1.94	0.49
1:A:130:PHE:CE1	1:A:144:TYR:HB2	2.48	0.49
2:B:183:TYR:OH	2:B:386:THR:HG23	2.12	0.49
1:A:536:VAL:HB	1:A:542:ILE:HD13	1.95	0.49
2:B:43[B]:LYS:NZ	7:B:626:HOH:O	2.45	0.49
1:A:385:LYS:NZ	7:A:714:HOH:O	2.32	0.48
2:B:224:GLU:C	2:B:226:PRO:HD3	2.38	0.48
1:A:395:LYS:HG3	5:A:604:PGE:H32	1.95	0.48
1:A:211:ARG:NH2	7:A:707:HOH:O	2.19	0.48
1:A:257:ILE:HG23	1:A:283:LEU:HD21	1.96	0.48
1:A:450:THR:O	1:A:451:LYS:HB2	2.14	0.48
1:C:370:GLU:O	1:C:374:LYS:CD	2.57	0.48
1:A:101:LYS:NZ	7:A:722:HOH:O	2.43	0.48
1:C:58:THR:HG23	1:C:76:ASP:O	2.13	0.48
1:C:17:ASP:O	1:C:83:ARG:HD3	2.14	0.48
1:C:229:TRP:CZ2	1:C:230:MET:HE2	2.48	0.48
1:A:230:MET:HE3	1:A:232:TYR:HE2	1.78	0.47
2:B:30[B]:LYS:NZ	7:B:606:HOH:O	2.40	0.47
1:A:225:PRO:HB3	1:A:236:PRO:HD3	1.94	0.47
1:C:431:LYS:NZ	7:C:727:HOH:O	2.46	0.47
1:A:399:GLU:OE2	7:A:709:HOH:O	2.20	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:41:MET:SD	1:C:73:LYS:HE2	2.55	0.47
1:A:169[A]:GLU:HB3	1:A:170:PRO:HD3	1.96	0.47
1:A:253:THR:HB	1:A:256:ASP:OD2	2.14	0.47
2:B:407:GLN:HE21	5:B:502:PGE:C3	2.28	0.47
2:D:191:SER:HB2	2:D:193:LEU:HD13	1.97	0.47
2:B:90:VAL:O	2:B:91:GLN:HB2	2.14	0.47
6:C:620:EDO:O2	7:C:704:HOH:O	2.18	0.47
1:C:213:GLY:HA3	6:C:613:EDO:H21	1.97	0.46
2:D:90:VAL:HG12	2:D:92:LEU:HD12	1.96	0.46
1:C:405:TYR:CE2	1:C:407[A]:GLN:HB2	2.49	0.46
2:B:323[A]:LYS:NZ	2:B:344:GLU:OE2	2.46	0.46
1:A:114:ALA:HB3	1:A:160:PHE:CE1	2.50	0.46
1:A:364:ASP:OD1	6:A:618:EDO:H12	2.15	0.46
1:C:157:PRO:O	1:C:161[B]:GLN:HG2	2.14	0.46
1:A:295:LEU:HD13	1:A:300:GLU:HG2	1.98	0.46
1:A:19:PRO:HA	1:A:79:GLU:OE1	2.16	0.46
1:A:288:ALA:N	1:A:291:GLU:OE1	2.48	0.46
1:C:306:ASN:HA	1:C:309:ILE:HD12	1.96	0.46
2:D:358:ARG:CZ	2:D:367:GLN:HG3	2.45	0.46
1:A:49:LYS:HG2	1:A:144:TYR:CE1	2.51	0.46
6:B:523:EDO:C2	7:B:705:HOH:O	2.64	0.46
1:C:211:ARG:O	1:C:211:ARG:NH2	2.41	0.46
2:B:423:VAL:HG12	2:B:427:TYR:HD2	1.80	0.45
2:D:291:GLU:OE1	7:D:603:HOH:O	2.21	0.45
1:A:307[B]:ARG:NH2	7:A:729:HOH:O	2.49	0.45
1:A:416:PHE:CB	5:A:604:PGE:H3	2.47	0.45
1:C:544[B]:GLY:N	1:C:547[B]:GLN:OE1	2.49	0.45
1:A:449:GLU:HB3	1:C:-1:MET:HE3	1.98	0.45
2:B:90:VAL:O	2:B:92:LEU:HD12	2.16	0.45
1:A:130:PHE:C	1:A:143:ARG:NH1	2.75	0.45
1:A:503:LEU:O	1:A:507[A]:GLN:HG2	2.17	0.45
1:A:27:THR:OG1	1:A:30:LYS:HG3	2.17	0.45
2:B:88:TRP:CD1	2:B:89:GLU:N	2.85	0.45
1:A:40:GLU:O	1:A:43:LYS:HG2	2.16	0.44
1:C:232:TYR:CE1	1:C:241:VAL:HG22	2.53	0.44
2:D:24:TRP:CD2	5:D:502:PGE:H4	2.52	0.44
2:D:56:TYR:O	2:D:143:ARG:NH1	2.42	0.44
2:D:138:GLU:HG2	2:D:139:THR:HG23	1.98	0.44
2:B:425:LEU:HD23	2:B:425:LEU:H	1.83	0.44
1:C:126:LYS:HE2	1:C:127:TYR:CZ	2.53	0.44
1:A:253:THR:HG22	1:A:255:ASN:N	2.33	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:171:PHE:CE2	1:C:178:ILE:CD1	3.00	0.44
1:C:509:GLN:HB3	7:C:963:HOH:O	2.18	0.44
2:D:73[B]:LYS:NZ	2:D:146:TYR:OH	2.36	0.44
1:C:97:PRO:HD3	1:C:232:TYR:CE2	2.53	0.44
1:C:248:GLU:HG3	1:C:307[B]:ARG:NH2	2.32	0.44
2:B:206[B]:ARG:HG3	2:B:228:LEU:HG	1.99	0.44
1:C:406:TRP:CZ3	1:C:407[B]:GLN:OE1	2.71	0.44
1:C:394:GLN:NE2	7:C:713:HOH:O	2.29	0.44
2:D:90:VAL:HG12	2:D:92:LEU:CD1	2.48	0.43
2:D:358:ARG:NH1	2:D:367:GLN:CD	2.76	0.43
2:D:358:ARG:NH2	2:D:367:GLN:HG3	2.33	0.43
2:D:13:LYS:HB2	2:D:16:MET:CE	2.49	0.43
2:D:16:MET:HE3	2:D:83:ARG:HA	2.01	0.43
2:D:358:ARG:NH2	2:D:363:ASN:H	2.16	0.43
2:D:403:THR:H	5:D:502:PGE:H62	1.84	0.43
2:D:58:THR:HG23	2:D:76:ASP:O	2.18	0.43
1:C:39:THR:O	1:C:43[B]:LYS:HG2	2.19	0.43
1:C:133:PRO:O	1:C:134[B]:SER:C	2.61	0.43
1:C:101:LYS:HD3	1:C:321:PRO:HG3	2.00	0.43
2:B:50:ILE:HG13	2:B:143[A]:ARG:HB3	2.00	0.43
1:C:33:ALA:HB1	1:C:71:TRP:HB2	2.01	0.42
2:B:108:VAL:HG22	2:B:188:TYR:CD2	2.54	0.42
1:C:275:LYS:NZ	7:C:740:HOH:O	2.52	0.42
2:D:92:LEU:O	2:D:93:GLY:C	2.62	0.42
2:B:410:TRP:CB	5:B:501:PGE:H32	2.49	0.42
2:D:350:LYS:HE3	2:D:378:GLU:OE1	2.19	0.42
1:A:331:LYS:HE3	6:A:618:EDO:C1	2.50	0.42
1:A:337:TRP:HE1	1:A:367:GLN:NE2	2.14	0.42
2:D:86:ASP:H	6:D:505:EDO:HO1	1.66	0.42
1:C:357:MET:HE2	7:C:979:HOH:O	2.18	0.42
1:C:395[A]:LYS:HE2	1:C:414:TRP:CE2	2.55	0.42
2:D:193:LEU:N	2:D:193:LEU:HD12	2.35	0.42
1:A:17:ASP:CG	1:A:18:GLY:H	2.27	0.42
1:A:18:GLY:HA3	1:A:56:TYR:CD1	2.55	0.42
1:C:423:VAL:O	7:C:706:HOH:O	2.22	0.42
1:A:186:ASP:HB3	1:A:229:TRP:HD1	1.84	0.42
2:B:147:ASN:HB3	6:B:513:EDO:C1	2.49	0.42
2:B:423:VAL:HG12	2:B:427:TYR:CD2	2.55	0.42
2:D:319:TYR:OH	2:D:385:LYS:HE2	2.20	0.42
2:B:407:GLN:HE21	5:B:502:PGE:H32	1.84	0.42
2:B:126[A]:LYS:NZ	7:B:639:HOH:O	2.53	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:175:ASN:O	1:C:178:ILE:HG12	2.20	0.42
1:C:402:TRP:CZ3	1:C:403:THR:HG22	2.54	0.42
2:B:166[A]:LYS:NZ	7:B:637:HOH:O	2.53	0.41
2:B:422:LEU:N	1:C:138:GLU:CD	2.78	0.41
1:A:41:MET:HE2	1:A:116:PHE:HE2	1.84	0.41
1:A:253:THR:HG22	1:A:256:ASP:H	1.85	0.41
1:C:157:PRO:HB3	1:C:184:MET:HE1	2.01	0.41
1:C:433:PRO:HG2	6:D:512:EDO:H21	2.02	0.41
1:A:131:THR:OG1	1:A:143:ARG:CD	2.69	0.41
1:A:229:TRP:CZ3	1:A:230:MET:HE2	2.54	0.41
1:C:413:GLU:HG2	1:C:414:TRP:N	2.36	0.41
2:B:256:ASP:HA	2:B:259:LYS:HE2	2.02	0.41
1:C:413:GLU:O	7:C:708:HOH:O	2.22	0.41
2:B:30[A]:LYS:HE2	2:B:71:TRP:CZ3	2.56	0.41
1:C:202:ILE:O	1:C:206:ARG:HG3	2.21	0.41
1:C:374:LYS:HE2	7:C:979:HOH:O	2.21	0.41
1:A:172:LYS:HE2	1:A:180:ILE:HB	2.02	0.41
1:A:180:ILE:HA	1:A:188:TYR:O	2.20	0.41
2:B:365:VAL:HG11	2:B:401:TRP:HB2	2.03	0.41
2:B:388[A]:LYS:HZ2	2:B:388[A]:LYS:HG3	1.60	0.41
2:B:410:TRP:HB2	5:B:501:PGE:H32	2.02	0.41
1:C:63:ILE:HG22	1:C:64:LYS:N	2.36	0.41
1:C:286:THR:O	1:C:286:THR:HG23	2.21	0.41
1:A:21:VAL:HG23	1:A:79:GLU:HG3	2.04	0.41
2:B:147:ASN:HB3	6:B:513:EDO:H12	2.03	0.41
2:D:411:ILE:H	5:D:501:PGE:C3	2.34	0.41
1:C:1:PRO:HB3	6:C:613:EDO:H12	2.02	0.40
2:D:358:ARG:NE	2:D:361:HIS:O	2.54	0.40
1:A:337:TRP:O	1:A:353[A]:LYS:HA	2.21	0.40
2:D:13:LYS:HB2	2:D:16:MET:HE3	2.01	0.40
2:D:365:VAL:HG11	2:D:401:TRP:HB2	2.03	0.40
1:A:253:THR:HG21	7:A:928:HOH:O	2.20	0.40
1:A:451:LYS:HZ3	1:A:471:ASN:C	2.29	0.40
1:C:224:GLU:O	1:C:224:GLU:HG2	2.21	0.40
1:C:441:TYR:O	1:C:457:TYR:HA	2.22	0.40
1:A:94:ILE:HG22	1:A:183:TYR:OH	2.22	0.40
1:A:116:PHE:O	1:A:148:VAL:HG11	2.22	0.40
1:A:252:TRP:CD1	1:A:295:LEU:HD11	2.56	0.40
1:C:22[B]:LYS:H	1:C:22[B]:LYS:HD2	1.86	0.40
2:D:246:LEU:HD11	2:D:264:LEU:HD21	2.02	0.40

