



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 11:06 AM UTC

PDB ID : 4XPI / pdb_00004xpi
Title : Fe protein independent substrate reduction by nitrogenase variants altered in intramolecular electron transfer
Authors : Danyal, K.; Rasmusen, A.J.; Keable, S.M.; Shaw, S.; Zadvornyy, O.; Duval, S.; Dean, D.R.; Raugei, S.; Peters, J.W.; Seefeldt, L.C.
Deposited on : 2015-01-17
Resolution : 1.97 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

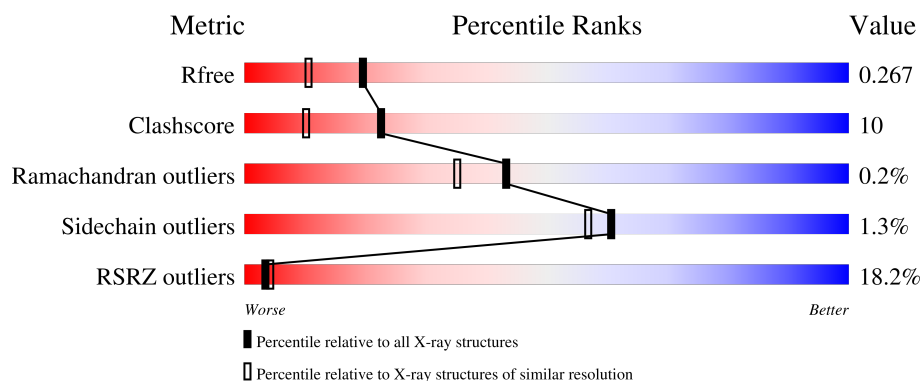
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.97 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	1506 (1.98-1.98)
Clashscore	190562	1534 (1.98-1.98)
Ramachandran outliers	187476	1518 (1.98-1.98)
Sidechain outliers	187428	1518 (1.98-1.98)
RSRZ outliers	180081	1506 (1.98-1.98)

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	490	22% 77% 19% ..
1	C	490	36% 68% 28% ..
2	B	522	7% 82% 17% .
2	D	522	8% 84% 15% .

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
5	GOL	B	607	-	-	X	-
5	GOL	B	608	-	X	X	-
5	GOL	C	508	-	-	X	-

2 Entry composition

There are 9 unique types of molecules in this entry. The entry contains 17075 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 Nitrogenase molybdenum-iron protein alpha chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	479	Total	C	N	O	S	1	2	0
			3805	2419	648	712	26			
1	C	478	Total	C	N	O	S	0	1	0
			3797	2414	647	711	25			

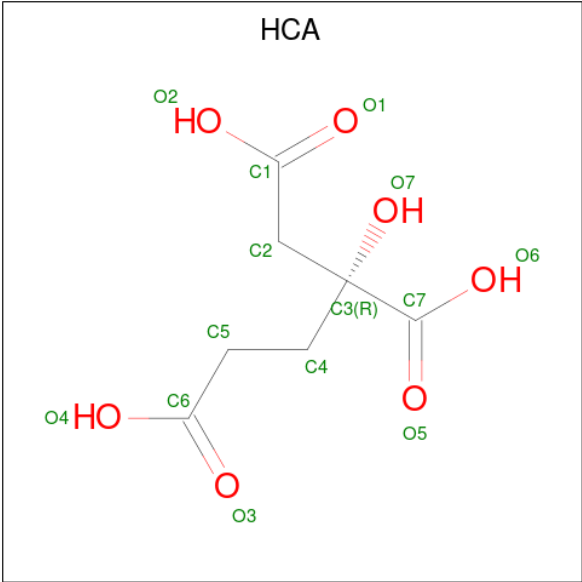
- Molecule 2 is a protein called Nitrogenase molybdenum-iron protein beta chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	522	Total	C	N	O	S	0	1	0
			4178	2666	708	776	28			
2	D	522	Total	C	N	O	S	0	0	0
			4172	2663	707	774	28			

There are 2 discrepancies between the modelled and reference sequences:

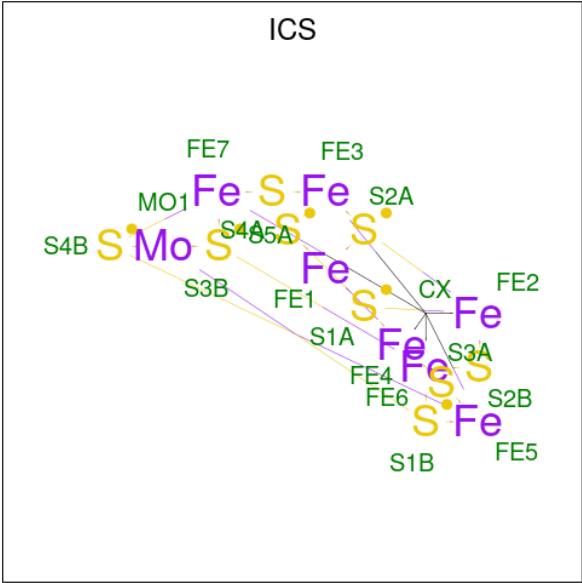
Chain	Residue	Modelled	Actual	Comment	Reference
B	98	HIS	TYR	engineered mutation	UNP P07329
D	98	HIS	TYR	engineered mutation	UNP P07329

- Molecule 3 is 3-HYDROXY-3-CARBOXY-ADIPIC ACID (CCD ID: HCA) (formula: $C_7H_{10}O_7$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			14	7	7		
3	C	1	Total	C	O	0	0
			14	7	7		

- Molecule 4 is iron-sulfur-molybdenum cluster with interstitial carbon (CCD ID: ICS) (formula: CFe₇MoS₉).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	A	1	Total	C	Fe	Mo	S	0	0
			18	1	7	1	9		

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	C	1	Total	C	Fe	Mo	S	0	0
			18	1	7	1	9		

- Molecule 5 is GLYCEROL (CCD ID: GOL) (formula: $C_3H_8O_3$).



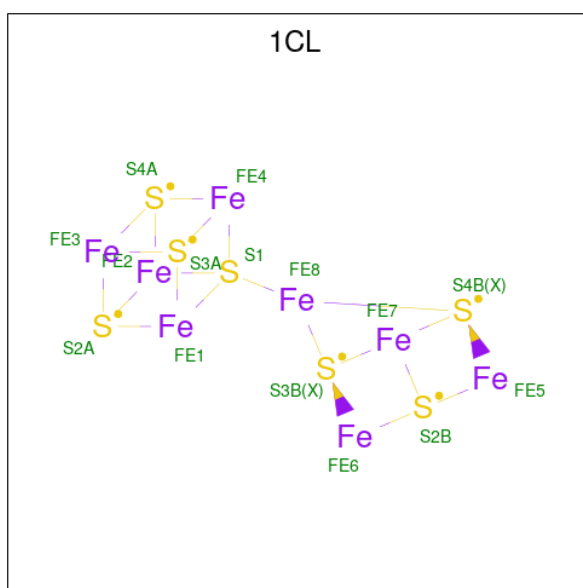
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	C	O	0	0
			6	3	3		
5	B	1	Total	C	O	0	0
			6	3	3		
5	B	1	Total	C	O	0	0
			6	3	3		
5	B	1	Total	C	O	0	0
			6	3	3		
5	B	1	Total	C	O	0	0
			6	3	3		
5	B	1	Total	C	O	0	0
			6	3	3		
5	C	1	Total	C	O	0	0
			6	3	3		
5	C	1	Total	C	O	0	0
			6	3	3		
5	C	1	Total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

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	C	1	Total	C	O	0	0
			6	3	3		
5	C	1	Total	C	O	0	0
			6	3	3		
5	C	1	Total	C	O	0	0
			6	3	3		
5	D	1	Total	C	O	0	0
			6	3	3		
5	D	1	Total	C	O	0	0
			6	3	3		

- Molecule 6 is FE(8)-S(7) CLUSTER, OXIDIZED (CCD ID: 1CL) (formula: Fe_8S_7).



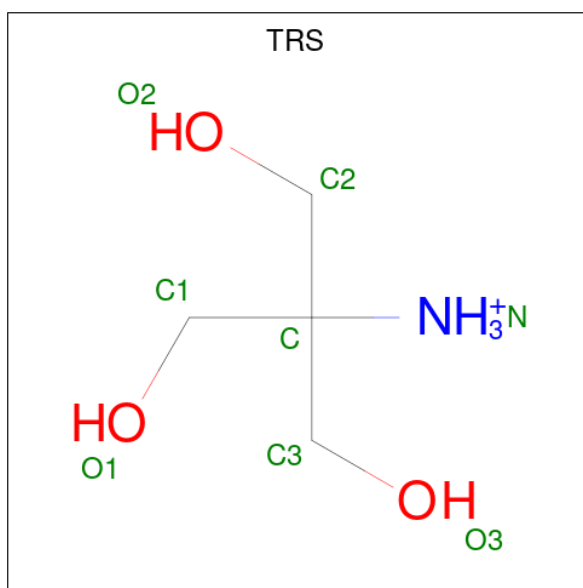
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	A	1	Total	Fe	S	0	0
			15	8	7		
6	C	1	Total	Fe	S	0	0
			15	8	7		

- Molecule 7 is CALCIUM ION (CCD ID: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	B	2	Total	Ca	0	0
			2	2		

- Molecule 8 is 2-AMINO-2-HYDROXYMETHYL-PROPANE-1,3-DIOL (CCD ID: TRS)

(formula: $C_4H_{12}NO_3$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
8	B	1	Total	C	N	O	0	0
			8	4	1	3		
8	D	1	Total	C	N	O	0	0
			8	4	1	3		

