



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 1, 2026 – 07:07 PM UTC

PDB ID : 4DCX / pdb_00004dcx
Title : X-ray structure of NikA in complex with Fe(1R,2R)-N,N'-Bis(2-pyridylmethyl)-N,N'-dicarboxymethyl-1,2-cyclohexanediamine
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Deposited on : 2012-01-18
Resolution : 2.00 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

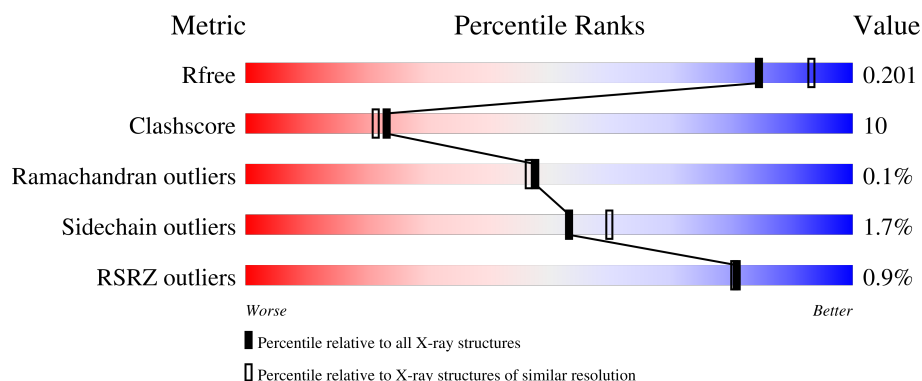
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.00 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	10052 (2.00-2.00)
Clashscore	190562	11152 (2.00-2.00)
Ramachandran outliers	187476	11031 (2.00-2.00)
Sidechain outliers	187428	11029 (2.00-2.00)
RSRZ outliers	180081	10067 (2.00-2.00)

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	502	85% 14% .
1	B	502	% 80% 18% ..

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
3	ACT	A	615	-	-	X	-
3	ACT	A	616	-	-	X	-
3	ACT	A	617	-	-	X	-
3	ACT	B	606	-	-	X	-
4	GOL	A	627	-	-	X	-
4	GOL	B	612	-	-	X	-
4	GOL	B	618	-	-	X	-

2 Entry composition [i](#)

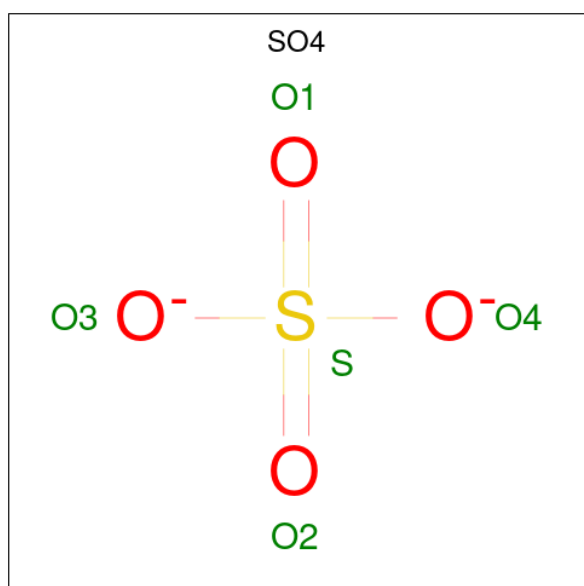
There are 6 unique types of molecules in this entry. The entry contains 9194 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Nickel-binding periplasmic protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	497	Total	C	N	O	S	9	20	0
			4050	2606	676	755	13			
1	B	497	Total	C	N	O	S	11	9	0
			3992	2562	671	748	11			

- Molecule 2 is SULFATE ION (CCD ID: SO4) (formula: O₄S).



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

- Molecule 3 is ACETATE ION (CCD ID: ACT) (formula: C₂H₃O₂).



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

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

- Molecule 4 is GLYCEROL (CCD ID: GOL) (formula: $C_3H_8O_3$).



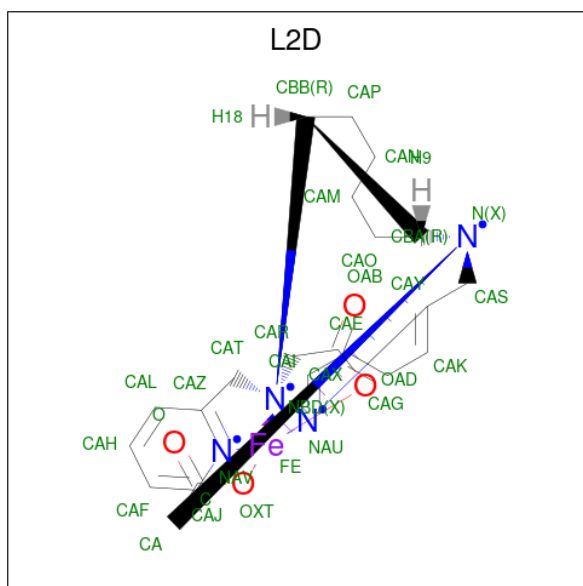
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			6	3	3		
4	A	1	Total	C	O	0	0
			6	3	3		
4	A	1	Total	C	O	0	0
			6	3	3		
4	A	1	Total	C	O	0	0
			6	3	3		
4	A	1	Total	C	O	0	0
			6	3	3		
4	A	1	Total	C	O	0	0
			6	3	3		
4	A	1	Total	C	O	0	0
			6	3	3		
4	B	1	Total	C	O	0	0
			6	3	3		
4	B	1	Total	C	O	0	0
			6	3	3		
4	B	1	Total	C	O	0	0
			6	3	3		
4	B	1	Total	C	O	0	0
			6	3	3		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	B	1	Total	C	O	0	0
			6	3	3		
4	B	1	Total	C	O	0	0
			6	3	3		
4	B	1	Total	C	O	0	0
			6	3	3		
4	B	1	Total	C	O	0	0
			6	3	3		

- Molecule 5 is {2,2'-[(1R,2R)-cyclohexane-1,2-diylbis{[(pyridin-2-yl-kappaN)methyl]imino-kappaN}]}diacetato-kappaO(2-)}iron (CCD ID: L2D) (formula: C₂₂H₂₆FeN₄O₄).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
5	A	1	Total	C	Fe	N	O	0	0
			31	22	1	4	4		
5	B	1	Total	C	Fe	N	O	0	0
			31	22	1	4	4		

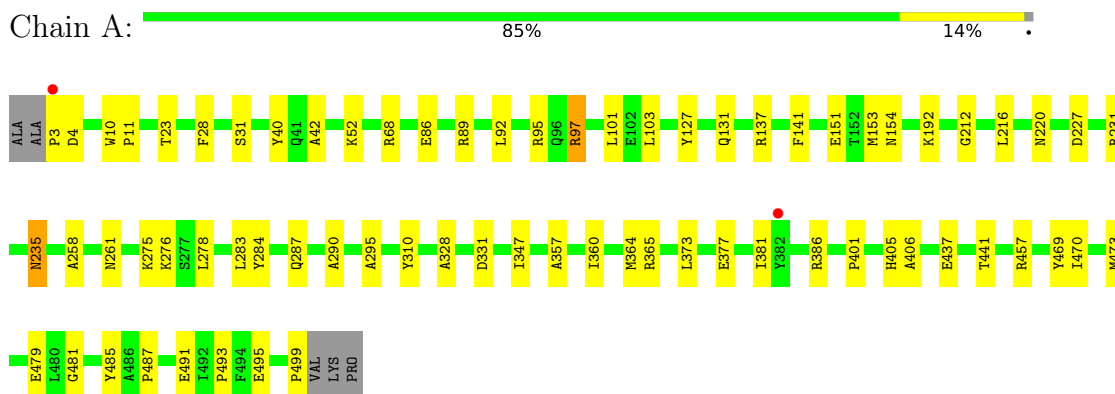
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	511	Total	O	2	0
			511	511		
6	B	347	Total	O	0	1
			348	348		