All (2) symmetry-related close contacts are listed below. The label for Atom-2 includes the sym-

metry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:A:908:HOH:O	7:D:757:HOH:O[1_656]	2.08	0.12
1:A:399:GLU:OE1	7:D:662:HOH:O[1_656]	2.19	0.01

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	569/557 (102%)	556 (98%)	13 (2%)	0	100	100
1	C	596/557 (107%)	581 (98%)	10 (2%)	5 (1%)	16	6
2	B	453/429 (106%)	441 (97%)	10 (2%)	2 (0%)	30	19
2	D	433/429 (101%)	419 (97%)	10 (2%)	4 (1%)	14	5
All	All	2051/1972 (104%)	1997 (97%)	43 (2%)	11 (0%)	24	14

All (11) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	134[A]	SER
1	C	134[B]	SER
1	C	135[A]	ILE
1	C	135[B]	ILE
2	D	225	PRO
2	D	357	MET
2	B	225	PRO
2	D	226	PRO
2	D	356	ARG
1	C	272	PRO
2	B	224	GLU

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	509/497 (102%)	505 (99%)	4 (1%)	73	70
1	C	536/497 (108%)	513 (96%)	23 (4%)	26	13
2	B	417/390 (107%)	410 (98%)	7 (2%)	53	45
2	D	398/390 (102%)	392 (98%)	6 (2%)	57	49
All	All	1860/1774 (105%)	1820 (98%)	40 (2%)	57	34

All (40) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	253	THR
1	A	374	LYS
1	A	547[A]	GLN
1	A	547[B]	GLN
2	B	6	GLU
2	B	65[A]	LYS
2	B	65[B]	LYS
2	B	113	ASP
2	B	166[A]	LYS
2	B	166[B]	LYS
2	B	425	LEU
1	C	40[A]	GLU
1	C	40[B]	GLU
1	C	53[A]	GLU
1	C	53[B]	GLU
1	C	68	SER
1	C	72[A]	ARG
1	C	72[B]	ARG
1	C	164[A]	MET
1	C	164[B]	MET
1	C	195	ILE
1	C	212[A]	TRP
1	C	212[B]	TRP
1	C	275	LYS