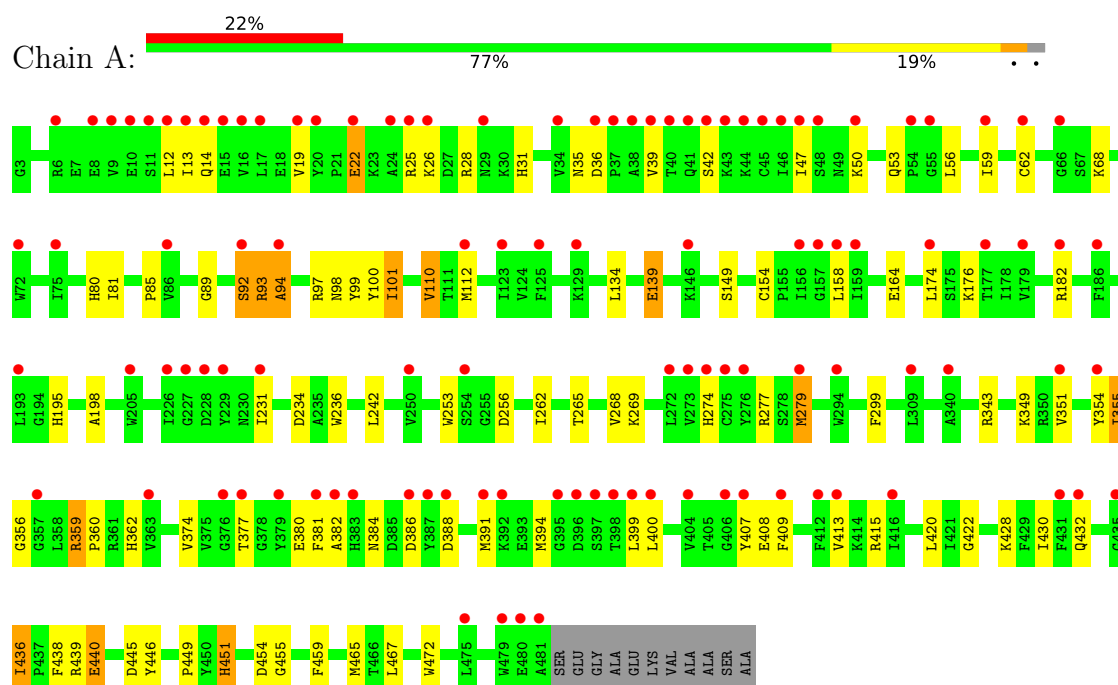
- Molecule 9 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
9	A	211	Total	O	0	0
			211	211		
9	B	257	Total	O	0	0
			257	257		
9	C	202	Total	O	0	0
			202	202		
9	D	251	Total	O	0	0
			251	251		

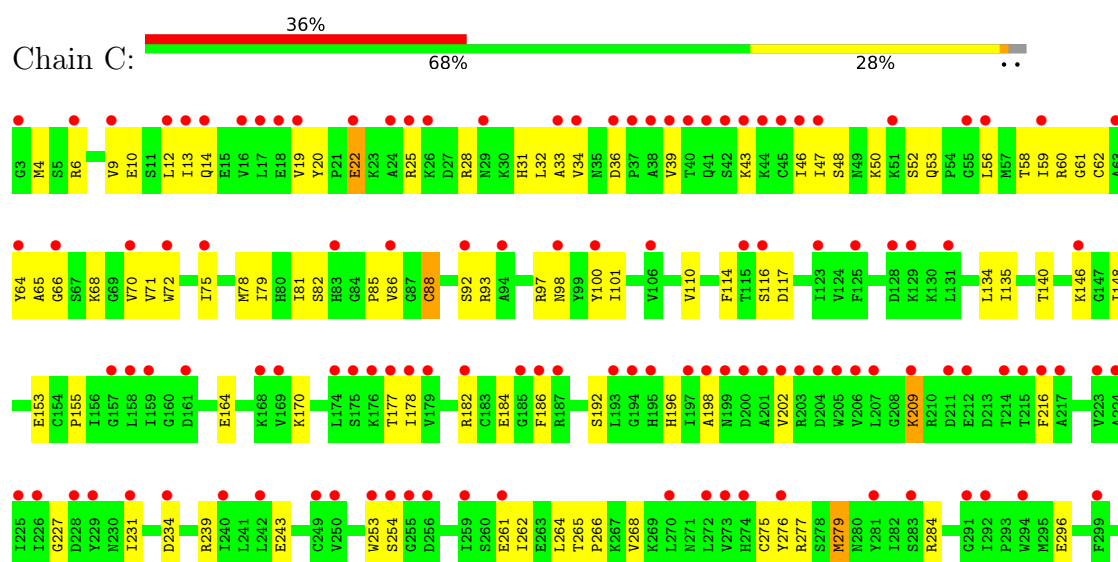
3 Residue-property plots

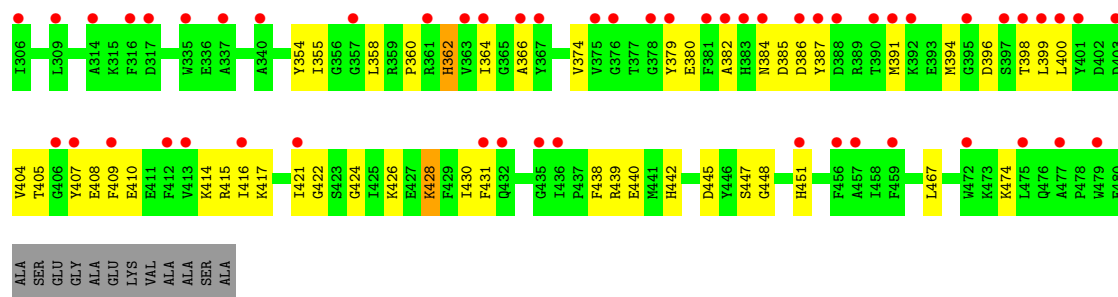
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. 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: Nitrogenase molybdenum-iron protein alpha chain

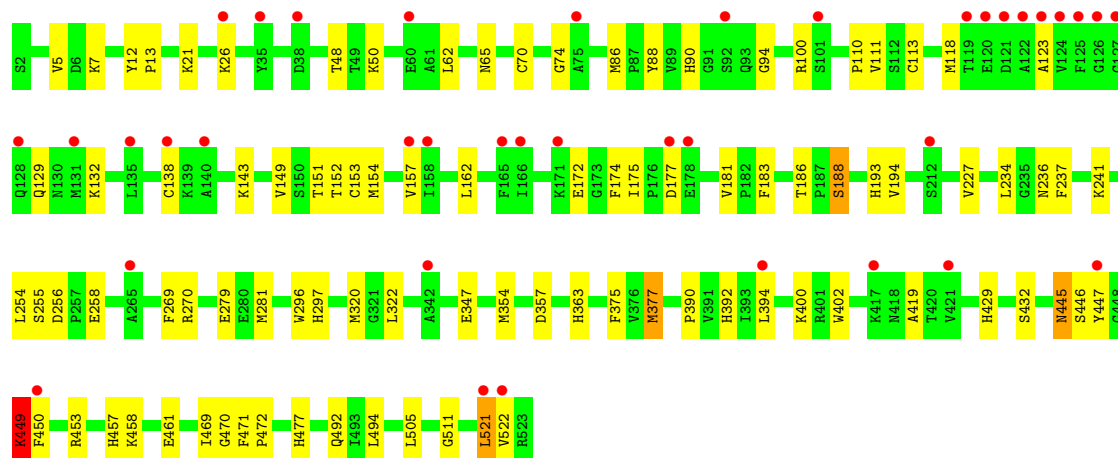
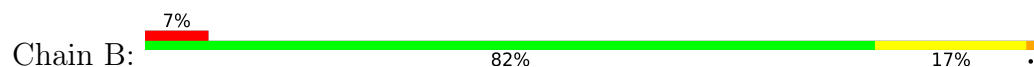


- Molecule 1: Nitrogenase molybdenum-iron protein alpha chain

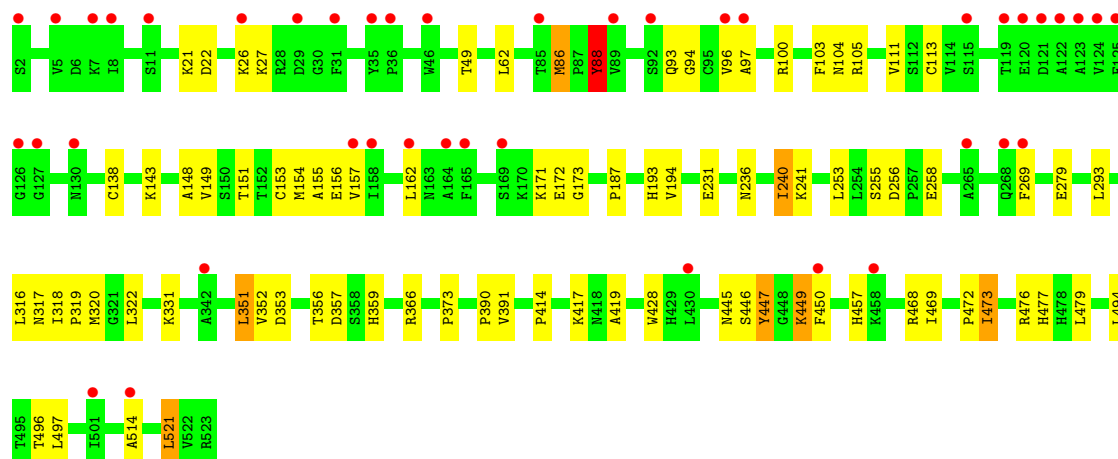
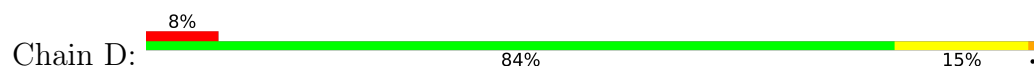




• Molecule 2: Nitrogenase molybdenum-iron protein beta chain



• Molecule 2: Nitrogenase molybdenum-iron protein beta chain



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	80.80Å 130.83Å 108.11Å 90.00° 111.14° 90.00°	Depositor
Resolution (Å)	35.00 – 1.97 35.00 – 1.97	Depositor EDS
% Data completeness (in resolution range)	96.4 (35.00-1.97) 96.4 (35.00-1.97)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.96 (at 1.98Å)	Xtriage
Refinement program	REFMAC 5.6.0117	Depositor
R, R_{free}	0.213 , 0.264 0.218 , 0.267	Depositor DCC
R_{free} test set	7091 reflections (4.83%)	wwPDB-VP
Wilson B-factor (Å ²)	27.7	Xtriage
Anisotropy	0.531	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 49.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	0.000 for h,-k,-h-l	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	17075	wwPDB-VP
Average B, all atoms (Å ²)	41.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 24.75 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 3.6143e-03. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

¹Intensities estimated from amplitudes.