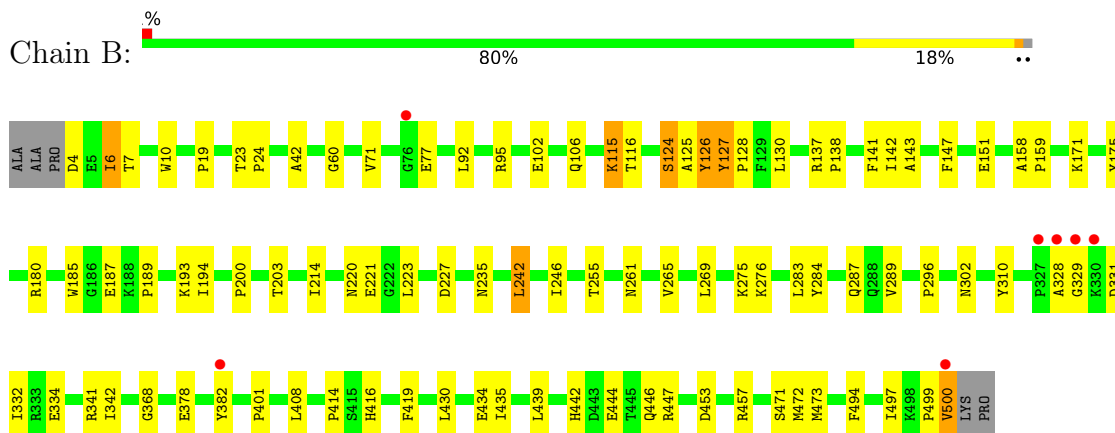
3 Residue-property plots [i](#)

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: Nickel-binding periplasmic protein



• Molecule 1: Nickel-binding periplasmic protein



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	86.35Å 95.64Å 125.19Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	47.82 – 2.00 47.82 – 2.00	Depositor EDS
% Data completeness (in resolution range)	99.6 (47.82-2.00) 99.6 (47.82-2.00)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.07	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.64 (at 2.00Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.7_650)	Depositor
R, R_{free}	0.155 , 0.203 0.154 , 0.201	Depositor DCC
R_{free} test set	3519 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	27.5	Xtriage
Anisotropy	0.346	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 68.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	9194	wwPDB-VP
Average B, all atoms (Å ²)	36.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.34% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: L2D, SO4, ACT, GOL

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	0.47	0/4219	0.76	5/5743 (0.1%)
1	B	0.41	0/4122	0.74	1/5616 (0.0%)
All	All	0.44	0/8341	0.75	6/11359 (0.1%)

There are no bond length outliers.

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	235	ASN	CA-C-N	5.49	125.16	119.56
1	A	235	ASN	C-N-CA	5.49	125.16	119.56
1	B	141	PHE	N-CA-C	5.32	117.09	108.41
1	A	295	ALA	CA-C-N	5.09	124.75	119.56
1	A	295	ALA	C-N-CA	5.09	124.75	119.56
1	A	141	PHE	N-CA-C	5.08	116.81	108.52

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	4050	0	4059	68	0
1	B	3992	0	3967	89	0
2	A	10	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	B	5	0	0	0	0
3	A	68	0	51	13	0
3	B	40	0	30	13	0
4	A	60	0	80	16	0
4	B	48	0	64	21	0
5	A	31	0	26	0	0
5	B	31	0	26	2	0
6	A	511	0	0	23	0
6	B	348	0	0	15	0
All	All	9194	0	8303	171	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 10.