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Mol	Chain	Res	Type
1	C	301	LEU
1	C	332	GLN
1	C	358[A]	ARG
1	C	358[B]	ARG
1	C	428[A]	GLN
1	C	428[B]	GLN
1	C	512[A]	LYS
1	C	512[B]	LYS
1	C	547[A]	GLN
1	C	547[B]	GLN
2	D	6	GLU
2	D	73[A]	LYS
2	D	73[B]	LYS
2	D	197[A]	GLN
2	D	197[B]	GLN
2	D	362	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (13) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	394	GLN
1	A	480	GLN
2	B	147	ASN
2	B	161	GLN
2	B	255	ASN
1	C	255	ASN
1	C	471	ASN
1	C	487	GLN
1	C	507	GLN
2	D	137	ASN
2	D	255	ASN
2	D	269	GLN
2	D	336	GLN

5.3.3 RNA ⓘ

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](#)

Of 81 ligands modelled in this entry, 4 are monoatomic - leaving 77 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
6	EDO	A	605	-	3,3,3	0.43	0	2,2,2	0.31	0
6	EDO	C	616	-	3,3,3	0.41	0	2,2,2	0.32	0
6	EDO	B	522	-	3,3,3	0.42	0	2,2,2	0.28	0
6	EDO	A	606	-	3,3,3	0.42	0	2,2,2	0.10	0
5	PGE	B	503	-	9,9,9	0.31	0	8,8,8	0.45	0
6	EDO	C	619	-	3,3,3	0.45	0	2,2,2	0.36	0
6	EDO	D	506	-	3,3,3	0.41	0	2,2,2	0.37	0
5	PGE	B	502	-	9,9,9	0.33	0	8,8,8	0.69	0
6	EDO	C	626	-	3,3,3	0.41	0	2,2,2	0.36	0
6	EDO	A	609	-	3,3,3	0.40	0	2,2,2	0.42	0
6	EDO	B	521	-	3,3,3	0.37	0	2,2,2	0.27	0
6	EDO	A	618	-	3,3,3	0.31	0	2,2,2	0.42	0
6	EDO	A	615	-	3,3,3	0.39	0	2,2,2	0.39	0
6	EDO	B	505	-	3,3,3	0.46	0	2,2,2	0.36	0
6	EDO	C	609	-	3,3,3	0.37	0	2,2,2	0.41	0
6	EDO	D	510	-	3,3,3	0.37	0	2,2,2	0.47	0
6	EDO	B	511	-	3,3,3	0.41	0	2,2,2	0.51	0
6	EDO	C	611	-	3,3,3	0.42	0	2,2,2	0.22	0
6	EDO	D	507	-	3,3,3	0.42	0	2,2,2	0.33	0
6	EDO	C	613	-	3,3,3	0.43	0	2,2,2	0.14	0
6	EDO	C	623	-	3,3,3	0.51	0	2,2,2	0.25	0
6	EDO	C	604	-	3,3,3	0.41	0	2,2,2	0.36	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
6	EDO	D	505	-	3,3,3	0.42	0	2,2,2	0.37	0
6	EDO	B	515	-	3,3,3	0.40	0	2,2,2	0.40	0
6	EDO	B	509	-	3,3,3	0.43	0	2,2,2	0.34	0
6	EDO	B	516	-	3,3,3	0.39	0	2,2,2	0.28	0
6	EDO	C	618	-	3,3,3	0.44	0	2,2,2	0.30	0
6	EDO	B	506	-	3,3,3	0.46	0	2,2,2	0.24	0
6	EDO	A	607	-	3,3,3	0.41	0	2,2,2	0.36	0
6	EDO	C	605	-	3,3,3	0.25	0	2,2,2	0.92	0
5	PGE	A	604	-	9,9,9	0.25	0	8,8,8	0.60	0
6	EDO	C	615	-	3,3,3	0.50	0	2,2,2	0.11	0
6	EDO	C	622	-	3,3,3	0.40	0	2,2,2	0.39	0
6	EDO	D	503	-	3,3,3	0.49	0	2,2,2	0.14	0
6	EDO	B	508	-	3,3,3	0.31	0	2,2,2	0.71	0
6	EDO	C	608	-	3,3,3	0.47	0	2,2,2	0.19	0
6	EDO	D	508	-	3,3,3	0.45	0	2,2,2	0.27	0
6	EDO	B	510	-	3,3,3	0.54	0	2,2,2	0.14	0
6	EDO	C	621	-	3,3,3	0.48	0	2,2,2	0.30	0
6	EDO	D	509	-	3,3,3	0.36	0	2,2,2	0.46	0
6	EDO	A	612	-	3,3,3	0.47	0	2,2,2	0.31	0
6	EDO	B	517	-	3,3,3	0.40	0	2,2,2	0.42	0
6	EDO	A	614	-	3,3,3	0.43	0	2,2,2	0.30	0
5	PGE	B	501	-	9,9,9	0.37	0	8,8,8	0.77	0
6	EDO	D	512	-	3,3,3	0.34	0	2,2,2	0.37	0
6	EDO	D	513	-	3,3,3	0.38	0	2,2,2	0.29	0
6	EDO	C	614	-	3,3,3	0.43	0	2,2,2	0.31	0
6	EDO	A	617	-	3,3,3	0.40	0	2,2,2	0.38	0
6	EDO	B	523	-	3,3,3	0.48	0	2,2,2	0.19	0
5	PGE	B	504	-	9,9,9	0.28	0	8,8,8	0.43	0
4	ZW2	C	603	3	21,21,21	3.86	13 (61%)	24,30,30	5.05	11 (45%)
6	EDO	C	620	-	3,3,3	0.40	0	2,2,2	0.32	0
6	EDO	D	514	-	3,3,3	0.55	0	2,2,2	0.24	0
5	PGE	D	501	-	9,9,9	0.29	0	8,8,8	0.52	0
6	EDO	C	624	-	3,3,3	0.37	0	2,2,2	0.34	0
4	ZW2	A	603	3	21,21,21	4.17	10 (47%)	24,30,30	4.76	10 (41%)
6	EDO	A	613	-	3,3,3	0.38	0	2,2,2	0.31	0
6	EDO	C	617	-	3,3,3	0.34	0	2,2,2	0.46	0
6	EDO	A	610	-	3,3,3	0.30	0	2,2,2	0.49	0
6	EDO	B	519	-	3,3,3	0.51	0	2,2,2	0.13	0
6	EDO	C	625	-	3,3,3	0.44	0	2,2,2	0.34	0
6	EDO	A	611	-	3,3,3	0.39	0	2,2,2	0.36	0
6	EDO	B	512	-	3,3,3	0.37	0	2,2,2	0.41	0
6	EDO	B	514	-	3,3,3	0.55	0	2,2,2	0.31	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
5	PGE	D	502	-	9,9,9	0.32	0	8,8,8	0.58	0
6	EDO	C	612	-	3,3,3	0.44	0	2,2,2	0.28	0
6	EDO	B	513	-	3,3,3	0.35	0	2,2,2	0.40	0
6	EDO	B	507	-	3,3,3	0.25	0	2,2,2	0.56	0
6	EDO	B	518	-	3,3,3	0.43	0	2,2,2	0.35	0
6	EDO	C	610	-	3,3,3	0.41	0	2,2,2	0.63	0
6	EDO	D	511	-	3,3,3	0.43	0	2,2,2	0.30	0
6	EDO	C	607	-	3,3,3	0.45	0	2,2,2	0.26	0
6	EDO	C	606	-	3,3,3	0.36	0	2,2,2	0.35	0
6	EDO	B	520	-	3,3,3	0.38	0	2,2,2	0.28	0
6	EDO	D	504	-	3,3,3	0.38	0	2,2,2	0.48	0
6	EDO	A	608	-	3,3,3	0.45	0	2,2,2	0.31	0
6	EDO	A	616	-	3,3,3	0.33	0	2,2,2	0.42	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
6	EDO	A	605	-	-	0/1/1/1	-
6	EDO	C	616	-	-	1/1/1/1	-
6	EDO	B	522	-	-	1/1/1/1	-
6	EDO	A	606	-	-	0/1/1/1	-
5	PGE	B	503	-	-	4/7/7/7	-
6	EDO	C	619	-	-	0/1/1/1	-
6	EDO	D	506	-	-	0/1/1/1	-
5	PGE	B	502	-	-	4/7/7/7	-
6	EDO	C	626	-	-	1/1/1/1	-
6	EDO	A	609	-	-	1/1/1/1	-
6	EDO	B	521	-	-	1/1/1/1	-
6	EDO	A	618	-	-	0/1/1/1	-
6	EDO	A	615	-	-	1/1/1/1	-
6	EDO	B	505	-	-	0/1/1/1	-
6	EDO	C	609	-	-	1/1/1/1	-
6	EDO	D	510	-	-	0/1/1/1	-
6	EDO	B	511	-	-	0/1/1/1	-
6	EDO	C	611	-	-	0/1/1/1	-
6	EDO	D	507	-	-	0/1/1/1	-
6	EDO	C	613	-	-	0/1/1/1	-
6	EDO	C	623	-	-	0/1/1/1	-
6	EDO	C	604	-	-	1/1/1/1	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
6	EDO	D	505	-	-	0/1/1/1	-
6	EDO	B	515	-	-	0/1/1/1	-
6	EDO	B	509	-	-	0/1/1/1	-
6	EDO	B	516	-	-	0/1/1/1	-
6	EDO	C	618	-	-	1/1/1/1	-
6	EDO	B	506	-	-	0/1/1/1	-
6	EDO	A	607	-	-	0/1/1/1	-
6	EDO	C	605	-	-	0/1/1/1	-
5	PGE	A	604	-	-	4/7/7/7	-
6	EDO	C	615	-	-	1/1/1/1	-
6	EDO	C	622	-	-	0/1/1/1	-
6	EDO	D	503	-	-	0/1/1/1	-
6	EDO	B	508	-	-	0/1/1/1	-
6	EDO	C	608	-	-	0/1/1/1	-
6	EDO	D	508	-	-	0/1/1/1	-
6	EDO	B	510	-	-	1/1/1/1	-
6	EDO	C	621	-	-	0/1/1/1	-
6	EDO	D	509	-	-	1/1/1/1	-
6	EDO	A	612	-	-	0/1/1/1	-
6	EDO	B	517	-	-	1/1/1/1	-
6	EDO	A	614	-	-	1/1/1/1	-
5	PGE	B	501	-	-	3/7/7/7	-
6	EDO	D	512	-	-	0/1/1/1	-
6	EDO	D	513	-	-	1/1/1/1	-
6	EDO	C	614	-	-	0/1/1/1	-
6	EDO	A	617	-	-	1/1/1/1	-
6	EDO	B	523	-	-	0/1/1/1	-
5	PGE	B	504	-	-	6/7/7/7	-
4	ZW2	C	603	3	-	1/4/4/4	0/3/3/3
6	EDO	C	620	-	-	1/1/1/1	-
6	EDO	D	514	-	-	0/1/1/1	-
5	PGE	D	501	-	-	4/7/7/7	-
6	EDO	C	624	-	-	0/1/1/1	-
4	ZW2	A	603	3	-	0/4/4/4	0/3/3/3
6	EDO	A	613	-	-	0/1/1/1	-
6	EDO	C	617	-	-	0/1/1/1	-
6	EDO	A	610	-	-	0/1/1/1	-
6	EDO	B	519	-	-	1/1/1/1	-
6	EDO	C	625	-	-	0/1/1/1	-
6	EDO	A	611	-	-	1/1/1/1	-
6	EDO	B	512	-	-	0/1/1/1	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
6	EDO	B	514	-	-	1/1/1/1	-
5	PGE	D	502	-	-	2/7/7/7	-
6	EDO	C	612	-	-	0/1/1/1	-
6	EDO	B	513	-	-	0/1/1/1	-
6	EDO	B	507	-	-	0/1/1/1	-
6	EDO	B	518	-	-	0/1/1/1	-
6	EDO	C	610	-	-	1/1/1/1	-
6	EDO	D	511	-	-	1/1/1/1	-
6	EDO	C	607	-	-	1/1/1/1	-
6	EDO	C	606	-	-	1/1/1/1	-
6	EDO	B	520	-	-	0/1/1/1	-
6	EDO	D	504	-	-	0/1/1/1	-
6	EDO	A	608	-	-	1/1/1/1	-
6	EDO	A	616	-	-	0/1/1/1	-