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

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: ICS, CA, GOL, 1CL, HCA, TRS

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	1.41	24/3899 (0.6%)	1.20	11/5257 (0.2%)
1	C	1.22	10/3888 (0.3%)	1.12	5/5242 (0.1%)
2	B	1.40	26/4284 (0.6%)	1.17	11/5791 (0.2%)
2	D	1.35	23/4278 (0.5%)	1.12	10/5783 (0.2%)
All	All	1.35	83/16349 (0.5%)	1.15	37/22073 (0.2%)

All (83) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	92	SER	CA-C	-21.24	1.22	1.52
2	B	477	HIS	CE1-NE2	12.19	1.44	1.32
2	B	357	ASP	C-O	11.08	1.38	1.24
1	A	430	ILE	C-O	10.84	1.36	1.24
2	D	357	ASP	C-O	10.08	1.36	1.24
2	D	450	PHE	N-CA	9.49	1.58	1.46
2	D	477	HIS	CG-CD2	9.48	1.46	1.35
2	B	471	PHE	CA-C	9.12	1.62	1.52
2	B	477	HIS	CG-CD2	8.69	1.45	1.35
1	C	92	SER	CA-C	-8.41	1.40	1.52
1	A	356	GLY	C-O	-8.23	1.12	1.23
2	D	477	HIS	CE1-NE2	8.10	1.40	1.32
2	D	496	THR	C-O	8.10	1.33	1.24
1	A	451	HIS	ND1-CE1	7.97	1.40	1.32
2	D	357	ASP	N-CA	7.94	1.56	1.46
2	B	450	PHE	N-CA	7.73	1.56	1.46
1	C	93	ARG	CA-C	7.72	1.63	1.52
1	A	359	ARG	C-O	-7.67	1.17	1.24
2	B	477	HIS	ND1-CE1	7.63	1.40	1.32
2	D	469	ILE	N-CA	-7.33	1.37	1.46
1	A	93	ARG	CA-C	7.11	1.61	1.52
2	D	193	HIS	CE1-NE2	7.07	1.39	1.32

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	80	HIS	ND1-CE1	6.94	1.39	1.32
2	B	357	ASP	N-CA	6.93	1.54	1.46
2	B	429	HIS	CE1-NE2	6.88	1.39	1.32
2	D	473	ILE	C-O	6.76	1.31	1.24
1	A	85	PRO	C-O	6.76	1.32	1.24
1	A	440	GLU	CD-OE2	-6.68	1.12	1.25
1	A	94	ALA	CA-C	6.51	1.61	1.52
1	C	424	GLY	C-O	6.49	1.31	1.23
2	B	457	HIS	ND1-CE1	6.46	1.39	1.32
1	A	451	HIS	CG-CD2	6.42	1.43	1.35
2	D	497	LEU	C-O	6.37	1.31	1.24
2	B	227	VAL	CA-C	-6.35	1.47	1.53
1	A	81	ILE	N-CA	6.27	1.53	1.46
2	D	447	TYR	C-O	-6.26	1.16	1.24
1	C	85	PRO	C-O	6.12	1.31	1.24
2	B	449	LYS	C-O	6.12	1.31	1.24
2	D	86	MET	N-CA	6.08	1.53	1.45
1	A	101	ILE	N-CA	-6.06	1.38	1.46
2	D	476	ARG	N-CA	-6.06	1.38	1.45
1	A	454	ASP	C-O	-6.05	1.17	1.24
2	B	143	LYS	N-CA	6.01	1.50	1.46
1	C	101	ILE	C-O	-5.96	1.17	1.24
2	B	193	HIS	CG-ND1	-5.94	1.31	1.38
2	D	477	HIS	ND1-CE1	5.92	1.38	1.32
2	B	469	ILE	C-O	-5.88	1.18	1.24
2	D	359	HIS	CG-ND1	-5.86	1.31	1.38
2	D	155	ALA	C-O	-5.80	1.17	1.24
1	A	343	ARG	C-O	-5.78	1.19	1.24
1	A	80	HIS	CG-ND1	-5.70	1.31	1.38
1	A	459	PHE	N-CA	-5.68	1.39	1.46
1	C	428	LYS	CA-C	5.67	1.60	1.52
2	D	457	HIS	ND1-CE1	5.66	1.38	1.32
1	A	195	HIS	CG-CD2	5.65	1.42	1.35
2	D	143	LYS	C-O	-5.58	1.21	1.23
1	C	66	GLY	N-CA	5.53	1.53	1.45
2	D	148	ALA	C-O	-5.42	1.17	1.24
1	C	362	HIS	CD2-NE2	-5.39	1.31	1.37
1	A	195	HIS	CE1-NE2	5.39	1.38	1.32
2	B	237	PHE	C-O	5.37	1.30	1.24
2	B	522	VAL	CA-C	5.35	1.59	1.52
1	C	430	ILE	C-O	5.34	1.30	1.24
2	B	354	MET	C-O	5.32	1.30	1.24

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	457	HIS	CG-CD2	5.32	1.41	1.35
2	B	511	GLY	N-CA	5.32	1.53	1.45
2	D	468	ARG	C-O	-5.32	1.17	1.24
2	B	74	GLY	CA-C	-5.28	1.46	1.52
2	D	457	HIS	CG-CD2	5.24	1.41	1.35
1	A	436	ILE	CA-C	-5.20	1.48	1.53
2	B	234	LEU	C-O	5.20	1.30	1.24
2	B	505	LEU	C-O	5.16	1.30	1.24
2	B	392	HIS	CG-ND1	-5.15	1.32	1.38
2	D	88	TYR	C-O	-5.12	1.18	1.23
1	A	242	LEU	CA-CB	-5.11	1.45	1.53
2	D	428	TRP	CD2-CE2	5.10	1.50	1.41
1	A	198	ALA	C-O	-5.10	1.18	1.24
2	B	445	ASN	CA-CB	5.09	1.61	1.53
1	C	72	TRP	CA-C	-5.06	1.47	1.52
2	B	152	THR	N-CA	5.03	1.51	1.45
1	A	89	GLY	N-CA	5.03	1.52	1.45
1	A	149	SER	CA-C	-5.03	1.46	1.52
2	B	110	PRO	C-O	-5.01	1.18	1.23

All (37) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	409	PHE	N-CA-C	-8.83	100.63	111.40
1	C	409	PHE	N-CA-C	-6.93	103.17	111.69
1	A	430	ILE	N-CA-C	6.56	116.71	110.42
1	A	110	VAL	N-CA-C	6.48	117.23	110.62
1	A	99	TYR	N-CA-C	6.33	119.42	110.50
1	A	22	GLU	N-CA-C	6.24	118.08	111.28
1	C	60	ARG	N-CA-C	6.23	118.34	110.24
2	D	521	LEU	N-CA-CB	6.19	119.32	110.16
1	A	256	ASP	N-CA-C	6.12	119.98	111.90
2	D	351	LEU	N-CA-C	-5.95	104.70	111.07
1	C	424	GLY	N-CA-C	5.94	121.96	112.58
2	B	186	THR	CA-C-N	5.93	126.13	119.90
2	B	186	THR	C-N-CA	5.93	126.13	119.90
2	D	240	ILE	N-CA-C	-5.82	104.84	110.72
1	A	81	ILE	CB-CA-C	-5.81	103.93	110.96
2	B	505	LEU	N-CA-C	5.80	117.28	111.07
1	A	139	GLU	N-CA-C	5.76	117.56	111.28
2	D	103	PHE	N-CA-C	5.66	117.45	111.28
2	B	449	LYS	N-CA-C	-5.65	105.20	111.36

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	449	LYS	CA-C-N	-5.59	111.81	120.31
2	B	449	LYS	C-N-CA	-5.59	111.81	120.31
1	C	239	ARG	N-CA-C	5.56	118.06	111.33
2	D	93	GLN	N-CA-C	5.53	118.07	111.71
2	D	357	ASP	N-CA-C	5.42	117.94	111.71
2	D	320	MET	CG-SD-CE	5.40	112.78	100.90
1	A	94	ALA	N-CA-C	5.38	122.25	110.80
2	B	183	PHE	N-CA-C	5.38	116.97	108.96
1	A	154	CYS	N-CA-C	5.37	121.68	109.81
2	D	105	ARG	N-CA-C	5.34	117.19	111.36
2	B	521	LEU	N-CA-CB	5.32	118.04	110.16
1	A	236	TRP	N-CA-C	5.28	117.72	111.33
1	C	209	LYS	N-CA-C	5.27	117.77	111.71
2	D	449	LYS	N-CA-C	-5.20	105.73	111.71
2	B	377	MET	CG-SD-CE	-5.15	89.56	100.90
2	B	188	SER	CA-CB-OG	5.04	121.18	111.10
2	B	432	SER	N-CA-C	5.02	117.13	111.11
2	D	104	ASN	CB-CA-C	-5.02	102.41	110.74

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	3805	0	3747	84	0
1	C	3797	0	3737	138	0
2	B	4178	0	4089	66	0
2	D	4172	0	4085	49	0
3	A	14	0	6	1	0
3	C	14	0	6	2	0
4	A	18	0	0	0	0
4	C	18	0	0	0	0
5	A	6	0	8	0	0
5	B	36	0	48	17	0
5	C	36	0	48	18	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	D	12	0	16	0	0
6	A	15	0	0	0	0
6	C	15	0	0	0	0
7	B	2	0	0	0	0
8	B	8	0	12	2	0
8	D	8	0	12	1	0
9	A	211	0	0	23	0
9	B	257	0	0	26	0
9	C	202	0	0	53	0
9	D	251	0	0	16	0
All	All	17075	0	15814	334	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 (334) 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:C:71:VAL:HG13	9:C:796:HOH:O	1.24	1.35
1:C:428:LYS:HB2	9:C:766:HOH:O	1.39	1.17
1:C:385:ASP:HB2	9:C:691:HOH:O	1.38	1.17
1:C:253:TRP:HB3	1:C:279:MET:HE1	1.38	1.01
1:C:358:LEU:HB2	9:C:615:HOH:O	1.61	0.99
1:C:46:ILE:HD12	9:C:730:HOH:O	1.60	0.98
2:B:111:VAL:HG12	9:B:735:HOH:O	1.67	0.95
5:C:504:GOL:O3	9:C:601:HOH:O	1.81	0.93
1:C:428:LYS:HD2	9:C:609:HOH:O	1.69	0.91
1:C:36:ASP:O	1:C:39:VAL:HG22	1.69	0.91
2:D:318:ILE:HA	9:D:701:HOH:O	1.69	0.91
1:A:394:MET:HB2	9:A:719:HOH:O	1.72	0.90
2:D:111:VAL:HG12	9:D:727:HOH:O	1.72	0.89
2:B:296:TRP:CD1	2:B:377:MET:HE1	2.08	0.88
2:B:269:PHE:CD2	9:B:819:HOH:O	2.26	0.88
2:D:269:PHE:CD2	9:D:871:HOH:O	2.27	0.88
1:C:438:PHE:HB2	9:C:667:HOH:O	1.75	0.87
1:C:25:ARG:NH1	9:C:602:HOH:O	2.08	0.86
5:C:504:GOL:C3	9:C:601:HOH:O	2.23	0.86
1:C:140:THR:HG21	5:C:507:GOL:H12	1.55	0.86
2:D:194:VAL:HG21	9:D:925:HOH:O	1.76	0.85
1:A:440:GLU:HG3	9:A:785:HOH:O	1.75	0.85
1:A:428:LYS:HB2	9:A:785:HOH:O	1.76	0.84