All (171) 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:331:ASP:HB2	3:B:606:ACT:H3	1.32	1.06
1:B:235:ASN:HD21	4:B:616:GOL:H2	1.19	1.02
3:B:606:ACT:C	4:B:618:GOL:H12	1.94	0.97
1:A:52:LYS:HE3	1:A:68:ARG:HA	1.47	0.93
3:B:606:ACT:H2	4:B:618:GOL:H31	1.49	0.93
1:B:310:TYR:HB2	4:B:612:GOL:H12	1.51	0.90
1:B:6:ILE:HD11	1:B:194:ILE:HG12	1.50	0.90
1:B:331:ASP:HB2	3:B:606:ACT:CH3	2.07	0.84
1:B:331:ASP:CB	3:B:606:ACT:H3	2.07	0.84
1:B:10:TRP:HZ2	4:B:615:GOL:H11	1.40	0.83
1:A:499:PRO:HB2	6:A:1101:HOH:O	1.80	0.82
1:A:227:ASP:HB3	1:A:284[B]:TYR:CZ	2.15	0.81
3:B:606:ACT:CH3	4:B:618:GOL:H12	2.09	0.81
1:A:437:GLU:O	1:A:441[B]:THR:HG23	1.81	0.80
1:B:10:TRP:CZ2	4:B:615:GOL:H11	2.19	0.77
1:B:235:ASN:HD21	4:B:616:GOL:C2	1.96	0.77
1:A:365:ARG:HH22	4:A:622:GOL:H32	1.53	0.74
1:A:52:LYS:CE	1:A:68:ARG:HA	2.18	0.73
1:A:151[B]:GLU:HG3	6:A:953:HOH:O	1.88	0.72
1:B:414:PRO:HA	1:B:419:PHE:CD1	2.25	0.72
3:B:605:ACT:H1	6:B:1008:HOH:O	1.89	0.72
1:A:331:ASP:H	4:A:622:GOL:H11	1.55	0.72
1:B:332:ILE:HG12	3:B:606:ACT:H1	1.70	0.71
1:A:328:ALA:HB2	3:A:615:ACT:H2	1.71	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:441[B]:THR:HG22	6:A:1096:HOH:O	1.90	0.70
1:B:7:THR:HG22	1:B:214:ILE:HG22	1.73	0.69
1:B:499:PRO:O	1:B:500:VAL:HB	1.91	0.68
1:B:227:ASP:HB3	1:B:284:TYR:CZ	2.30	0.66
1:B:19:PRO:HG3	1:B:142:ILE:HB	1.78	0.66
3:B:606:ACT:H2	4:B:618:GOL:H12	1.77	0.65
1:A:92:LEU:HD12	4:A:621:GOL:H31	1.79	0.64
1:B:378:GLU:HG2	1:B:382:TYR:CE2	2.34	0.63
1:A:491:GLU:OE1	4:A:627:GOL:H32	1.99	0.62
1:B:6:ILE:CD1	1:B:194:ILE:HG12	2.25	0.62
1:A:328:ALA:HB2	3:A:615:ACT:CH3	2.29	0.61
1:B:310:TYR:CB	4:B:612:GOL:H12	2.26	0.61
1:B:444:GLU:HG3	6:B:928:HOH:O	1.99	0.61
1:B:246:ILE:CD1	1:B:472:MET:HE3	2.30	0.61
1:A:89:ARG:HG3	4:A:626:GOL:H12	1.82	0.61
1:B:221:GLU:OE2	4:B:613:GOL:H31	2.01	0.61
1:A:275:LYS:HB2	4:A:625:GOL:H32	1.83	0.60
1:A:495:GLU:H	1:A:495:GLU:CD	2.09	0.60
1:B:143:ALA:HB1	6:B:1020:HOH:O	2.00	0.60
1:B:416:HIS:HB2	6:B:964:HOH:O	2.01	0.60
1:B:442:HIS:CD2	4:B:617:GOL:H32	2.38	0.59
1:B:115:LYS:H	1:B:115:LYS:HD2	1.67	0.59
1:A:276:LYS:HD2	6:A:1167:HOH:O	2.01	0.59
1:A:231[A]:ARG:NH2	6:A:1162:HOH:O	2.37	0.58
1:A:360:ILE:O	1:A:364[B]:MET:HG2	2.03	0.58
1:B:331:ASP:H	3:B:606:ACT:C	2.16	0.58
4:A:623:GOL:H11	6:A:876:HOH:O	2.02	0.58
1:B:275:LYS:HB2	4:B:612:GOL:H2	1.86	0.58
1:A:347:ILE:HD13	1:A:381:ILE:HG13	1.86	0.58
1:A:86:GLU:HG2	6:A:1117:HOH:O	2.04	0.58
1:A:377:GLU:HG2	6:A:1168:HOH:O	2.03	0.57
3:B:609:ACT:H1	6:B:956:HOH:O	2.03	0.57
1:A:52:LYS:NZ	6:A:869:HOH:O	2.30	0.57
1:A:278:LEU:HD23	1:A:278:LEU:C	2.29	0.57
1:B:220:ASN:O	1:B:473:MET:HE2	2.05	0.57
1:B:125:ALA:HB3	1:B:442:HIS:CE1	2.40	0.56
1:B:276:LYS:H	4:B:612:GOL:H31	1.70	0.56
1:B:151:GLU:HG3	6:B:735:HOH:O	2.05	0.56
1:B:180:ARG:HG3	1:B:189:PRO:HG2	1.88	0.56
1:A:89:ARG:HD3	4:A:626:GOL:H31	1.87	0.55
1:B:193:LYS:HD2	6:B:1032:HOH:O	2.05	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:71:VAL:HG22	1:B:185:TRP:CG	2.42	0.55
3:A:616:ACT:H1	6:A:917:HOH:O	2.06	0.55
1:B:171:LYS:HD3	1:B:175:TYR:OH	2.07	0.54
1:B:414:PRO:HA	1:B:419:PHE:CG	2.41	0.54
1:B:472:MET:HA	1:B:472:MET:HE2	1.89	0.54
1:A:153[B]:MET:HE2	6:A:1206:HOH:O	2.08	0.54
1:A:235:ASN:HD21	3:A:618:ACT:C	2.21	0.54
1:A:479:GLU:HG2	6:A:1092:HOH:O	2.08	0.53
1:B:106:GLN:NE2	1:B:124:SER:H	2.07	0.53
1:A:365:ARG:NH2	4:A:622:GOL:H32	2.23	0.53
1:B:242:LEU:HD22	1:B:471:SER:HB2	1.91	0.53
1:A:92:LEU:O	1:A:95[A]:ARG:HB2	2.09	0.52
1:B:223:LEU:HA	4:B:619:GOL:H12	1.92	0.52
1:A:491:GLU:HB3	4:A:627:GOL:H11	1.91	0.52
1:B:296:PRO:HB3	1:B:302:ASN:HD22	1.74	0.52
1:A:258:ALA:HA	1:A:261:ASN:OD1	2.10	0.51
1:A:485:TYR:CD1	3:A:614:ACT:H2	2.45	0.51
1:B:171:LYS:HD3	1:B:175:TYR:CZ	2.45	0.51
1:A:491:GLU:CD	4:A:627:GOL:H32	2.36	0.51
1:A:52:LYS:HE3	1:A:68:ARG:CA	2.32	0.50
1:A:31:SER:HB3	4:A:627:GOL:H12	1.93	0.50
1:B:124:SER:HB3	6:B:985:HOH:O	2.11	0.49
1:B:200:PRO:HD2	6:B:969:HOH:O	2.12	0.49