All (23) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	603	ZW2	C4-N1	10.55	1.46	1.38
4	C	603	ZW2	C3-S	-8.05	1.63	1.73
4	A	603	ZW2	C3-S	-7.74	1.63	1.73
4	C	603	ZW2	C4-N1	7.54	1.44	1.38
4	A	603	ZW2	C3-N2	7.34	1.47	1.38
4	C	603	ZW2	C3-N2	6.99	1.47	1.38
4	A	603	ZW2	C4-N2	5.53	1.47	1.38
4	A	603	ZW2	C5-C2	5.15	1.54	1.42
4	A	603	ZW2	C2-C3	5.07	1.42	1.37
4	C	603	ZW2	C5-C2	5.07	1.54	1.42
4	C	603	ZW2	C4-N2	5.02	1.46	1.38
4	C	603	ZW2	C2-C3	4.48	1.42	1.37
4	A	603	ZW2	C5-C6	4.28	1.44	1.36
4	C	603	ZW2	C5-C6	4.16	1.44	1.36
4	C	603	ZW2	C1-N1	4.10	1.44	1.39
4	A	603	ZW2	C1-N1	3.48	1.43	1.39
4	C	603	ZW2	C6-S	-2.93	1.64	1.73
4	A	603	ZW2	C6-S	-2.83	1.64	1.73
4	C	603	ZW2	O3-C4	-2.78	1.18	1.23
4	A	603	ZW2	C2-C1	2.76	1.51	1.45
4	C	603	ZW2	C2-C1	2.71	1.51	1.45
4	C	603	ZW2	O1-N1	2.41	1.41	1.38
4	C	603	ZW2	O2-C1	-2.26	1.18	1.23