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:6:ARG:NH2	1:C:396:ASP:OD1	2.11	0.83
1:A:36:ASP:O	1:A:39:VAL:HG22	1.80	0.82
1:C:28:ARG:HD3	1:C:408:GLU:OE2	1.79	0.82
1:C:186:PHE:HB3	9:D:773:HOH:O	1.78	0.81
1:A:445:ASP:OD2	9:A:601:HOH:O	2.00	0.80
1:C:13:ILE:HG21	9:C:741:HOH:O	1.81	0.79
1:C:416:ILE:HG13	9:C:737:HOH:O	1.82	0.79
2:B:90:HIS:HB2	9:B:801:HOH:O	1.82	0.78
2:D:100:ARG:HG3	9:D:932:HOH:O	1.84	0.78
1:A:440:GLU:CG	9:A:785:HOH:O	2.27	0.78
2:B:461:GLU:OE1	9:B:701:HOH:O	2.01	0.77
1:A:139:GLU:HG3	1:A:174:LEU:HD13	1.69	0.75
1:A:432:GLN:OE1	9:A:602:HOH:O	2.05	0.74
2:B:88:TYR:HE2	9:B:801:HOH:O	1.70	0.74
2:D:293:LEU:O	9:D:701:HOH:O	2.03	0.74
1:C:61:GLY:HA3	9:C:656:HOH:O	1.86	0.74
1:C:234:ASP:HB3	1:C:451:HIS:ND1	2.03	0.74
1:C:58:THR:HB	5:C:508:GOL:O1	1.89	0.72
1:C:64:TYR:HB2	9:C:627:HOH:O	1.88	0.72
1:C:385:ASP:CB	9:C:691:HOH:O	2.14	0.72
1:A:445:ASP:CG	9:A:601:HOH:O	2.34	0.70
2:B:129:GLN:HA	9:B:718:HOH:O	1.90	0.70
1:C:410:GLU:OE2	1:C:414:LYS:NZ	2.23	0.69
1:A:42:SER:N	1:A:388:ASP:OD1	2.19	0.69
1:A:53:GLN:HB2	1:A:56:LEU:HD12	1.73	0.69
5:C:504:GOL:H31	9:C:601:HOH:O	1.91	0.69
1:C:275:CYS:HB2	9:C:765:HOH:O	1.93	0.68
2:B:363:HIS:ND1	9:B:706:HOH:O	2.28	0.68
1:C:253:TRP:HB3	1:C:279:MET:CE	2.20	0.67
2:B:347:GLU:OE2	9:B:702:HOH:O	2.12	0.67
1:C:78:MET:HE2	9:C:628:HOH:O	1.95	0.67
1:C:12:LEU:HD13	1:C:415:ARG:HG2	1.76	0.66
1:C:4:MET:SD	9:C:737:HOH:O	2.54	0.66
1:A:351:VAL:CG2	1:A:374:VAL:HG22	2.26	0.66
2:D:373:PRO:HD2	9:D:925:HOH:O	1.96	0.66
1:C:467:LEU:O	1:C:467:LEU:HD23	1.96	0.66
1:C:28:ARG:CD	1:C:408:GLU:OE2	2.42	0.65
1:C:33:ALA:HB3	9:C:730:HOH:O	1.97	0.65
1:C:53:GLN:HB2	1:C:56:LEU:HD12	1.79	0.65
1:A:253:TRP:HB3	1:A:279:MET:HE1	1.78	0.65
1:A:428:LYS:NZ	9:A:605:HOH:O	2.28	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:209:LYS:HE2	9:C:659:HOH:O	1.97	0.64
2:B:236:ASN:ND2	5:B:607:GOL:H12	2.13	0.64
1:A:93:ARG:NH2	5:B:608:GOL:O2	2.31	0.64
1:C:10:GLU:HG3	1:C:34:VAL:HG21	1.79	0.64
2:B:129:GLN:OE1	9:B:703:HOH:O	2.15	0.63
1:A:101:ILE:HD12	5:B:603:GOL:H31	1.80	0.63
1:C:416:ILE:CG1	9:C:737:HOH:O	2.42	0.63
2:D:353:ASP:OD2	9:D:702:HOH:O	2.16	0.63
1:A:62:CYS:HA	9:A:641:HOH:O	1.98	0.62
1:C:32:LEU:HD21	9:C:753:HOH:O	1.98	0.62
1:A:391:MET:HA	9:A:719:HOH:O	2.00	0.62
1:A:35:ASN:HB2	1:A:400:LEU:HD11	1.82	0.62
1:C:192:SER:OG	9:C:603:HOH:O	2.16	0.62
1:A:134:LEU:HG	2:B:62:LEU:HB2	1.82	0.61
1:C:71:VAL:CG1	9:C:796:HOH:O	2.04	0.61
2:B:377:MET:HE2	2:B:402:TRP:HE1	1.65	0.61
1:C:53:GLN:O	5:C:508:GOL:C1	2.49	0.61
1:C:81:ILE:C	9:C:630:HOH:O	2.43	0.60
1:C:440:GLU:HG3	9:C:766:HOH:O	2.00	0.60
1:C:53:GLN:N	5:C:508:GOL:H11	2.16	0.60
1:C:14:GLN:HB3	9:C:764:HOH:O	2.01	0.60
1:C:400:LEU:CB	9:C:730:HOH:O	2.49	0.60
2:B:123:ALA:HB2	2:B:154:MET:HE3	1.83	0.59
2:B:7:LYS:HD3	9:B:810:HOH:O	2.02	0.59
2:B:446:SER:O	2:B:449:LYS:HG2	2.02	0.59
1:C:467:LEU:HD23	1:C:467:LEU:C	2.28	0.59
1:C:68:LYS:HD3	1:C:68:LYS:C	2.28	0.59
1:A:269:LYS:NZ	9:A:609:HOH:O	2.34	0.58
2:B:65:ASN:HD21	5:B:608:GOL:H31	1.67	0.58
9:C:604:HOH:O	2:D:26:LYS:HB2	2.04	0.58
2:B:172:GLU:OE1	9:B:704:HOH:O	2.17	0.58
1:C:47:ILE:CD1	1:C:50:LYS:HG3	2.34	0.58
1:C:438:PHE:CB	9:C:667:HOH:O	2.41	0.58
2:D:366:ARG:NH2	2:D:391:VAL:HG21	2.18	0.57
1:C:400:LEU:HB3	9:C:730:HOH:O	2.03	0.57
1:C:254:SER:HB3	9:C:748:HOH:O	2.04	0.57
1:C:47:ILE:HD12	1:C:50:LYS:HG3	1.86	0.57
1:A:112:MET:HG2	5:B:608:GOL:O2	2.05	0.57
1:A:39:VAL:O	1:A:39:VAL:HG23	2.05	0.56
1:A:445:ASP:O	1:A:446:TYR:HB2	2.05	0.56
2:B:90:HIS:CE1	2:B:118:MET:SD	2.99	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:405:THR:HG22	5:C:508:GOL:O3	2.05	0.56
2:B:100:ARG:HG3	9:B:947:HOH:O	2.04	0.56
1:C:216:PHE:CD1	1:C:264:LEU:HD22	2.41	0.56
1:A:47:ILE:HD12	1:A:50:LYS:HG2	1.89	0.55
1:C:48:SER:OG	1:C:384:ASN:ND2	2.38	0.55
2:D:390:PRO:O	2:D:419:ALA:HB2	2.06	0.55
1:C:39:VAL:O	1:C:39:VAL:HG23	2.07	0.55
1:A:164:GLU:OE1	1:A:182:ARG:NH2	2.41	0.54
1:C:417:LYS:NZ	9:C:605:HOH:O	2.22	0.54
2:D:113:CYS:HB2	9:D:727:HOH:O	2.06	0.54
1:A:22:GLU:HG3	1:A:25:ARG:NH2	2.23	0.54
1:C:265:THR:O	1:C:268:VAL:HG22	2.06	0.54
1:A:354:TYR:OH	1:A:380:GLU:HA	2.08	0.54
2:B:151:THR:HG23	2:B:162:LEU:HD11	1.89	0.54
1:C:164:GLU:OE1	1:C:182:ARG:NH2	2.40	0.54
1:C:65:ALA:O	1:C:70:VAL:HG23	2.08	0.53
1:A:68:LYS:HD3	1:A:68:LYS:C	2.33	0.53
1:C:53:GLN:O	5:C:508:GOL:H12	2.08	0.53
1:C:59:ILE:HD12	1:C:354:TYR:CE2	2.43	0.53
1:A:440:GLU:HG3	9:A:601:HOH:O	2.08	0.53
1:C:110:VAL:O	5:C:505:GOL:H11	2.08	0.53
1:A:164:GLU:OE2	1:A:182:ARG:NE	2.41	0.53
1:A:28:ARG:HD3	1:A:408:GLU:OE2	2.08	0.53
2:B:7:LYS:HE2	9:B:946:HOH:O	2.09	0.53
1:A:139:GLU:OE2	1:A:176:LYS:HE2	2.10	0.52
1:A:349:LYS:HE2	9:A:630:HOH:O	2.09	0.52
1:A:384:ASN:ND2	9:A:607:HOH:O	2.40	0.52
1:A:428:LYS:HD2	9:A:601:HOH:O	2.10	0.52
1:C:198:ALA:O	1:C:202:VAL:HG23	2.09	0.52
1:C:354:TYR:OH	1:C:380:GLU:HA	2.08	0.52
2:D:153:CYS:O	2:D:157:VAL:HG23	2.10	0.52
1:C:177:THR:HG21	9:C:659:HOH:O	2.10	0.52
1:C:400:LEU:HB2	9:C:730:HOH:O	2.10	0.52
1:C:428:LYS:NZ	9:C:607:HOH:O	2.28	0.52
2:B:50:LYS:HB2	8:B:604:TRS:N	2.24	0.51
2:B:390:PRO:O	2:B:419:ALA:HB2	2.10	0.51
1:C:404:VAL:HG23	9:C:753:HOH:O	2.10	0.51
1:A:12:LEU:HD13	1:A:415:ARG:HG2	1.92	0.51
2:B:453:ARG:NH1	5:B:608:GOL:O1	2.43	0.51
1:C:261:GLU:CD	2:D:27:LYS:HZ3	2.19	0.51
2:D:445:ASN:HB2	2:D:472:PRO:O	2.10	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:14:GLN:NE2	9:A:623:HOH:O	2.43	0.51
1:C:32:LEU:CD2	9:C:753:HOH:O	2.57	0.51
2:B:322:LEU:HD21	1:C:474:LYS:HB3	1.92	0.51
2:B:494:LEU:C	2:B:494:LEU:HD23	2.36	0.51
1:C:140:THR:CG2	5:C:507:GOL:H12	2.36	0.51
1:C:355:ILE:HB	1:C:360:PRO:HD3	1.92	0.51
1:C:354:TYR:CZ	1:C:404:VAL:HG12	2.46	0.51
1:A:445:ASP:O	1:A:446:TYR:CB	2.57	0.50
1:A:432:GLN:HG2	1:A:472:TRP:HH2	1.76	0.50
1:A:274:HIS:HE1	1:A:299:PHE:H	1.58	0.50
1:A:265:THR:O	1:A:268:VAL:HG22	2.11	0.50
1:C:135:ILE:HD12	1:C:170:LYS:HG3	1.92	0.50
1:C:52:SER:HB3	5:C:508:GOL:H11	1.92	0.50
1:A:28:ARG:CD	1:A:408:GLU:OE2	2.60	0.50
2:B:132:LYS:HD2	9:B:718:HOH:O	2.10	0.50
3:C:501:HCA:O7	3:C:501:HCA:O1	2.28	0.50
2:B:445:ASN:HA	9:B:725:HOH:O	2.11	0.50
9:A:637:HOH:O	2:B:26:LYS:HB2	2.12	0.49
2:D:154:MET:SD	9:D:773:HOH:O	2.59	0.49
1:C:75:ILE:HD13	1:C:262:ILE:HD11	1.95	0.49
5:B:603:GOL:H2	9:B:875:HOH:O	2.12	0.49
1:C:110:VAL:O	5:C:505:GOL:C1	2.60	0.49
3:A:501:HCA:O7	3:A:501:HCA:O2	2.29	0.49
1:A:377:THR:HG22	1:A:394:MET:HE2	1.93	0.49
1:A:47:ILE:HD11	9:A:611:HOH:O	2.11	0.49
1:A:253:TRP:HB3	1:A:279:MET:CE	2.41	0.49
2:B:123:ALA:HB2	2:B:154:MET:CE	2.43	0.49
2:D:171:LYS:HE2	9:D:815:HOH:O	2.13	0.49
2:B:153:CYS:O	2:B:157:VAL:HG23	2.13	0.48
1:C:19:VAL:HG11	1:C:407:TYR:CZ	2.48	0.48
1:C:75:ILE:HD11	9:C:748:HOH:O	2.12	0.48
1:C:243:GLU:OE1	9:C:604:HOH:O	2.20	0.48
1:A:413:VAL:CG1	1:A:436:ILE:CD1	2.91	0.48
2:D:319:PRO:HD3	9:D:701:HOH:O	2.12	0.48