1:B:276:LYS:HD3	1:B:289:VAL:HG21	1.93	0.49
1:A:101[B]:LEU:HD21	1:A:103:LEU:HB3	1.94	0.48
1:B:102:GLU:HB3	1:B:126:TYR:OH	2.13	0.48
1:A:42:ALA:HB3	1:B:42:ALA:HB3	1.96	0.48
1:A:52:LYS:HG3	1:A:68:ARG:HG2	1.95	0.48
1:B:430:LEU:C	1:B:430:LEU:HD23	2.38	0.48
1:A:10:TRP:CD1	1:A:11:PRO:HD2	2.49	0.48
1:B:275:LYS:HG3	4:B:612:GOL:H11	1.95	0.48
1:A:457:ARG:HH22	3:A:609:ACT:H3	1.78	0.48
1:A:310:TYR:H	4:A:625:GOL:H2	1.78	0.48
4:A:624:GOL:H32	6:A:1197:HOH:O	2.13	0.48
1:A:101[B]:LEU:CD2	1:A:103:LEU:HB3	2.43	0.47
1:B:125:ALA:O	1:B:126:TYR:C	2.57	0.47
1:A:52:LYS:HE2	3:A:617:ACT:CH3	2.44	0.47
1:B:124:SER:C	1:B:126:TYR:H	2.23	0.47
1:A:137:ARG:HA	6:A:1153:HOH:O	2.14	0.47
4:A:623:GOL:H12	6:A:909:HOH:O	2.15	0.47
1:B:106:GLN:HE22	1:B:124:SER:H	1.60	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:331:ASP:O	1:B:368:GLY:HA2	2.14	0.47
1:A:386:ARG:HE	3:A:616:ACT:CH3	2.28	0.47
1:B:283:LEU:HD13	1:B:287[B]:GLN:OE1	2.15	0.47
1:A:220:ASN:O	1:A:473:MET:HE2	2.15	0.46
5:B:620:L2D:H7	5:B:620:L2D:H11	1.69	0.46
1:A:3:PRO:HG2	1:A:4:ASP:H	1.80	0.46
1:B:127:TYR:HA	4:B:617:GOL:H31	1.97	0.46
1:B:457:ARG:HG3	6:B:972:HOH:O	2.15	0.46
1:B:246:ILE:HD13	1:B:472:MET:HE3	1.97	0.46
1:B:127:TYR:CD2	1:B:447:ARG:NH1	2.84	0.45
1:B:446:GLN:HA	1:B:446:GLN:OE1	2.16	0.45
1:A:328:ALA:CB	3:A:615:ACT:H2	2.42	0.45
1:B:408:LEU:O	1:B:435:ILE:HD13	2.17	0.45
1:B:494:PHE:HA	1:B:497:ILE:HD13	1.98	0.45
1:A:386:ARG:HE	3:A:616:ACT:H2	1.82	0.45
1:A:52:LYS:HE2	3:A:617:ACT:H1	1.99	0.45
1:B:142:ILE:HG23	1:B:147:PHE:HE2	1.83	0.44
5:B:620:L2D:H16	5:B:620:L2D:H21	1.68	0.44
1:B:457:ARG:HD2	6:B:996:HOH:O	2.17	0.44
1:A:154:ASN:HA	6:A:1165:HOH:O	2.16	0.44
1:B:246:ILE:HD11	1:B:472:MET:HE3	1.98	0.44
1:B:126:TYR:CD1	1:B:128:PRO:HD2	2.53	0.44
1:A:23[A]:THR:HG22	6:A:1080:HOH:O	2.18	0.43
1:A:405:HIS:CG	1:A:406:ALA:N	2.86	0.43
1:A:493:PRO:HA	1:A:495:GLU:OE2	2.18	0.43
4:B:614:GOL:H2	6:B:977:HOH:O	2.19	0.43
1:A:131:GLN:HG2	6:A:1079:HOH:O	2.19	0.43
3:A:615:ACT:H3	6:A:1012:HOH:O	2.18	0.43
1:B:265:VAL:O	1:B:269:LEU:HG	2.18	0.43
1:B:328:ALA:HA	1:B:329:GLY:HA2	1.71	0.43
1:B:92:LEU:O	1:B:95:ARG:HB2	2.18	0.43
1:B:401:PRO:HB2	6:B:806:HOH:O	2.18	0.43
1:B:223:LEU:HB3	1:B:473:MET:CE	2.49	0.43
3:A:613:ACT:H2	3:A:617:ACT:H3	2.00	0.43
1:B:203:THR:HG22	3:B:610:ACT:H2	2.01	0.43
1:A:40:TYR:CE1	1:A:401:PRO:HB3	2.53	0.42
1:B:60:GLY:O	1:B:125:ALA:HA	2.19	0.42
1:B:158:ALA:HA	1:B:159:PRO:HD3	1.84	0.42
1:B:127:TYR:HA	4:B:617:GOL:H11	2.00	0.42
1:A:283:LEU:HD13	1:A:287[B]:GLN:CD	2.45	0.42
1:B:23[B]:THR:HG23	1:B:24:PRO:HA	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:B:606:ACT:H2	4:B:618:GOL:C3	2.35	0.42
4:A:627:GOL:H31	6:A:1050:HOH:O	2.19	0.42
1:B:137:ARG:HB2	1:B:138:PRO:HA	2.02	0.42
1:B:115:LYS:H	1:B:115:LYS:CD	2.28	0.41
1:A:290:ALA:HA	1:A:469:TYR:CE2	2.55	0.41
1:A:287[B]:GLN:CD	1:A:470:ILE:HG22	2.46	0.41
1:B:275:LYS:H	4:B:612:GOL:H11	1.85	0.41
1:B:341:ARG:C	1:B:342:ILE:HG13	2.45	0.41
1:A:487:PRO:HD2	6:A:803:HOH:O	2.20	0.41
1:A:97:ARG:HG2	6:A:1087:HOH:O	2.19	0.41
1:A:481:GLY:HA2	1:B:444:GLU:CG	2.51	0.41
1:B:71:VAL:HG22	1:B:185:TRP:CB	2.50	0.41
1:B:434:GLU:OE1	1:B:453[B]:ASP:OD2	2.38	0.41
1:B:4:ASP:HA	1:B:499:PRO:CB	2.51	0.41
1:B:116:THR:HG22	6:B:1024:HOH:O	2.20	0.41
1:B:127:TYR:N	1:B:128:PRO:CD	2.83	0.41
1:B:447:ARG:HG3	1:B:447:ARG:HH11	1.86	0.41
1:A:283:LEU:HD13	1:A:287[B]:GLN:OE1	2.21	0.41
1:A:481:GLY:CA	1:B:444:GLU:HG2	2.50	0.41
1:B:77:GLU:OE1	6:B:1020:HOH:O	2.22	0.40
1:B:255:THR:O	1:B:261:ASN:HA	2.20	0.40
1:A:357:ALA:HB1	1:A:373:LEU:HD22	2.04	0.40
1:A:28:PHE:CD2	1:A:28:PHE:C	2.99	0.40
1:A:212:GLY:HA2	6:A:937:HOH:O	2.21	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	516/502 (103%)	499 (97%)	17 (3%)	0	100 100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	504/502 (100%)	486 (96%)	17 (3%)	1 (0%)	43	42
All	All	1020/1004 (102%)	985 (97%)	34 (3%)	1 (0%)	48	46