All (21) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	C	603	ZW2	C6-S-C3	21.52	100.69	91.41
4	A	603	ZW2	C6-S-C3	21.21	100.55	91.41
4	C	603	ZW2	O1-N1-C1	5.98	124.53	116.67
4	C	603	ZW2	O3-C4-N1	-5.67	116.79	123.45
4	A	603	ZW2	O1-N1-C4	5.34	120.26	116.38
4	C	603	ZW2	C2-C3-S	-4.04	110.23	111.64
4	C	603	ZW2	N2-C4-N1	3.72	120.57	115.65
4	C	603	ZW2	C8-C7-C6	-3.25	109.05	114.34
4	A	603	ZW2	C2-C3-S	-3.22	110.51	111.64
4	A	603	ZW2	C8-C7-C6	-2.89	109.64	114.34
4	C	603	ZW2	S-C3-N2	2.71	128.94	120.90
4	A	603	ZW2	S-C3-N2	2.70	128.91	120.90
4	C	603	ZW2	O2-C1-C2	-2.68	119.28	124.96
4	A	603	ZW2	N2-C4-N1	2.59	119.07	115.65
4	A	603	ZW2	C7-C6-S	2.44	126.69	121.68
4	C	603	ZW2	O1-N1-C4	-2.39	114.64	116.38
4	A	603	ZW2	C5-C2-C3	-2.33	109.62	111.67
4	A	603	ZW2	O3-C4-N1	-2.29	120.76	123.45
4	C	603	ZW2	C7-C6-S	2.20	126.22	121.68
4	A	603	ZW2	C2-C1-N1	2.08	118.93	113.58
4	C	603	ZW2	C2-C1-N1	2.05	118.84	113.58

There are no chirality outliers.

All (53) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	B	501	PGE	O2-C3-C4-O3
5	B	504	PGE	O2-C3-C4-O3
5	B	502	PGE	O2-C3-C4-O3
5	D	501	PGE	O2-C3-C4-O3
5	A	604	PGE	O1-C1-C2-O2
5	B	501	PGE	O1-C1-C2-O2
5	B	504	PGE	O1-C1-C2-O2
5	B	504	PGE	O3-C5-C6-O4
6	B	517	EDO	O1-C1-C2-O2
6	B	522	EDO	O1-C1-C2-O2
5	B	503	PGE	O1-C1-C2-O2
6	A	614	EDO	O1-C1-C2-O2
6	B	514	EDO	O1-C1-C2-O2
6	C	607	EDO	O1-C1-C2-O2
6	C	620	EDO	O1-C1-C2-O2

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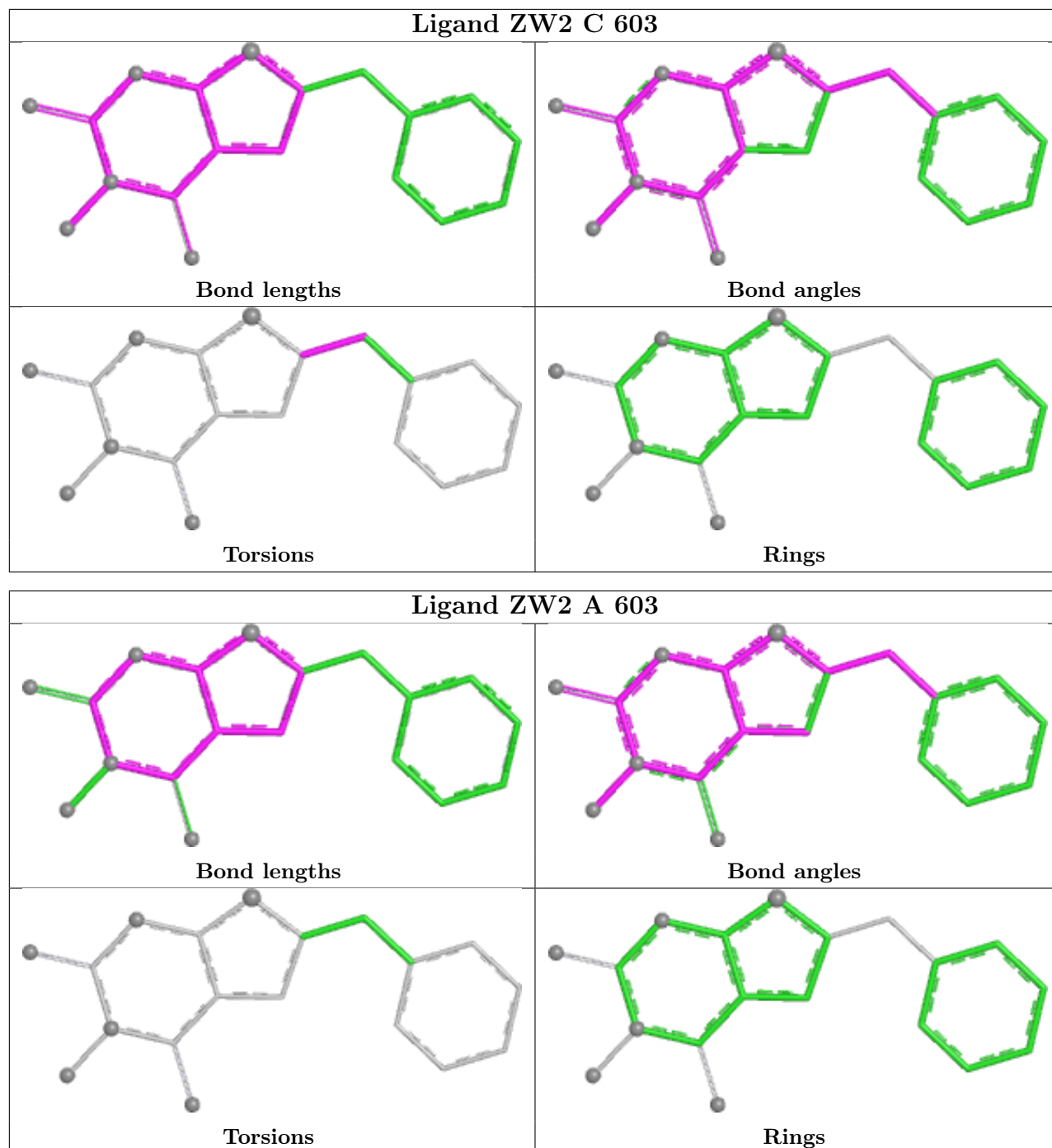
Mol	Chain	Res	Type	Atoms
4	C	603	ZW2	C5-C6-C7-C8
5	D	502	PGE	C4-C3-O2-C2
5	B	504	PGE	C1-C2-O2-C3
5	B	503	PGE	C3-C4-O3-C5
6	C	618	EDO	O1-C1-C2-O2
5	B	503	PGE	O3-C5-C6-O4
5	B	501	PGE	C6-C5-O3-C4
6	D	511	EDO	O1-C1-C2-O2
5	A	604	PGE	O2-C3-C4-O3
5	B	503	PGE	C4-C3-O2-C2
5	B	504	PGE	C6-C5-O3-C4
5	A	604	PGE	C6-C5-O3-C4
5	D	501	PGE	O3-C5-C6-O4
6	A	615	EDO	O1-C1-C2-O2
6	A	617	EDO	O1-C1-C2-O2
6	C	616	EDO	O1-C1-C2-O2
5	B	502	PGE	C4-C3-O2-C2
5	D	502	PGE	C6-C5-O3-C4
5	B	502	PGE	O1-C1-C2-O2
5	D	501	PGE	C1-C2-O2-C3
5	B	502	PGE	C6-C5-O3-C4
6	A	609	EDO	O1-C1-C2-O2
6	B	510	EDO	O1-C1-C2-O2
6	A	608	EDO	O1-C1-C2-O2
6	A	611	EDO	O1-C1-C2-O2
6	B	521	EDO	O1-C1-C2-O2
6	C	606	EDO	O1-C1-C2-O2
6	C	609	EDO	O1-C1-C2-O2
6	C	626	EDO	O1-C1-C2-O2
6	D	513	EDO	O1-C1-C2-O2
6	C	604	EDO	O1-C1-C2-O2
6	C	610	EDO	O1-C1-C2-O2
6	B	519	EDO	O1-C1-C2-O2
6	C	615	EDO	O1-C1-C2-O2
5	D	501	PGE	C3-C4-O3-C5
5	B	504	PGE	C4-C3-O2-C2
5	A	604	PGE	O3-C5-C6-O4
6	D	509	EDO	O1-C1-C2-O2