1:A:62:CYS:HB3	2:B:94:GLY:HA3	1.93	0.48
2:B:241:LYS:NZ	2:B:256:ASP:OD2	2.47	0.48
1:C:53:GLN:O	5:C:508:GOL:H11	2.12	0.48
1:A:274:HIS:CE1	1:A:299:PHE:H	2.31	0.48
1:C:100:TYR:CE2	1:C:110:VAL:HB	2.48	0.48
2:B:132:LYS:CD	9:B:718:HOH:O	2.62	0.47
2:B:400:LYS:H	5:B:602:GOL:H32	1.79	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:100:TYR:CE2	1:A:110:VAL:HB	2.49	0.47
1:C:81:ILE:HD12	1:C:134:LEU:HD21	1.96	0.47
1:A:93:ARG:NH2	5:B:608:GOL:C2	2.77	0.47
2:D:473:ILE:HG21	2:D:479:LEU:HD12	1.97	0.47
1:C:442:HIS:HB3	3:C:501:HCA:O5	2.13	0.47
2:B:111:VAL:CG1	9:B:735:HOH:O	2.42	0.47
1:C:134:LEU:HG	2:D:62:LEU:HB2	1.97	0.47
1:C:405:THR:HG22	5:C:508:GOL:C3	2.45	0.47
1:A:428:LYS:HB2	1:A:438:PHE:CE2	2.50	0.47
2:D:494:LEU:C	2:D:494:LEU:HD23	2.40	0.47
1:A:12:LEU:HD12	9:A:649:HOH:O	2.15	0.47
1:C:146:LYS:NZ	9:C:625:HOH:O	2.48	0.47
1:A:445:ASP:OD1	9:A:601:HOH:O	2.19	0.47
2:D:446:SER:O	2:D:449:LYS:HG2	2.14	0.47
1:A:422:GLY:HA2	1:A:439:ARG:O	2.15	0.47
1:C:31:HIS:NE2	1:C:47:ILE:HD11	2.30	0.47
1:C:79:ILE:HG23	1:C:114:PHE:CD2	2.50	0.47
2:D:173:GLY:HA2	9:D:791:HOH:O	2.14	0.46
1:A:351:VAL:HG21	1:A:374:VAL:HG22	1.97	0.46
1:A:47:ILE:HD12	1:A:50:LYS:CG	2.45	0.46
1:C:9:VAL:CG1	1:C:34:VAL:HG22	2.45	0.46
1:C:59:ILE:O	1:C:426:LYS:NZ	2.47	0.46
1:C:20:TYR:CE2	1:C:28:ARG:HG3	2.51	0.46
1:C:253:TRP:CZ2	1:C:262:ILE:HG23	2.50	0.46
1:C:431:PHE:HB2	9:C:667:HOH:O	2.14	0.46
1:C:62:CYS:HB3	2:D:94:GLY:HA3	1.97	0.46
1:C:155:PRO:HB3	2:D:157:VAL:HG21	1.97	0.46
1:C:192:SER:CB	9:C:603:HOH:O	2.63	0.46
2:B:88:TYR:O	2:B:149:VAL:HA	2.16	0.45
1:C:440:GLU:CG	9:C:766:HOH:O	2.61	0.45
1:A:467:LEU:HD23	1:A:467:LEU:C	2.41	0.45
1:C:428:LYS:HG3	1:C:438:PHE:CD2	2.51	0.45
1:A:234:ASP:HB3	1:A:451:HIS:ND1	2.30	0.45
1:C:277:ARG:HD2	1:C:386:ASP:OD2	2.16	0.45
2:B:50:LYS:HB2	8:B:604:TRS:HN3	1.80	0.45
1:A:399:LEU:HD12	1:A:400:LEU:H	1.81	0.45
2:B:270:ARG:NH2	9:B:720:HOH:O	2.50	0.45
2:D:22:ASP:O	2:D:26:LYS:HG2	2.17	0.45
2:D:151:THR:CG2	2:D:162:LEU:HD21	2.46	0.45
1:A:59:ILE:HD12	1:A:354:TYR:CE2	2.52	0.44
2:B:70:CYS:HB2	2:B:188:SER:HB2	1.98	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:209:LYS:NZ	9:C:617:HOH:O	2.44	0.44
1:C:296:GLU:HB3	9:C:727:HOH:O	2.16	0.44
1:A:440:GLU:HG2	9:A:785:HOH:O	2.08	0.44
1:C:265:THR:HB	1:C:266:PRO:HD3	1.99	0.44
2:B:5:VAL:HG12	9:B:887:HOH:O	2.16	0.44
2:B:445:ASN:HB2	2:B:472:PRO:O	2.17	0.44
1:C:276:TYR:OH	1:C:284:ARG:NH2	2.50	0.44
2:D:86:MET:HG2	2:D:138:CYS:SG	2.57	0.44
1:A:93:ARG:HH21	5:B:608:GOL:HO2	1.63	0.44
1:C:82:SER:N	9:C:630:HOH:O	2.50	0.44
1:C:421:ILE:O	1:C:438:PHE:HA	2.17	0.44
2:D:322:LEU:HD13	2:D:351:LEU:HD23	1.99	0.44
2:B:7:LYS:CD	9:B:946:HOH:O	2.66	0.44
1:A:134:LEU:HD23	1:A:134:LEU:C	2.43	0.44
2:B:132:LYS:HD3	2:B:174:PHE:CE2	2.53	0.44
5:B:605:GOL:H12	9:B:829:HOH:O	2.17	0.44
1:C:382:ALA:HB3	1:C:387:TYR:CE2	2.53	0.44
1:A:381:PHE:HA	9:A:747:HOH:O	2.18	0.44
2:B:492:GLN:HB3	5:B:605:GOL:H31	2.00	0.44
1:C:6:ARG:HG2	1:C:10:GLU:OE2	2.18	0.44
2:B:194:VAL:HB	2:B:297:HIS:CG	2.53	0.43
1:C:227:GLY:H	1:C:279:MET:HE3	1.83	0.43
2:D:390:PRO:O	2:D:419:ALA:CB	2.65	0.43
5:B:606:GOL:H12	5:B:607:GOL:O2	2.18	0.43
2:D:241:LYS:NZ	2:D:256:ASP:OD2	2.49	0.43
2:B:86:MET:HG2	2:B:138:CYS:SG	2.58	0.43
1:C:79:ILE:O	1:C:148:ILE:HA	2.18	0.43
1:C:234:ASP:HB3	1:C:451:HIS:CG	2.54	0.43
1:C:9:VAL:HG12	1:C:34:VAL:HG22	2.01	0.43
1:C:62:CYS:HA	9:C:644:HOH:O	2.18	0.43
1:C:366:ALA:HB3	9:C:786:HOH:O	2.17	0.43
2:D:49:THR:HB	8:D:602:TRS:C3	2.49	0.43
2:D:96:VAL:O	2:D:97:ALA:C	2.60	0.43
2:B:90:HIS:CB	9:B:801:HOH:O	2.53	0.43
2:B:320:MET:SD	5:B:607:GOL:C3	3.07	0.43
1:C:9:VAL:O	1:C:13:ILE:HD13	2.19	0.43
2:D:317:ASN:ND2	9:D:725:HOH:O	2.52	0.43
1:C:196:HIS:ND1	9:C:606:HOH:O	2.22	0.43
1:C:405:THR:HG22	5:C:508:GOL:H32	2.01	0.43
1:A:112:MET:HA	5:B:608:GOL:HO2	1.84	0.42
1:A:382:ALA:HB1	1:A:386:ASP:HB2	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:279:GLU:CD	2:B:279:GLU:H	2.27	0.42
2:B:447:TYR:CD1	2:D:521:LEU:HD22	2.54	0.42
1:A:359:ARG:N	1:A:360:PRO:CD	2.82	0.42
2:B:12:TYR:HA	2:B:13:PRO:HA	1.83	0.42
1:C:184:GLU:HA	9:C:627:HOH:O	2.19	0.42
1:C:253:TRP:HA	1:C:254:SER:HA	1.75	0.42
2:D:352:VAL:O	2:D:356:THR:HG23	2.19	0.42
2:B:377:MET:HE2	2:B:377:MET:HB3	1.84	0.42
1:C:97:ARG:O	1:C:231:ILE:HA	2.19	0.42
1:C:134:LEU:HD23	1:C:134:LEU:C	2.44	0.42
2:D:156:GLU:HG3	2:D:187:PRO:HB3	2.01	0.42
1:A:158:LEU:HD11	2:B:154:MET:HG3	2.01	0.42
1:C:364:ILE:HG12	1:C:374:VAL:HG21	2.01	0.42
2:B:470:GLY:N	9:B:725:HOH:O	2.52	0.42
2:D:240:ILE:HG13	2:D:293:LEU:HD11	2.01	0.42
1:A:399:LEU:HD12	1:A:400:LEU:N	2.35	0.42
1:C:86:VAL:O	1:C:86:VAL:HG22	2.19	0.42
1:C:399:LEU:HD12	1:C:400:LEU:H	1.85	0.42
2:D:154:MET:CG	9:D:773:HOH:O	2.68	0.42
1:A:413:VAL:HG11	1:A:436:ILE:HD12	2.02	0.41
1:A:420:LEU:HB2	1:A:467:LEU:HD12	2.01	0.41
1:A:449:PRO:O	1:A:455:GLY:HA2	2.19	0.41
2:B:470:GLY:CA	9:B:725:HOH:O	2.67	0.41
1:A:19:VAL:HG11	1:A:407:TYR:CZ	2.55	0.41
2:D:316:LEU:HD11	2:D:331:LYS:HG2	2.02	0.41
1:A:42:SER:OG	1:A:384:ASN:HB3	2.20	0.41
2:B:175:ILE:CD1	2:B:181:VAL:HG21	2.51	0.41
1:C:382:ALA:HB1	1:C:386:ASP:HB2	2.03	0.41
1:A:42:SER:CB	1:A:388:ASP:OD1	2.69	0.41
2:B:521:LEU:HD22	2:D:447:TYR:CD1	2.55	0.41
1:A:31:HIS:NE2	1:A:47:ILE:HD11	2.36	0.41
2:B:254:LEU:HD22	2:B:281:MET:SD	2.61	0.41
2:B:521:LEU:HD11	2:D:446:SER:C	2.45	0.41
1:C:52:SER:HB3	5:C:508:GOL:C1	2.50	0.41
1:C:394:MET:HE3	1:C:398:THR:CB	2.50	0.41
2:D:253:LEU:HD23	2:D:256:ASP:CG	2.46	0.41
2:D:414:PRO:O	2:D:417:LYS:HG3	2.21	0.41
1:A:22:GLU:HG2	1:A:26:LYS:HE3	2.02	0.41
1:C:68:LYS:NZ	5:C:505:GOL:H31	2.35	0.41
1:C:88:CYS:SG	1:C:153:GLU:CD	3.04	0.41
1:C:422:GLY:HA2	1:C:439:ARG:O	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:447:SER:OG	1:C:448:GLY:N	2.53	0.41
2:B:113:CYS:CB	9:B:947:HOH:O	2.69	0.41
1:C:62:CYS:SG	1:C:64:TYR:HB3	2.61	0.41
2:D:151:THR:HG22	2:D:162:LEU:HD21	2.03	0.41
1:A:274:HIS:CD2	1:A:451:HIS:CE1	3.08	0.41
1:A:355:ILE:HB	1:A:360:PRO:HD3	2.02	0.41
2:B:48:THR:OG1	2:B:458:LYS:HE3	2.21	0.41
2:B:151:THR:CG2	2:B:162:LEU:HD11	2.50	0.41
1:C:22:GLU:OE2	1:C:25:ARG:NH2	2.54	0.41
1:C:39:VAL:HG23	1:C:391:MET:SD	2.61	0.41
1:C:116:SER:O	1:C:117:ASP:C	2.63	0.41
1:C:440:GLU:HG3	9:C:609:HOH:O	2.20	0.41
2:D:88:TYR:O	2:D:149:VAL:HA	2.21	0.41
2:D:231:GLU:CD	2:D:236:ASN:HD22	2.29	0.41
2:B:394:LEU:HD23	2:B:394:LEU:C	2.46	0.41
1:A:428:LYS:CB	9:A:785:HOH:O	2.51	0.40
5:B:603:GOL:O2	2:D:514:ALA:O	2.35	0.40
1:C:135:ILE:HD13	1:C:178:ILE:HD13	2.03	0.40
1:A:253:TRP:CZ2	1:A:262:ILE:HG23	2.57	0.40
1:A:277:ARG:HD2	1:A:386:ASP:OD2	2.20	0.40
2:B:375:PHE:HD1	5:B:607:GOL:C3	2.35	0.40
1:C:379:TYR:CG	1:C:382:ALA:HB2	2.57	0.40
2:D:449:LYS:HE3	2:D:449:LYS:HB2	1.79	0.40
1:A:97:ARG:O	1:A:231:ILE:HA	2.22	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	479/490 (98%)	457 (95%)	20 (4%)	2 (0%)	30 20