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	126	TYR

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	443/425 (104%)	439 (99%)	4 (1%)	70	78
1	B	431/425 (101%)	421 (98%)	10 (2%)	44	49
All	All	874/850 (103%)	860 (98%)	14 (2%)	53	62

All (14) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	97	ARG
1	A	127	TYR
1	A	192	LYS
1	A	216	LEU
1	B	6	ILE
1	B	115	LYS
1	B	124	SER
1	B	127	TYR
1	B	130	LEU
1	B	187	GLU
1	B	242	LEU
1	B	334	GLU
1	B	439	LEU
1	B	500	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (9) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	41	GLN
1	A	288	GLN
1	A	416	HIS
1	B	106	GLN
1	B	154	ASN
1	B	281	ASN
1	B	288	GLN
1	B	302	ASN
1	B	361	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](#)

50 ligands are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
4	GOL	A	627	-	5,5,5	0.36	0	5,5,5	0.38	0
4	GOL	B	617	-	5,5,5	0.37	0	5,5,5	0.23	0
5	L2D	B	620	-	32,38,38	2.30	12 (37%)	33,69,69	1.76	6 (18%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	SO4	A	602	-	4,4,4	0.22	0	6,6,6	0.11	0
3	ACT	A	605	-	3,3,3	0.81	0	3,3,3	1.33	0
2	SO4	B	601	-	4,4,4	0.20	0	6,6,6	0.14	0
4	GOL	A	623	-	5,5,5	0.43	0	5,5,5	0.38	0
3	ACT	A	614	-	3,3,3	0.81	0	3,3,3	1.23	0
3	ACT	B	604	-	3,3,3	0.90	0	3,3,3	1.19	0
4	GOL	A	622	-	5,5,5	0.43	0	5,5,5	0.28	0
4	GOL	A	621	-	5,5,5	0.30	0	5,5,5	0.53	0
3	ACT	A	603	-	3,3,3	0.83	0	3,3,3	1.31	0
3	ACT	A	619	-	3,3,3	0.84	0	3,3,3	1.45	0
3	ACT	B	602	-	3,3,3	0.84	0	3,3,3	1.41	0
3	ACT	A	617	-	3,3,3	0.79	0	3,3,3	0.67	0
4	GOL	B	613	-	5,5,5	0.42	0	5,5,5	0.44	0
4	GOL	B	618	-	5,5,5	0.37	0	5,5,5	0.41	0
3	ACT	A	616	-	3,3,3	0.74	0	3,3,3	1.18	0
5	L2D	A	630	-	32,38,38	1.65	7 (21%)	33,69,69	2.21	9 (27%)
4	GOL	B	612	-	5,5,5	0.42	0	5,5,5	0.32	0
3	ACT	B	605	-	3,3,3	0.82	0	3,3,3	1.43	0
3	ACT	B	607	-	3,3,3	0.79	0	3,3,3	1.41	0
3	ACT	A	610	-	3,3,3	0.82	0	3,3,3	1.52	0
4	GOL	B	616	-	5,5,5	0.34	0	5,5,5	0.15	0
3	ACT	A	604	-	3,3,3	0.75	0	3,3,3	1.29	0
3	ACT	A	618	-	3,3,3	0.79	0	3,3,3	1.24	0
3	ACT	B	610	-	3,3,3	0.82	0	3,3,3	1.36	0
4	GOL	B	615	-	5,5,5	0.36	0	5,5,5	0.67	0
4	GOL	A	624	-	5,5,5	0.35	0	5,5,5	0.32	0
4	GOL	A	629	-	5,5,5	0.45	0	5,5,5	0.24	0
4	GOL	B	614	-	5,5,5	0.41	0	5,5,5	0.28	0
2	SO4	A	601	-	4,4,4	0.29	0	6,6,6	0.09	0
4	GOL	A	626	-	5,5,5	0.36	0	5,5,5	0.38	0
4	GOL	A	620	-	5,5,5	0.33	0	5,5,5	0.44	0
3	ACT	A	612	-	3,3,3	0.81	0	3,3,3	1.31	0
3	ACT	A	613	-	3,3,3	0.83	0	3,3,3	1.35	0
3	ACT	B	606	-	3,3,3	0.76	0	3,3,3	1.27	0
3	ACT	A	615	-	3,3,3	0.84	0	3,3,3	1.08	0
3	ACT	A	609	-	3,3,3	0.82	0	3,3,3	1.31	0
3	ACT	A	611	-	3,3,3	0.81	0	3,3,3	1.38	0
3	ACT	B	608	-	3,3,3	0.80	0	3,3,3	1.37	0
4	GOL	A	625	-	5,5,5	0.45	0	5,5,5	0.31	0
3	ACT	A	607	-	3,3,3	0.80	0	3,3,3	1.32	0
3	ACT	B	603	-	3,3,3	0.82	0	3,3,3	1.33	0
3	ACT	A	608	-	3,3,3	0.88	0	3,3,3	1.43	0
4	GOL	A	628	-	5,5,5	0.35	0	5,5,5	0.43	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	ACT	B	611	-	3,3,3	0.81	0	3,3,3	1.29	0
3	ACT	A	606	-	3,3,3	0.78	0	3,3,3	1.37	0
4	GOL	B	619	-	5,5,5	0.31	0	5,5,5	0.38	0
3	ACT	B	609	-	3,3,3	0.79	0	3,3,3	1.44	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	GOL	A	627	-	-	1/4/4/4	-
4	GOL	B	615	-	-	4/4/4/4	-
4	GOL	A	624	-	-	2/4/4/4	-
4	GOL	A	629	-	-	2/4/4/4	-
4	GOL	A	625	-	-	1/4/4/4	-
4	GOL	B	617	-	-	4/4/4/4	-
4	GOL	B	614	-	-	1/4/4/4	-
4	GOL	B	616	-	-	2/4/4/4	-
4	GOL	A	623	-	-	4/4/4/4	-
4	GOL	A	626	-	-	2/4/4/4	-
4	GOL	A	628	-	-	2/4/4/4	-
4	GOL	A	622	-	-	2/4/4/4	-
4	GOL	A	620	-	-	2/4/4/4	-
4	GOL	B	613	-	-	4/4/4/4	-
4	GOL	A	621	-	-	2/4/4/4	-
4	GOL	B	612	-	-	4/4/4/4	-
4	GOL	B	618	-	-	3/4/4/4	-
4	GOL	B	619	-	-	2/4/4/4	-

All (19) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	B	620	L2D	FE-NBD	-5.73	2.00	2.24
5	B	620	L2D	CAS-N	-5.68	1.42	1.49
5	A	630	L2D	FE-NBD	-4.84	2.04	2.24
5	B	620	L2D	CAZ-NAV	-4.63	1.31	1.35
5	A	630	L2D	CAS-N	-4.03	1.44	1.49
5	B	620	L2D	CAR-NBD	-3.73	1.44	1.49

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	B	620	L2D	CBA-N	-3.22	1.46	1.50
5	B	620	L2D	CAY-NAU	-3.21	1.32	1.39
5	B	620	L2D	CA-N	-2.97	1.45	1.49
5	A	630	L2D	FE-N	-2.69	2.13	2.24
5	B	620	L2D	CAT-NBD	-2.59	1.46	1.49
5	B	620	L2D	OXT-C	-2.48	1.23	1.28
5	B	620	L2D	FE-N	2.30	2.33	2.24
5	B	620	L2D	OAD-CAX	-2.25	1.23	1.28
5	A	630	L2D	CAS-CAY	2.16	1.53	1.49
5	B	620	L2D	CBB-NBD	-2.11	1.48	1.50
5	A	630	L2D	CAY-NAU	-2.09	1.34	1.39
5	A	630	L2D	CBA-N	-2.09	1.48	1.50
5	A	630	L2D	CA-C	2.01	1.56	1.52

All (15) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	A	630	L2D	CAP-CBB-NBD	-6.30	108.45	114.45
5	B	620	L2D	CAP-CBB-NBD	-4.78	109.90	114.45
5	B	620	L2D	CAO-CBA-N	-4.30	110.35	114.45
5	A	630	L2D	CAO-CBA-N	-4.28	110.37	114.45
5	A	630	L2D	CAY-CAS-N	-3.88	100.27	109.17
5	A	630	L2D	CAS-N-CBA	-3.55	106.71	112.82
5	A	630	L2D	C-CA-N	3.37	115.03	111.38
5	A	630	L2D	CA-N-CBA	3.21	118.35	112.82
5	A	630	L2D	CA-N-CAS	-3.20	105.91	111.98
5	B	620	L2D	CAT-NBD-CAR	-3.12	106.07	111.98
5	B	620	L2D	CAT-CAZ-NAV	3.03	122.10	119.28
5	B	620	L2D	CA-N-CBA	2.85	117.72	112.82
5	A	630	L2D	CAR-NBD-CBB	-2.76	108.07	112.82
5	B	620	L2D	CAJ-CAF-CAH	-2.26	117.45	120.51
5	A	630	L2D	CAT-NBD-CAR	-2.04	108.11	111.98

There are no chirality outliers.