There are no ring outliers.

16 monomers are involved in 36 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	A	606	EDO	1	0
5	B	502	PGE	5	0
6	A	618	EDO	4	0
6	C	613	EDO	2	0
6	D	505	EDO	1	0
5	A	604	PGE	4	0
5	B	501	PGE	4	0
6	D	512	EDO	1	0
6	B	523	EDO	1	0
5	B	504	PGE	2	0
6	C	620	EDO	1	0
5	D	501	PGE	4	0
6	C	625	EDO	1	0
5	D	502	PGE	2	0
6	B	513	EDO	2	0
6	A	608	EDO	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.



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	555/557 (99%)	1.05	110 (19%) 3 2	22, 62, 142, 182	16 (2%)
1	C	557/557 (100%)	0.68	45 (8%) 18 16	18, 52, 97, 148	41 (7%)
2	B	424/429 (98%)	0.44	37 (8%) 16 14	16, 43, 93, 157	31 (7%)
2	D	414/429 (96%)	0.66	46 (11%) 10 8	22, 47, 122, 178	19 (4%)
All	All	1950/1972 (98%)	0.73	238 (12%) 8 7	16, 51, 129, 182	107 (5%)

All (238) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	D	5	ILE	6.6
1	A	128	THR	6.0
2	B	225	PRO	6.0
1	C	406	TRP	5.8
1	A	24	TRP	5.7
1	A	80	LEU	5.4
1	A	135	ILE	5.4
1	A	74	LEU	5.2
1	A	59	PRO	5.2
1	A	26	LEU	5.1
2	D	88	TRP	5.0
1	A	130	PHE	5.0
1	C	266	TRP	4.9
2	B	229	TRP	4.9
2	D	227	PHE	4.8
1	A	62	ALA	4.8
2	D	232	TYR	4.7
2	D	229	TRP	4.7
1	A	90	VAL	4.7
2	B	92	LEU	4.7
2	D	228	LEU	4.7

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Mol	Chain	Res	Type	RSRZ
1	A	111	VAL	4.6
1	C	2	ILE	4.6
1	A	279	LEU	4.6
2	B	90	VAL	4.6
2	D	92	LEU	4.6
2	B	88	TRP	4.5
1	A	139	THR	4.5
2	B	212	TRP	4.4
1	A	132	ILE	4.4
1	C	0	VAL	4.4
1	A	129	ALA	4.3
1	A	92	LEU	4.3
2	D	426	TRP	4.3
1	A	19	PRO	4.3
1	A	77	PHE	4.2
2	D	4	PRO	4.2
1	A	71	TRP	4.0
2	D	94	ILE	4.0
1	C	139	THR	4.0
1	A	25	PRO	3.9
2	D	241	VAL	3.9
1	A	18	GLY	3.9
1	A	2	ILE	3.8
1	A	61	PHE	3.8
1	A	115	TYR	3.7
2	B	228	LEU	3.7
1	A	60	VAL	3.7
1	A	293	ILE	3.7
2	D	212	TRP	3.7
2	D	358	ARG	3.7
2	B	216	THR	3.6
1	A	31	ILE	3.6
2	B	423	VAL	3.6
2	B	226	PRO	3.6
2	B	227	PHE	3.5
2	D	226	PRO	3.5
1	A	63	ILE	3.5
1	A	21	VAL	3.5
1	C	136	ASN	3.5
1	A	38	CYS	3.5
2	B	215	THR	3.5
2	B	422	LEU	3.5

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Mol	Chain	Res	Type	RSRZ
2	D	214	LEU	3.5
2	D	93	GLY	3.4
1	A	1	PRO	3.4
1	A	127	TYR	3.3
1	A	58	THR	3.3
1	A	140	PRO	3.3
2	D	359	GLY	3.3
2	B	214	LEU	3.3
2	D	7	THR	3.3
2	D	357	MET	3.2
2	B	217	PRO	3.2
1	A	12	LEU	3.2
2	D	360	ALA	3.2
1	A	133	PRO	3.2
1	A	73	LYS	3.2
2	D	230	MET	3.1
1	C	90	VAL	3.1
1	A	286	THR	3.1
2	D	90	VAL	3.1
1	A	87	PHE	3.1
2	D	422	LEU	3.0
1	A	81	ASN	3.0
1	A	225	PRO	3.0
2	D	313	PRO	3.0
1	A	357	MET	3.0
2	B	87	PHE	3.0
1	C	333	GLY	3.0
1	C	359	GLY	3.0
1	C	274	ILE	3.0
1	A	88	TRP	2.9
1	A	295	LEU	2.9
2	D	424	LYS	2.9
1	A	301	LEU	2.9
2	B	427	TYR	2.9
2	D	419	THR	2.9
1	A	226	PRO	2.9
1	A	346	PHE	2.9
1	C	355	ALA	2.9
1	C	426	TRP	2.9
2	B	218	ASP	2.9
1	A	282	LEU	2.9
2	D	193	LEU	2.9

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Mol	Chain	Res	Type	RSRZ
1	A	75	VAL	2.8
1	C	225	PRO	2.8
2	B	318	TYR	2.8
2	D	9	PRO	2.8
2	D	95	PRO	2.8
2	B	426	TRP	2.8
1	A	37	ILE	2.8
1	A	257	ILE	2.8
1	C	178	ILE	2.8
1	A	84	THR	2.8
1	A	288	ALA	2.8
1	A	89	GLU	2.8
2	D	225	PRO	2.8
1	C	314	VAL	2.8
1	C	-1	MET	2.8
1	C	286	THR	2.8
2	B	240[A]	THR	2.8
1	C	357	MET	2.8
2	B	232[A]	TYR	2.7
1	A	30	LYS	2.7
2	D	361	HIS	2.7
2	D	362	THR	2.7
2	D	425	LEU	2.7
2	B	230	MET	2.7
1	A	222	GLN	2.7
1	C	212[A]	TRP	2.7
1	A	79	GLU	2.7
2	D	213	GLY	2.7
1	C	140	PRO	2.7
2	D	70	LYS	2.7
1	A	144	TYR	2.7
1	A	69	THR	2.7
1	A	47	ILE	2.7
1	A	16	MET	2.6
1	C	92	LEU	2.6
2	B	94[A]	ILE	2.6
1	C	184	MET	2.6
1	A	56	TYR	2.6
1	A	354	TYR	2.6
1	A	22	LYS	2.6
1	C	220	LYS	2.6
2	D	139	THR	2.6