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	C	477/490 (97%)	448 (94%)	29 (6%)	0	100	100
2	B	521/522 (100%)	504 (97%)	16 (3%)	1 (0%)	43	35
2	D	520/522 (100%)	501 (96%)	18 (4%)	1 (0%)	43	35
All	All	1997/2024 (99%)	1910 (96%)	83 (4%)	4 (0%)	43	35

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	94	ALA
2	B	255	SER
2	D	255	SER
1	A	355	ILE

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	409/413 (99%)	403 (98%)	6 (2%)	57	52
1	C	408/413 (99%)	401 (98%)	7 (2%)	53	48
2	B	455/454 (100%)	451 (99%)	4 (1%)	70	67
2	D	454/454 (100%)	449 (99%)	5 (1%)	65	61
All	All	1726/1734 (100%)	1704 (99%)	22 (1%)	61	57

All (22) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	13	ILE
1	A	92	SER
1	A	98	ASN
1	A	279	MET
1	A	362	HIS
1	A	465	MET
2	B	21	LYS

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Mol	Chain	Res	Type
2	B	177	ASP
2	B	258	GLU
2	B	449	LYS
1	C	22	GLU
1	C	43	LYS
1	C	88	CYS
1	C	98	ASN
1	C	279	MET
1	C	362	HIS
1	C	445	ASP
2	D	21	LYS
2	D	88	TYR
2	D	172	GLU
2	D	258	GLU
2	D	279	GLU

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

Mol	Chain	Res	Type
1	A	29	ASN
1	A	274	HIS
1	A	384	ASN
1	A	451	HIS
2	B	65	ASN
2	B	163	ASN
2	B	363	HIS
1	C	98	ASN
1	C	321	GLN
1	C	384	ASN
2	D	163	ASN
2	D	317	ASN

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](#)

Of 25 ligands modelled in this entry, 2 are monoatomic - leaving 23 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	$\# Z > 2$
4	ICS	C	502	1	6,30,30	2.37	3 (50%)	-		
5	GOL	C	504	-	5,5,5	0.44	0	5,5,5	0.58	0
4	ICS	A	502	1	6,30,30	1.69	1 (16%)	-		
5	GOL	C	506	-	5,5,5	0.50	0	5,5,5	0.57	0
5	GOL	A	503	-	5,5,5	0.19	0	5,5,5	0.70	0
5	GOL	D	601	-	5,5,5	0.41	0	5,5,5	0.23	0
5	GOL	C	503	-	5,5,5	0.49	0	5,5,5	1.52	1 (20%)
5	GOL	C	505	-	5,5,5	1.02	1 (20%)	5,5,5	1.76	1 (20%)
5	GOL	B	603	-	5,5,5	0.48	0	5,5,5	0.80	0
5	GOL	B	602	-	5,5,5	0.65	0	5,5,5	0.85	0
3	HCA	C	501	-	13,13,13	1.26	1 (7%)	15,18,18	1.74	6 (40%)
3	HCA	A	501	-	13,13,13	1.17	1 (7%)	15,18,18	1.13	2 (13%)
8	TRS	D	602	-	7,7,7	0.28	0	9,9,9	0.75	0
5	GOL	B	607	-	5,5,5	0.32	0	5,5,5	0.98	0
6	1CL	C	509	2,1	0,22,22	-	-	-		
5	GOL	C	507	-	5,5,5	0.88	0	5,5,5	1.42	1 (20%)
5	GOL	B	606	-	5,5,5	0.42	0	5,5,5	1.04	0
5	GOL	B	605	-	5,5,5	0.24	0	5,5,5	0.93	0
5	GOL	C	508	-	5,5,5	0.65	0	5,5,5	0.74	0
5	GOL	B	608	-	5,5,5	1.11	1 (20%)	5,5,5	2.42	3 (60%)
6	1CL	A	504	2,1	0,22,22	-	-	-		
8	TRS	B	604	-	7,7,7	0.46	0	9,9,9	1.26	2 (22%)
5	GOL	D	603	-	5,5,5	0.39	0	5,5,5	0.44	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
5	GOL	C	504	-	-	4/4/4/4	-
5	GOL	C	506	-	-	2/4/4/4	-
5	GOL	A	503	-	-	4/4/4/4	-
5	GOL	D	601	-	-	1/4/4/4	-
5	GOL	C	503	-	-	3/4/4/4	-
5	GOL	C	505	-	-	2/4/4/4	-
5	GOL	B	603	-	-	2/4/4/4	-
5	GOL	B	602	-	-	2/4/4/4	-
3	HCA	C	501	-	-	2/17/17/17	-
3	HCA	A	501	-	-	8/17/17/17	-
8	TRS	D	602	-	-	8/9/9/9	-
5	GOL	B	607	-	-	2/4/4/4	-
6	1CL	C	509	2,1	-	-	0/10/8/8
5	GOL	C	507	-	-	2/4/4/4	-
5	GOL	B	606	-	-	2/4/4/4	-
5	GOL	B	605	-	-	4/4/4/4	-
5	GOL	C	508	-	-	2/4/4/4	-
5	GOL	B	608	-	-	4/4/4/4	-
6	1CL	A	504	2,1	-	-	0/10/8/8
8	TRS	B	604	-	-	4/9/9/9	-
5	GOL	D	603	-	-	2/4/4/4	-

All (8) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	C	502	ICS	S5A-FE3	-3.95	2.15	2.24
4	C	502	ICS	S3A-FE4	-3.56	2.16	2.24
4	A	502	ICS	S5A-FE3	-3.38	2.16	2.24
5	B	608	GOL	O3-C3	2.49	1.52	1.42
3	C	501	HCA	O5-C7	2.25	1.29	1.22
4	C	502	ICS	S3A-FE5	-2.10	2.19	2.24
5	C	505	GOL	O2-C2	2.07	1.49	1.43
3	A	501	HCA	O4-C6	-2.02	1.24	1.30

All (16) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	B	608	GOL	C3-C2-C1	3.87	126.00	111.80
3	C	501	HCA	O6-C7-C3	3.45	119.75	113.14
3	C	501	HCA	O1-C1-C2	-2.75	115.16	122.95
3	A	501	HCA	O7-C3-C7	-2.64	105.21	108.96
3	C	501	HCA	O5-C7-C3	-2.55	117.16	122.09
5	C	505	GOL	O3-C3-C2	2.37	121.04	110.38
3	C	501	HCA	O7-C3-C4	-2.36	105.12	108.88
5	C	503	GOL	O2-C2-C3	2.23	118.42	109.18
8	B	604	TRS	C3-C-N	2.23	113.86	108.17
5	B	608	GOL	O1-C1-C2	-2.17	100.63	110.38
5	C	507	GOL	C3-C2-C1	-2.13	103.99	111.80
3	C	501	HCA	O2-C1-C2	2.12	121.07	114.35
8	B	604	TRS	O3-C3-C	2.12	116.77	110.88
5	B	608	GOL	O3-C3-C2	2.08	119.75	110.38
3	A	501	HCA	O5-C7-C3	-2.06	118.09	122.09
3	C	501	HCA	C4-C5-C6	2.06	117.55	112.77

There are no chirality outliers.