All (44) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	622	GOL	O1-C1-C2-O2
4	A	622	GOL	O1-C1-C2-C3
4	A	623	GOL	C1-C2-C3-O3
4	A	624	GOL	O1-C1-C2-C3
4	A	626	GOL	O1-C1-C2-C3

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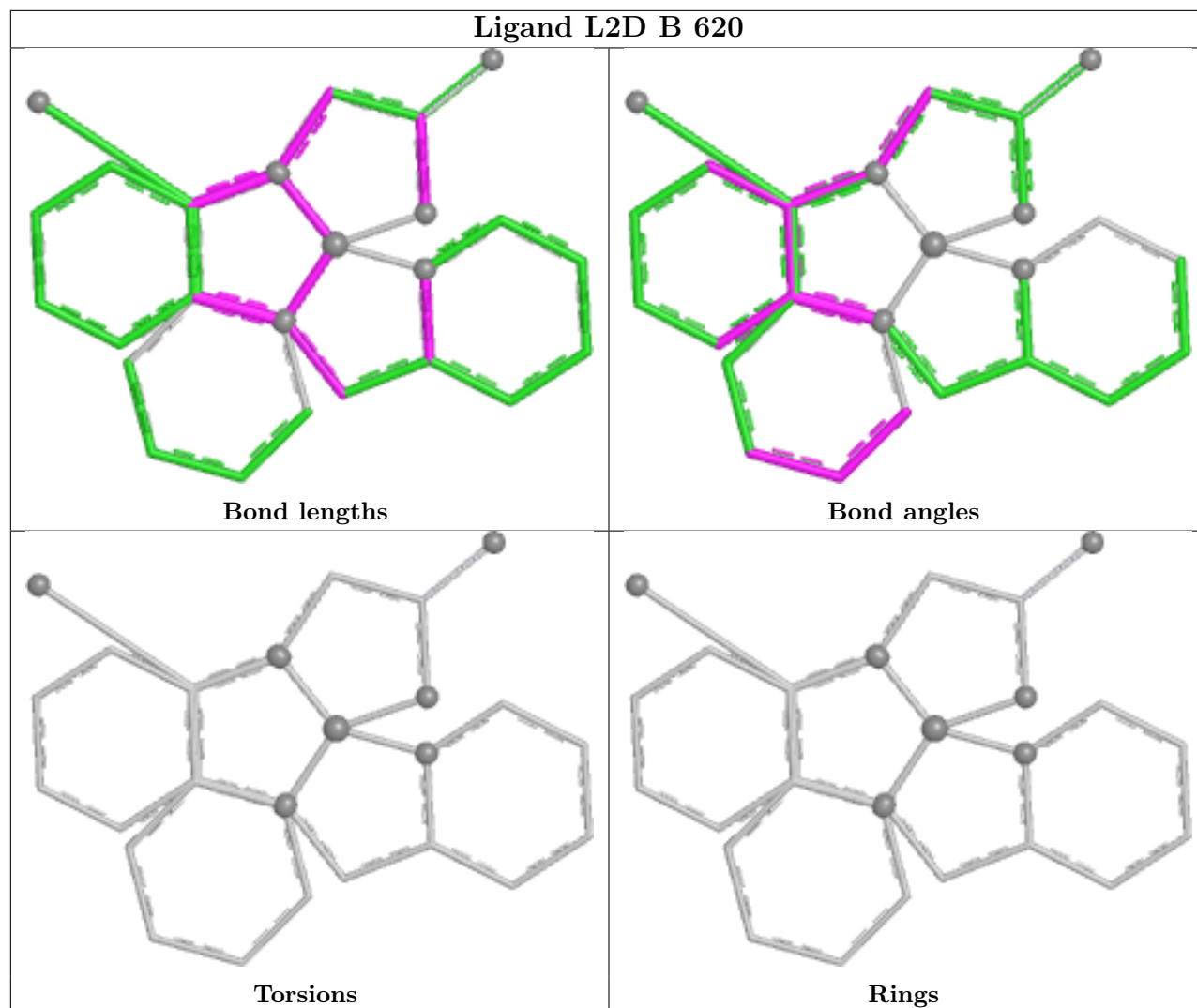
Mol	Chain	Res	Type	Atoms
4	A	628	GOL	O1-C1-C2-C3
4	A	629	GOL	O1-C1-C2-O2
4	A	629	GOL	O1-C1-C2-C3
4	B	612	GOL	O1-C1-C2-C3
4	B	612	GOL	C1-C2-C3-O3
4	B	613	GOL	O1-C1-C2-C3
4	B	615	GOL	O1-C1-C2-C3
4	B	616	GOL	O1-C1-C2-C3
4	B	618	GOL	O1-C1-C2-C3
4	A	620	GOL	O1-C1-C2-O2
4	A	626	GOL	O1-C1-C2-O2
4	B	612	GOL	O2-C2-C3-O3
4	A	620	GOL	O1-C1-C2-C3
4	A	621	GOL	O1-C1-C2-C3
4	A	623	GOL	O1-C1-C2-C3
4	B	615	GOL	C1-C2-C3-O3
4	B	617	GOL	O1-C1-C2-C3
4	B	617	GOL	C1-C2-C3-O3
4	B	618	GOL	C1-C2-C3-O3
4	B	619	GOL	O1-C1-C2-C3
4	A	621	GOL	O1-C1-C2-O2
4	B	613	GOL	O1-C1-C2-O2
4	B	615	GOL	O1-C1-C2-O2
4	B	615	GOL	O2-C2-C3-O3
4	B	616	GOL	O1-C1-C2-O2
4	B	617	GOL	O1-C1-C2-O2
4	B	617	GOL	O2-C2-C3-O3
4	B	619	GOL	O1-C1-C2-O2
4	A	623	GOL	O1-C1-C2-O2
4	A	623	GOL	O2-C2-C3-O3
4	A	624	GOL	O1-C1-C2-O2
4	A	628	GOL	O1-C1-C2-O2
4	B	612	GOL	O1-C1-C2-O2
4	B	613	GOL	O2-C2-C3-O3
4	B	618	GOL	O1-C1-C2-O2
4	B	613	GOL	C1-C2-C3-O3
4	B	614	GOL	O1-C1-C2-C3
4	A	625	GOL	O1-C1-C2-O2
4	A	627	GOL	O1-C1-C2-O2