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Mol	Chain	Res	Type	RSRZ
1	A	290	THR	2.6
2	B	421	PRO	2.6
2	B	241	VAL	2.6
1	C	354	TYR	2.5
2	B	304	ALA	2.5
1	A	179	VAL	2.5
1	A	184	MET	2.5
2	B	4	PRO	2.5
1	A	273	GLY	2.5
1	A	68	SER	2.5
1	C	195	ILE	2.5
1	A	112	GLY	2.4
1	C	232	TYR	2.4
2	D	354	TYR	2.4
1	C	116	PHE	2.4
1	C	43[A]	LYS	2.4
2	D	98	ALA	2.4
1	A	292	VAL	2.4
1	C	24	TRP	2.4
1	A	136	ASN	2.4
1	A	507[A]	GLN	2.4
1	C	332	GLN	2.4
1	A	228	LEU	2.4
1	C	452	LEU	2.4
1	A	124	PHE	2.4
1	A	216	THR	2.4
1	A	142	ILE	2.4
2	B	244	ILE	2.4
1	A	554	ALA	2.4
1	C	25	PRO	2.4
2	B	52	PRO	2.4
1	C	137	ASN	2.4
1	A	15	GLY	2.4
1	A	276	VAL	2.4
1	C	69	THR	2.3
1	A	166	LYS	2.3
1	C	70	LYS	2.3
2	D	200	THR	2.3
1	A	14	PRO	2.3
1	A	310	LEU	2.3
1	A	33	ALA	2.3
1	A	254	VAL	2.3

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Mol	Chain	Res	Type	RSRZ
1	A	27	THR	2.3
1	A	252	TRP	2.2
1	A	52	PRO	2.2
1	A	183	TYR	2.2
1	A	508	ALA	2.2
2	D	244	ILE	2.2
2	D	242	GLN	2.2
1	A	289	LEU	2.2
1	C	402	TRP	2.2
2	B	219	LYS	2.2
1	A	35	VAL	2.2
1	A	20	LYS	2.2
1	A	82	LYS	2.2
1	C	122	GLU	2.2
1	C	241	VAL	2.2
2	D	421	PRO	2.2
1	A	83	ARG	2.2
1	C	346	PHE	2.1
1	A	146	TYR	2.1
1	C	244	ILE	2.1
1	A	153	TRP	2.1
1	A	39	THR	2.1
1	A	113	ASP	2.1
1	A	261	VAL	2.1
2	D	8	VAL	2.1
1	C	301	LEU	2.1
2	B	243	PRO	2.1
2	B	425	LEU	2.1
1	A	91	GLN	2.1
1	A	131	THR	2.1
1	A	277	ARG	2.1
1	C	1	PRO	2.1
1	A	182[A]	GLN	2.1
1	A	223	LYS	2.1
2	B	139	THR	2.1
1	A	141	GLY	2.1
1	A	137	ASN	2.1
2	D	209	LEU	2.1
1	A	253	THR	2.0
1	A	419	THR	2.0
2	D	240	THR	2.0
1	C	221	HIS	2.0

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Mol	Chain	Res	Type	RSRZ
2	B	231	GLY	2.0
1	A	23	GLN	2.0
2	B	193	LEU	2.0
1	C	358[A]	ARG	2.0
2	D	231	GLY	2.0
1	C	272	PRO	2.0
2	B	1	PRO	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
6	EDO	A	608	4/4	0.37	0.20	123,126,126,128	0
6	EDO	C	625	4/4	0.41	0.27	149,154,162,167	0
6	EDO	C	605	4/4	0.70	0.20	88,89,91,95	0
6	EDO	C	619	4/4	0.71	0.18	84,85,88,88	0
6	EDO	C	612	4/4	0.72	0.20	75,82,83,84	0
6	EDO	B	512	4/4	0.73	0.19	59,68,69,72	0
6	EDO	C	615	4/4	0.75	0.19	59,68,73,75	0
6	EDO	C	613	4/4	0.76	0.14	89,93,93,94	0
6	EDO	A	609	4/4	0.76	0.27	91,99,105,105	0
6	EDO	C	607	4/4	0.76	0.18	91,94,96,98	0
5	PGE	B	504	10/10	0.76	0.21	63,78,89,93	10
6	EDO	D	508	4/4	0.76	0.19	78,82,83,85	0
6	EDO	D	505	4/4	0.77	0.17	105,109,111,113	0
6	EDO	B	515	4/4	0.77	0.14	82,87,89,89	0
6	EDO	D	513	4/4	0.77	0.15	70,79,82,85	0
6	EDO	C	616	4/4	0.78	0.15	66,73,79,81	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
6	EDO	C	614	4/4	0.78	0.14	92,93,95,97	0
5	PGE	B	502	10/10	0.78	0.21	53,63,71,76	0
6	EDO	C	610	4/4	0.80	0.17	66,70,72,73	0
6	EDO	C	618	4/4	0.81	0.16	58,69,69,74	0
6	EDO	A	612	4/4	0.81	0.18	52,59,63,71	0
6	EDO	C	604	4/4	0.81	0.12	71,77,78,79	0
5	PGE	A	604	10/10	0.82	0.18	45,73,83,84	0
6	EDO	B	509	4/4	0.84	0.23	61,69,80,84	0
6	EDO	B	510	4/4	0.84	0.19	40,54,63,65	0
6	EDO	D	504	4/4	0.84	0.16	56,67,78,80	0
6	EDO	A	607	4/4	0.84	0.17	73,83,86,89	0
6	EDO	D	506	4/4	0.84	0.19	84,85,85,86	0
5	PGE	B	503	10/10	0.84	0.19	44,67,78,79	0
6	EDO	D	509	4/4	0.84	0.14	54,67,69,75	0
6	EDO	B	522	4/4	0.84	0.16	64,72,72,73	0
6	EDO	B	505	4/4	0.85	0.18	56,56,57,63	0
6	EDO	C	617	4/4	0.85	0.16	69,69,70,72	0
6	EDO	B	518	4/4	0.85	0.15	79,87,91,91	0
6	EDO	B	519	4/4	0.85	0.18	69,78,86,91	0
6	EDO	C	621	4/4	0.85	0.17	76,79,80,82	0
6	EDO	A	613	4/4	0.85	0.13	91,91,92,94	0
6	EDO	A	614	4/4	0.86	0.13	76,77,79,81	0
6	EDO	C	622	4/4	0.86	0.17	86,87,92,93	0
6	EDO	C	623	4/4	0.86	0.14	54,60,61,67	0
6	EDO	B	513	4/4	0.86	0.15	44,46,57,58	0
6	EDO	B	523	4/4	0.86	0.15	44,59,61,62	0
6	EDO	A	617	4/4	0.87	0.14	64,68,73,80	0
6	EDO	C	611	4/4	0.87	0.15	58,68,70,71	0
6	EDO	C	626	4/4	0.87	0.18	94,97,98,98	0
5	PGE	D	502	10/10	0.88	0.17	43,55,68,70	10
6	EDO	D	511	4/4	0.88	0.13	52,72,77,82	0
6	EDO	B	516	4/4	0.88	0.17	55,70,74,80	0
6	EDO	D	514	4/4	0.88	0.15	49,59,60,62	0
6	EDO	A	618	4/4	0.89	0.12	60,71,76,80	0
6	EDO	C	608	4/4	0.89	0.14	46,65,77,85	0
6	EDO	D	507	4/4	0.89	0.13	68,70,73,77	0
6	EDO	A	611	4/4	0.89	0.13	67,73,74,76	0
6	EDO	B	517	4/4	0.90	0.14	48,53,69,70	0
5	PGE	B	501	10/10	0.90	0.16	38,52,68,74	0
6	EDO	B	514	4/4	0.90	0.14	77,79,84,86	0
6	EDO	B	520	4/4	0.90	0.14	46,58,65,66	0
6	EDO	B	521	4/4	0.90	0.15	44,51,63,64	0