All (60) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	501	HCA	C2-C3-C4-C5
5	A	503	GOL	O1-C1-C2-C3
5	A	503	GOL	C1-C2-C3-O3
5	B	603	GOL	O1-C1-C2-C3
5	B	605	GOL	C1-C2-C3-O3
5	B	608	GOL	O2-C2-C3-O3
5	C	503	GOL	C1-C2-C3-O3
5	C	504	GOL	O1-C1-C2-C3
5	C	504	GOL	C1-C2-C3-O3
5	C	508	GOL	C1-C2-C3-O3
8	D	602	TRS	C2-C-C1-O1
8	D	602	TRS	N-C-C1-O1
5	A	503	GOL	O1-C1-C2-O2
5	A	503	GOL	O2-C2-C3-O3
5	B	603	GOL	O1-C1-C2-O2
5	B	608	GOL	O1-C1-C2-O2
5	C	506	GOL	O2-C2-C3-O3
5	B	602	GOL	C1-C2-C3-O3
5	B	605	GOL	O1-C1-C2-C3
5	B	606	GOL	O1-C1-C2-C3
5	B	607	GOL	C1-C2-C3-O3
5	B	608	GOL	O1-C1-C2-C3

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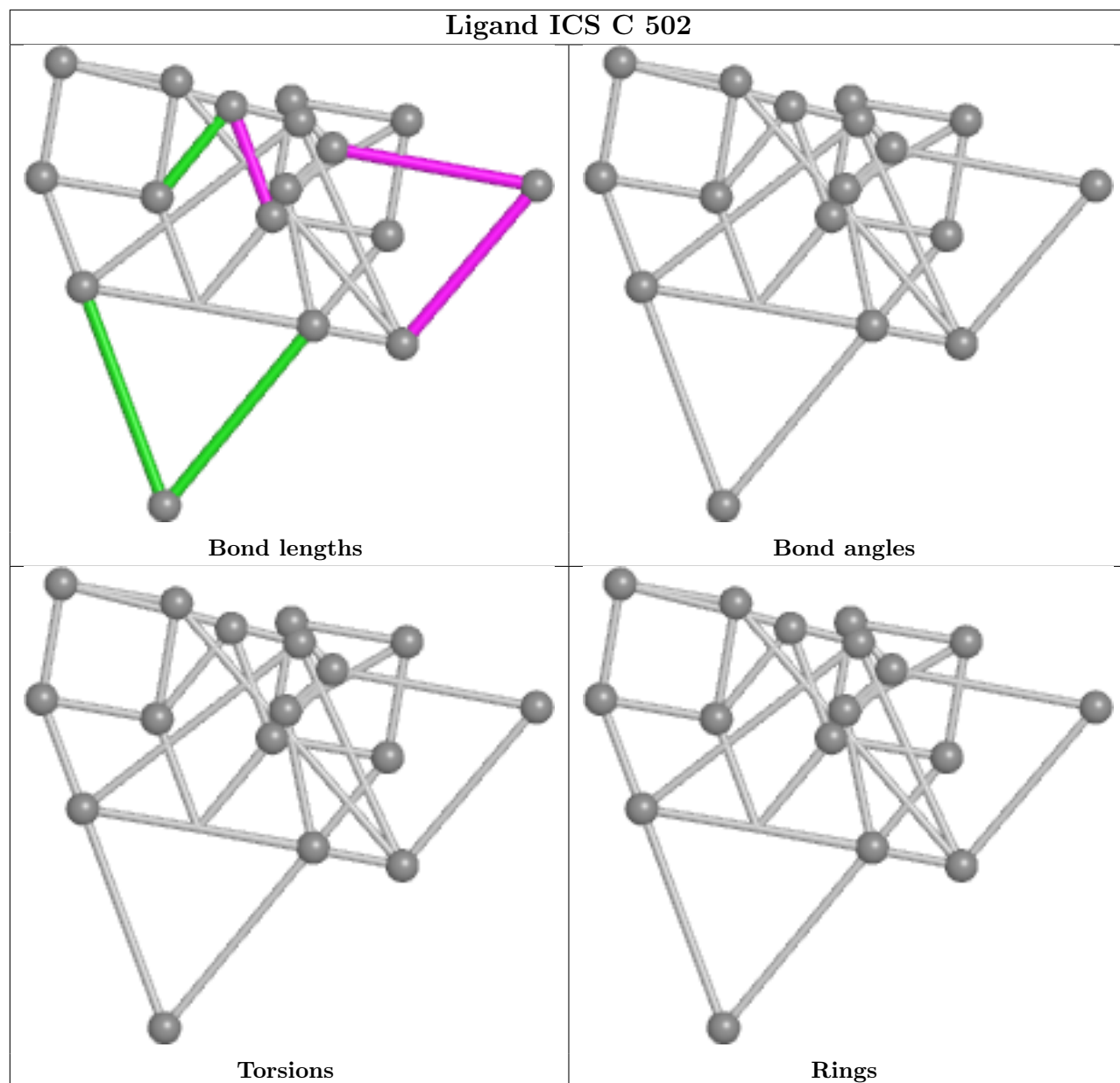
Mol	Chain	Res	Type	Atoms
5	B	608	GOL	C1-C2-C3-O3
5	C	503	GOL	O1-C1-C2-C3
5	C	506	GOL	C1-C2-C3-O3
5	C	507	GOL	C1-C2-C3-O3
5	D	603	GOL	O1-C1-C2-C3
5	B	605	GOL	O2-C2-C3-O3
5	B	607	GOL	O2-C2-C3-O3
5	C	504	GOL	O1-C1-C2-O2
5	C	504	GOL	O2-C2-C3-O3
5	C	508	GOL	O2-C2-C3-O3
8	D	602	TRS	C3-C-C1-O1
5	B	602	GOL	O2-C2-C3-O3
5	C	503	GOL	O2-C2-C3-O3
5	C	505	GOL	C1-C2-C3-O3
8	B	604	TRS	C1-C-C3-O3
8	B	604	TRS	C2-C-C3-O3
8	D	602	TRS	C2-C-C3-O3
5	B	605	GOL	O1-C1-C2-O2
5	C	507	GOL	O2-C2-C3-O3
3	A	501	HCA	C7-C3-C4-C5
3	C	501	HCA	C1-C2-C3-C7
5	D	603	GOL	O1-C1-C2-O2
8	D	602	TRS	C1-C-C3-O3
3	A	501	HCA	C1-C2-C3-C7
3	A	501	HCA	C4-C3-C7-O6
5	B	606	GOL	O1-C1-C2-O2
5	D	601	GOL	O2-C2-C3-O3
8	B	604	TRS	N-C-C3-O3
8	D	602	TRS	C1-C-C2-O2
8	D	602	TRS	N-C-C3-O3
5	C	505	GOL	O1-C1-C2-O2
3	A	501	HCA	C1-C2-C3-C4
8	B	604	TRS	C1-C-C2-O2
3	A	501	HCA	O2-C1-C2-C3
3	C	501	HCA	C1-C2-C3-C4
3	A	501	HCA	O1-C1-C2-C3
8	D	602	TRS	N-C-C2-O2
3	A	501	HCA	C4-C5-C6-O4

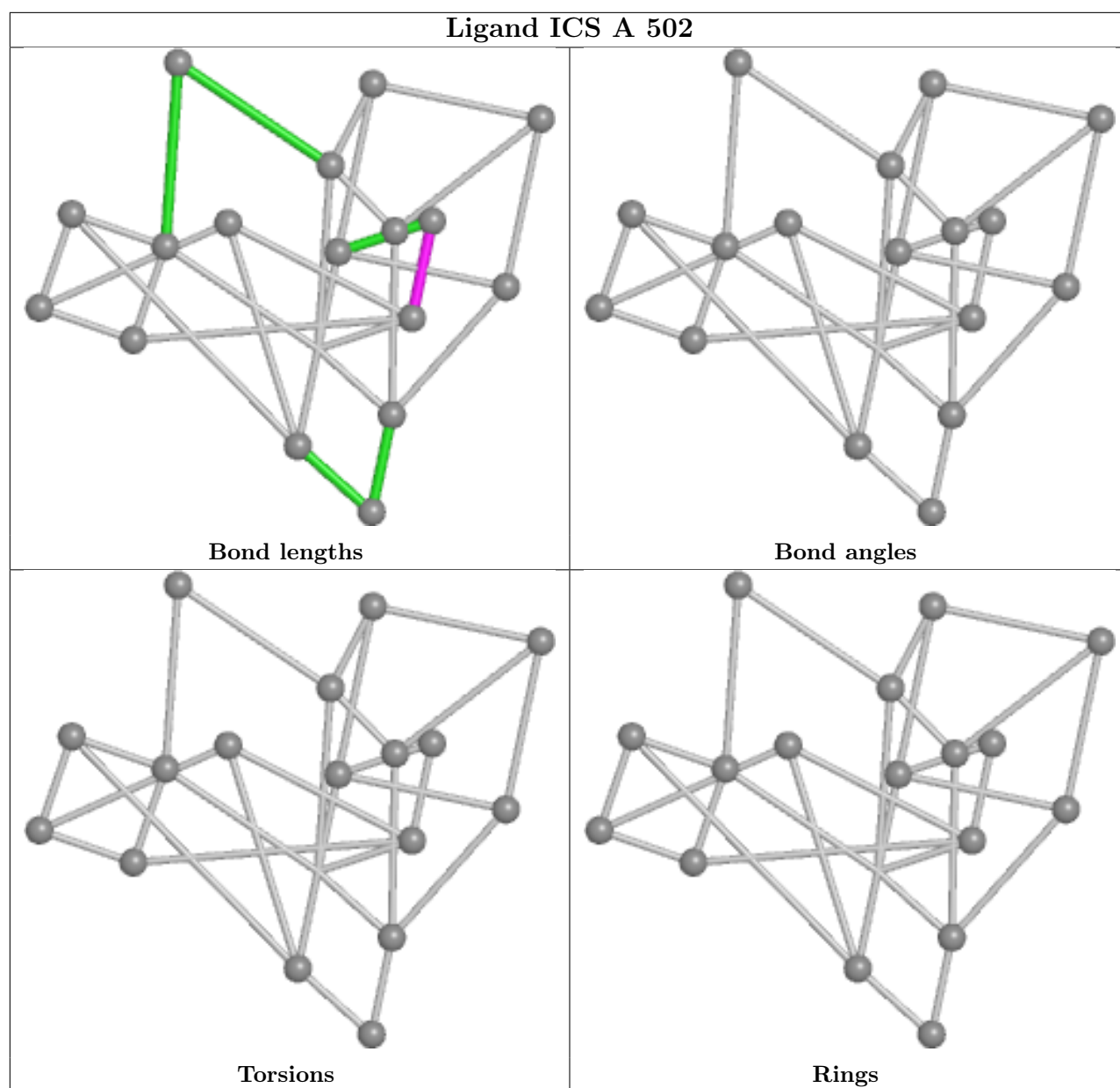
There are no ring outliers.