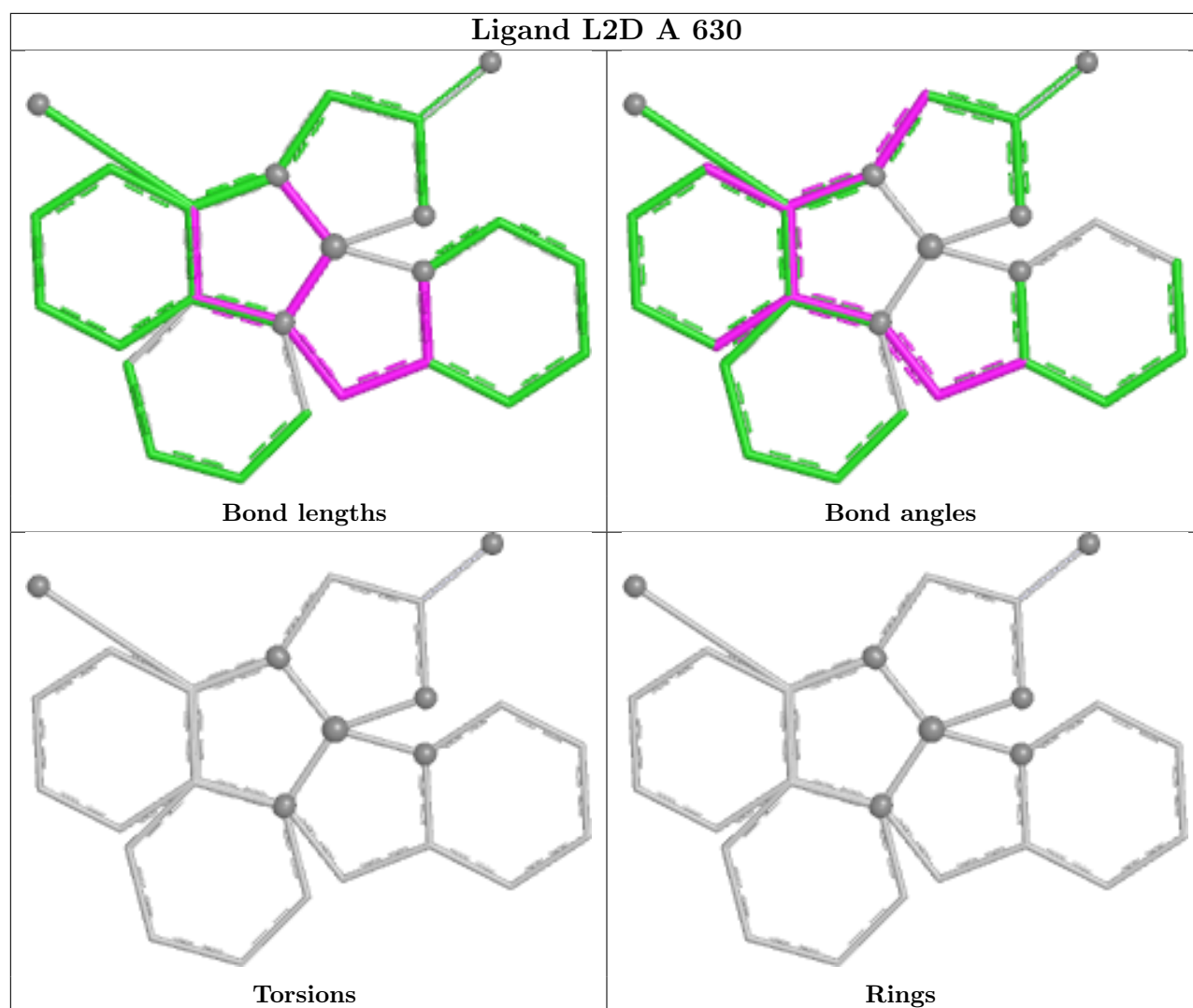
There are no ring outliers.

27 monomers are involved in 60 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	627	GOL	5	0
4	B	617	GOL	3	0
5	B	620	L2D	2	0
4	A	623	GOL	2	0
3	A	614	ACT	1	0
4	A	622	GOL	3	0
4	A	621	GOL	1	0
3	A	617	ACT	3	0
4	B	613	GOL	1	0
4	B	618	GOL	5	0
3	A	616	ACT	3	0
4	B	612	GOL	6	0
3	B	605	ACT	1	0
4	B	616	GOL	2	0
3	A	618	ACT	1	0
3	B	610	ACT	1	0
4	B	615	GOL	2	0
4	A	624	GOL	1	0
4	B	614	GOL	1	0
4	A	626	GOL	2	0
3	A	613	ACT	1	0
3	B	606	ACT	10	0
3	A	615	ACT	4	0
3	A	609	ACT	1	0
4	A	625	GOL	2	0
4	B	619	GOL	1	0
3	B	609	ACT	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 [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	497/502 (99%)	-0.58	2 (0%) 88 88	12, 27, 49, 85	21 (4%)
1	B	497/502 (99%)	-0.25	7 (1%) 73 73	13, 36, 71, 113	12 (2%)
All	All	994/1004 (99%)	-0.41	9 (0%) 81 80	12, 30, 63, 113	33 (3%)

All (9) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	3	PRO	3.5
1	B	500	VAL	3.5
1	B	328	ALA	3.1
1	B	327	PRO	2.8
1	B	329	GLY	2.7
1	B	330	LYS	2.5
1	B	76	GLY	2.5
1	B	382	TYR	2.4
1	A	382	TYR	2.2

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	ACT	A	617	4/4	0.55	0.20	63,64,70,79	0
3	ACT	A	619	4/4	0.69	0.16	64,72,72,78	0
3	ACT	A	616	4/4	0.70	0.19	35,39,40,43	4
3	ACT	B	603	4/4	0.70	0.12	77,82,82,84	0
3	ACT	A	603	4/4	0.71	0.16	63,69,69,70	0
3	ACT	A	608	4/4	0.71	0.24	48,59,64,68	4
3	ACT	A	613	4/4	0.74	0.11	64,68,69,69	0
4	GOL	A	624	6/6	0.74	0.16	59,79,85,87	0
4	GOL	A	628	6/6	0.74	0.17	74,77,82,85	0
3	ACT	A	609	4/4	0.75	0.09	79,83,83,83	0
3	ACT	A	605	4/4	0.76	0.14	74,82,83,86	0
3	ACT	A	612	4/4	0.77	0.14	72,74,74,74	0
4	GOL	A	629	6/6	0.77	0.19	52,67,74,77	0
3	ACT	B	610	4/4	0.78	0.12	38,63,69,72	0
2	SO4	A	602	5/5	0.78	0.15	91,96,101,101	0
3	ACT	A	618	4/4	0.78	0.14	68,69,71,73	0
3	ACT	B	604	4/4	0.78	0.12	55,59,62,64	0
4	GOL	B	614	6/6	0.78	0.20	80,81,82,84	0
4	GOL	B	618	6/6	0.78	0.15	60,70,75,83	0
4	GOL	B	616	6/6	0.79	0.14	75,78,79,80	0
3	ACT	A	610	4/4	0.79	0.13	54,55,55,59	0
3	ACT	A	615	4/4	0.80	0.15	34,38,39,40	4
4	GOL	A	627	6/6	0.81	0.15	33,45,56,58	0
3	ACT	A	607	4/4	0.81	0.14	44,54,56,57	4
3	ACT	B	602	4/4	0.81	0.17	68,69,71,75	0
3	ACT	B	608	4/4	0.82	0.14	81,82,82,83	0
3	ACT	B	607	4/4	0.83	0.11	51,60,61,64	0
4	GOL	B	617	6/6	0.83	0.13	90,91,92,95	0
3	ACT	B	609	4/4	0.83	0.12	66,71,73,75	0
3	ACT	B	611	4/4	0.84	0.15	44,45,49,55	4
3	ACT	A	614	4/4	0.85	0.13	55,58,60,66	4
3	ACT	A	611	4/4	0.85	0.15	77,81,81,82	0
4	GOL	B	613	6/6	0.86	0.13	38,52,61,61	0
3	ACT	A	604	4/4	0.86	0.14	45,54,54,60	0
4	GOL	A	621	6/6	0.86	0.14	35,44,59,63	0
3	ACT	B	605	4/4	0.86	0.11	46,54,56,58	0
4	GOL	B	612	6/6	0.86	0.16	61,69,71,78	0
4	GOL	A	625	6/6	0.87	0.12	45,52,55,58	0
3	ACT	B	606	4/4	0.87	0.12	59,60,61,61	4
4	GOL	A	623	6/6	0.88	0.10	29,54,61,61	0
3	ACT	A	606	4/4	0.88	0.12	37,38,41,52	0