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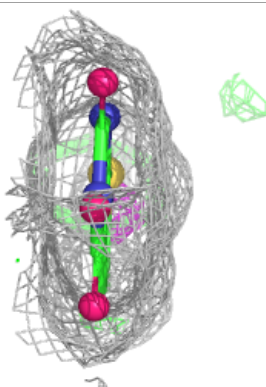
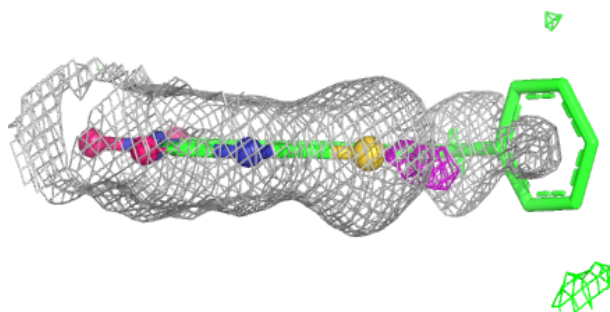
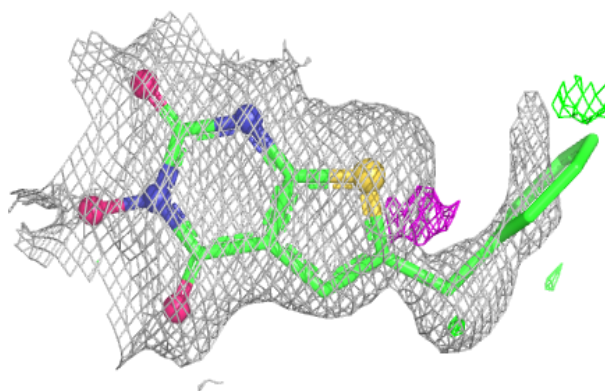
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
6	EDO	A	610	4/4	0.90	0.17	61,63,69,72	0
6	EDO	A	615	4/4	0.90	0.12	64,74,74,76	0
6	EDO	D	512	4/4	0.91	0.14	54,61,68,73	0
6	EDO	A	616	4/4	0.91	0.12	56,62,72,72	0
6	EDO	B	506	4/4	0.91	0.14	37,58,72,82	0
4	ZW2	A	603	19/19	0.92	0.14	47,62,120,120	0
6	EDO	C	609	4/4	0.92	0.18	53,69,77,84	0
5	PGE	D	501	10/10	0.92	0.13	54,72,75,77	0
6	EDO	C	624	4/4	0.92	0.14	53,59,72,76	0
6	EDO	B	507	4/4	0.93	0.14	41,60,70,81	0
6	EDO	D	503	4/4	0.93	0.12	47,60,64,65	0
6	EDO	C	606	4/4	0.93	0.13	64,67,67,68	0
6	EDO	A	606	4/4	0.93	0.13	41,53,57,58	0
4	ZW2	C	603	19/19	0.93	0.12	44,63,105,105	0
6	EDO	A	605	4/4	0.93	0.12	63,65,72,75	0
6	EDO	B	511	4/4	0.94	0.09	39,46,52,52	0
6	EDO	D	510	4/4	0.94	0.10	62,62,62,63	0
6	EDO	B	508	4/4	0.95	0.11	42,47,49,49	0
6	EDO	C	620	4/4	0.95	0.10	43,72,83,89	0
3	MN	A	602	1/1	0.99	0.03	41,41,41,41	0
3	MN	C	602	1/1	1.00	0.02	42,42,42,42	0
3	MN	A	601	1/1	1.00	0.02	41,41,41,41	0
3	MN	C	601	1/1	1.00	0.05	35,35,35,35	0

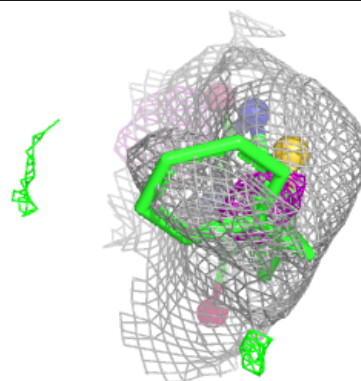
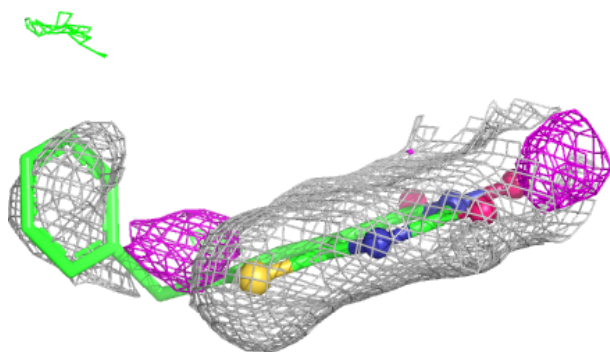
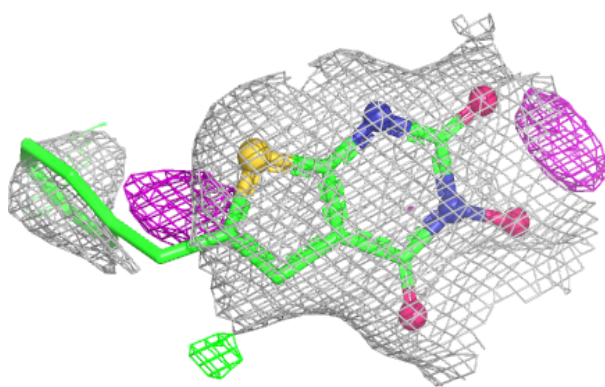
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

Electron density around ZW2 A 603:

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

**Electron density around ZW2 C 603:**

$2mF_o-DF_c$ (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.