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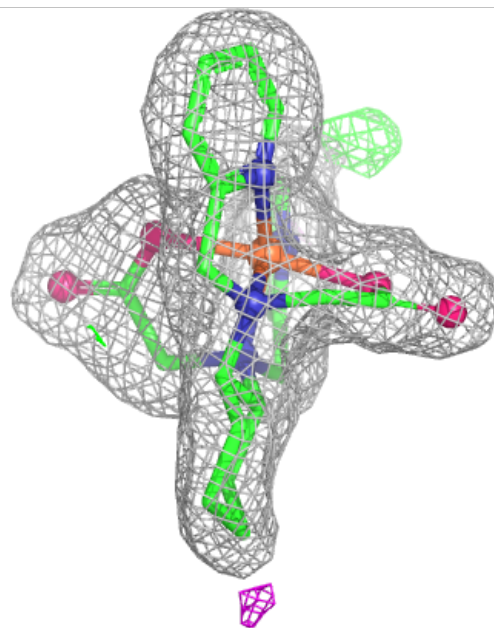
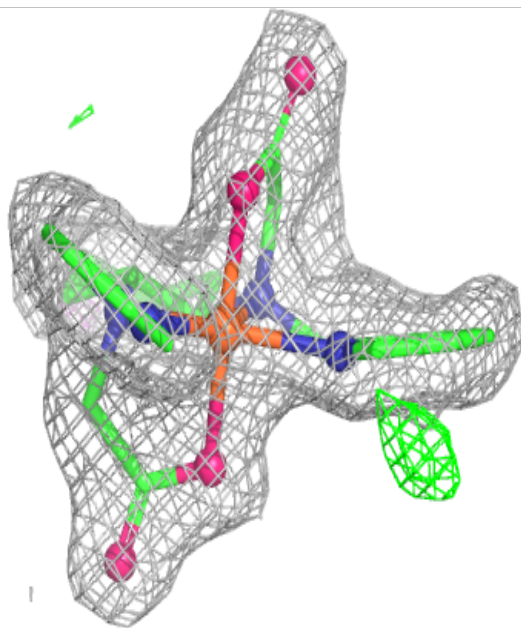
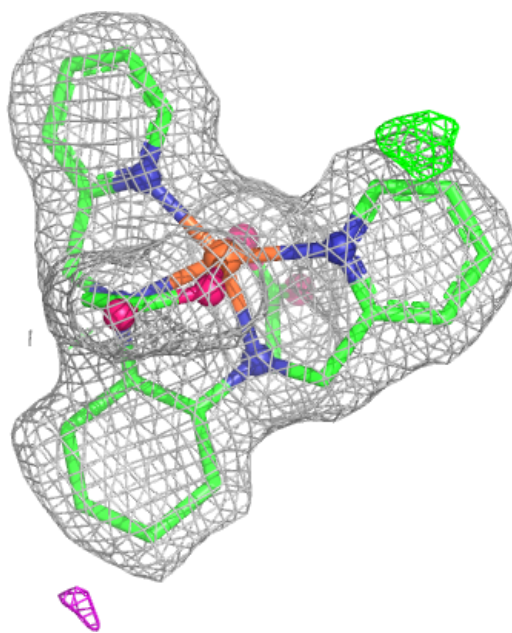
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
4	GOL	A	622	6/6	0.88	0.12	51,56,58,65	0
4	GOL	A	626	6/6	0.89	0.17	120,122,123,125	0
2	SO4	B	601	5/5	0.89	0.10	63,65,74,78	0
4	GOL	B	619	6/6	0.89	0.11	48,59,60,63	0
4	GOL	A	620	6/6	0.90	0.14	51,65,68,70	0
4	GOL	B	615	6/6	0.90	0.10	33,44,48,60	0
2	SO4	A	601	5/5	0.94	0.07	60,61,66,72	0
5	L2D	A	630	31/31	0.98	0.06	19,26,37,46	0
5	L2D	B	620	31/31	0.98	0.07	24,33,49,53	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.

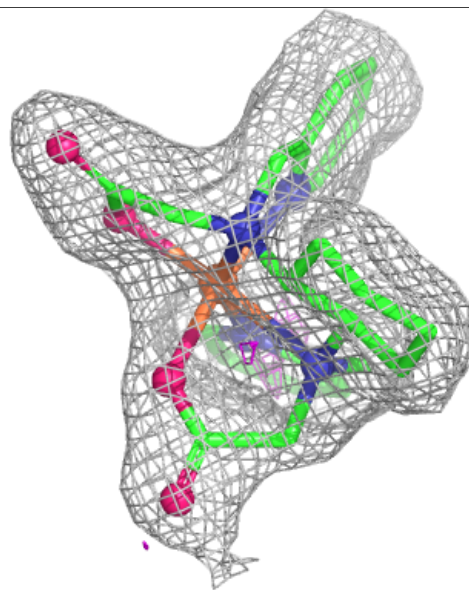
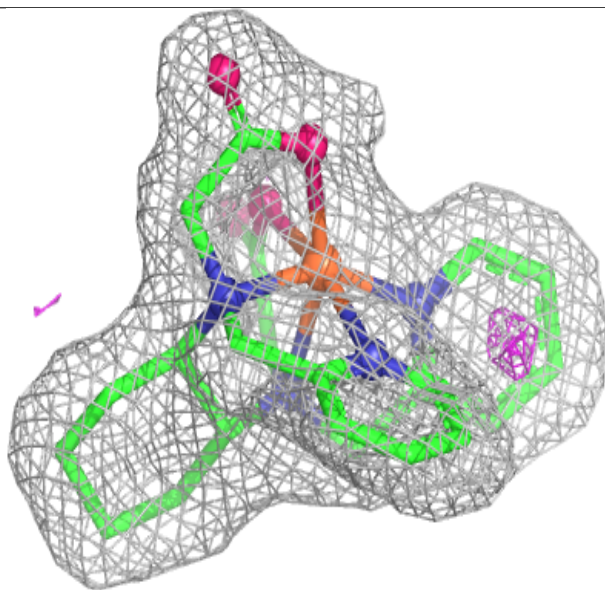
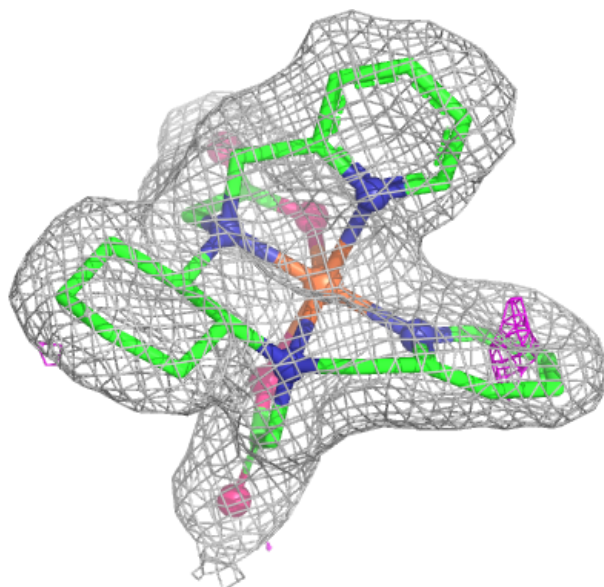
Electron density around L2D A 630:

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



Electron density around L2D B 620:

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



6.5 Other polymers ⓘ

There are no such residues in this entry.