14 monomers are involved in 41 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	C	504	GOL	3	0
5	C	505	GOL	3	0
5	B	603	GOL	3	0
5	B	602	GOL	1	0
3	C	501	HCA	2	0
3	A	501	HCA	1	0
8	D	602	TRS	1	0
5	B	607	GOL	4	0
5	C	507	GOL	2	0
5	B	606	GOL	1	0
5	B	605	GOL	2	0
5	C	508	GOL	10	0
5	B	608	GOL	7	0
8	B	604	TRS	2	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	479/490 (97%)	1.45	110 (22%) 2 2	18, 39, 64, 100	14 (2%)
1	C	478/490 (97%)	1.78	174 (36%) 1 1	19, 46, 76, 93	5 (1%)
2	B	522/522 (100%)	0.89	38 (7%) 21 28	18, 36, 53, 70	6 (1%)
2	D	522/522 (100%)	0.95	42 (8%) 18 25	22, 36, 54, 80	13 (2%)
All	All	2001/2024 (98%)	1.25	364 (18%) 3 4	18, 39, 63, 100	38 (1%)

All (364) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	D	123	ALA	8.2
1	A	45	CYS	6.6
2	D	121	ASP	5.8
1	C	40	THR	5.7
1	A	40	THR	5.5
1	C	45	CYS	4.9
2	D	122	ALA	4.6
1	C	24	ALA	4.5
1	A	39	VAL	4.4
2	D	125	PHE	4.4
2	D	265	ALA	4.4
2	B	123	ALA	4.2
1	A	481	ALA	4.2
2	B	125	PHE	4.1
1	C	14	GLN	4.1
1	C	217	ALA	4.1
1	A	38	ALA	4.1
1	A	47	ILE	4.0
2	B	121	ASP	4.0
1	A	9	VAL	4.0
1	C	17	LEU	3.9

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Mol	Chain	Res	Type	RSRZ
1	C	92	SER	3.8
1	A	17	LEU	3.8
1	C	205	TRP	3.8
1	C	47	ILE	3.8
1	A	392	LYS	3.8
1	A	19	VAL	3.8
2	B	342	ALA	3.7
2	D	124	VAL	3.7
2	B	127	GLY	3.7
1	C	38	ALA	3.7
1	C	75	ILE	3.7
1	A	42	SER	3.6
1	C	381	PHE	3.6
1	C	39	VAL	3.6
1	C	46	ILE	3.6
1	C	254	SER	3.6
1	C	174	LEU	3.6
1	C	475	LEU	3.6
1	C	43	LYS	3.5
1	C	392	LYS	3.5
1	A	475	LEU	3.5
1	A	388	ASP	3.5
1	C	388	ASP	3.5
1	A	351	VAL	3.5
1	A	24	ALA	3.5
1	C	37	PRO	3.5
1	A	157	GLY	3.5
1	A	25	ARG	3.4
1	C	19	VAL	3.4
1	C	206	VAL	3.4
1	C	363	VAL	3.4
1	C	383	HIS	3.4
1	C	41	GLN	3.4
1	A	43	LYS	3.4
1	C	9	VAL	3.4
1	C	94	ALA	3.4
1	C	364	ILE	3.4
1	C	435	GLY	3.4
1	A	92	SER	3.4
1	C	294	TRP	3.4
1	A	16	VAL	3.3
1	C	400	LEU	3.3

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Mol	Chain	Res	Type	RSRZ
1	C	193	LEU	3.3
1	A	409	PHE	3.3
2	D	127	GLY	3.3
1	C	176	LYS	3.2
1	A	13	ILE	3.2
1	A	407	TYR	3.2
1	C	231	ILE	3.2
2	B	265	ALA	3.2
1	C	158	LEU	3.2
1	A	479	TRP	3.2
2	B	126	GLY	3.2
2	D	157	VAL	3.1
1	A	6	ARG	3.1
1	A	50	LYS	3.1
2	B	122	ALA	3.1
1	A	75	ILE	3.1
1	C	16	VAL	3.1
1	A	55	GLY	3.1
1	A	404	VAL	3.1
1	A	14	GLN	3.1
1	C	412	PHE	3.1
1	C	177	THR	3.1
1	C	185	GLY	3.1
1	A	387	TYR	3.0
1	C	25	ARG	3.0
2	D	450	PHE	3.0
1	C	395	GLY	3.0
2	B	38	ASP	3.0
1	A	41	GLN	3.0
1	C	409	PHE	3.0
1	A	382	ALA	3.0
1	A	59	ILE	3.0
1	C	13	ILE	3.0
2	B	157	VAL	2.9
1	C	214	THR	2.9
1	C	398	THR	2.9
1	C	226	ILE	2.9
2	D	501	ILE	2.9
1	A	36	ASP	2.9
1	A	395	GLY	2.9
1	C	472	TRP	2.9
1	C	42	SER	2.9

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Mol	Chain	Res	Type	RSRZ
1	A	376	GLY	2.9
1	C	291	GLY	2.9
2	B	119	THR	2.9
1	C	201	ALA	2.9
1	A	480	GLU	2.9
1	C	391	MET	2.9
1	C	157	GLY	2.9
2	D	35	TYR	2.8
1	C	36	ASP	2.8
1	A	159	ILE	2.8
1	C	34	VAL	2.8
1	C	179	VAL	2.8
1	C	182	ARG	2.8
1	A	12	LEU	2.8
1	A	182	ARG	2.8
1	C	59	ILE	2.8
1	A	177	THR	2.8
1	C	44	LYS	2.8
1	C	186	PHE	2.8
1	C	18	GLU	2.8
1	C	292	ILE	2.8
1	C	416	ILE	2.8
1	C	202	VAL	2.8
2	D	5	VAL	2.8
1	C	125	PHE	2.7
1	A	383	HIS	2.7
1	C	194	GLY	2.7
2	D	119	THR	2.7
1	A	273	VAL	2.7
2	D	46	TRP	2.7
1	C	100	TYR	2.7
1	C	197	ILE	2.7
1	A	11	SER	2.7
1	C	397	SER	2.7
1	C	98	ASN	2.7
1	A	94	ALA	2.7
1	A	294	TRP	2.7
1	A	227	GLY	2.7
1	C	249	CYS	2.7
1	C	386	ASP	2.7
1	A	48	SER	2.7
1	C	272	LEU	2.7

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Mol	Chain	Res	Type	RSRZ
1	C	70	VAL	2.7
1	C	366	ALA	2.6
1	C	72	TRP	2.6
1	C	215	THR	2.6
1	C	316	PHE	2.6
1	C	209	LYS	2.6
1	C	56	LEU	2.6
1	A	34	VAL	2.6
1	C	55	GLY	2.6
1	C	376	GLY	2.6
2	D	514	ALA	2.6
1	C	64	TYR	2.6
1	C	175	SER	2.6
1	C	384	ASN	2.6
1	C	431	PHE	2.6
1	C	159	ILE	2.6
1	A	432	GLN	2.6
2	B	120	GLU	2.6
1	A	44	LYS	2.6
1	A	400	LEU	2.6
1	C	212	GLU	2.6
1	C	198	ALA	2.6
1	C	457	ALA	2.6
1	A	37	PRO	2.5
1	A	186	PHE	2.5
2	B	165	PHE	2.5
1	A	158	LEU	2.5
1	C	200	ASP	2.5
1	C	436	ILE	2.5
2	D	26	LYS	2.5
1	C	273	VAL	2.5
1	C	274	HIS	2.5
1	A	8	GLU	2.5
1	C	207	LEU	2.5
1	C	406	GLY	2.5
1	C	479	TRP	2.5
2	B	124	VAL	2.5
2	B	177	ASP	2.5
1	C	407	TYR	2.5
1	C	299	PHE	2.5
1	C	357	GLY	2.5
2	D	269	PHE	2.5

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Mol	Chain	Res	Type	RSRZ
1	A	46	ILE	2.5
1	C	240	ILE	2.5
2	B	166	ILE	2.5
2	D	158	ILE	2.5
1	C	253	TRP	2.5
1	A	179	VAL	2.5
2	B	135	LEU	2.4
2	D	120	GLU	2.4
1	A	397	SER	2.4
1	C	116	SER	2.4
2	B	101	SER	2.4
1	C	382	ALA	2.4
1	C	6	ARG	2.4
1	A	193	LEU	2.4
2	B	212	SER	2.4
1	A	123	ILE	2.4
1	A	386	ASP	2.4
1	C	421	ILE	2.4
1	C	250	VAL	2.4
1	C	66	GLY	2.4
1	C	129	LYS	2.4
1	C	146	LYS	2.4
2	B	394	LEU	2.4
2	D	458	LYS	2.4
1	A	354	TYR	2.4
1	C	228	ASP	2.4
1	A	22	GLU	2.4
1	C	451	HIS	2.4
1	C	223	VAL	2.4
1	A	391	MET	2.4
1	C	242	LEU	2.3
1	C	387	TYR	2.3
2	B	158	ILE	2.3
1	A	274	HIS	2.3
1	A	357	GLY	2.3
1	C	26	LYS	2.3
1	A	254	SER	2.3
1	C	256	ASP	2.3
1	A	62	CYS	2.3
1	C	270	LEU	2.3
1	A	276	TYR	2.3
1	A	412	PHE	2.3

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Mol	Chain	Res	Type	RSRZ
2	B	450	PHE	2.3
1	C	314	ALA	2.3
2	D	164	ALA	2.3
2	B	417	LYS	2.3
2	D	115	SER	2.3
1	C	203	ARG	2.3
1	A	250	VAL	2.3
2	D	268	GLN	2.3
1	A	398	THR	2.3
1	C	367	TYR	2.3
2	B	447	TYR	2.3
1	C	3	GLY	2.3
1	C	225	ILE	2.3
1	A	396	ASP	2.3
1	C	22	GLU	2.3
1	C	234	ASP	2.3
1	C	261	GLU	2.3
1	A	72	TRP	2.2
1	A	205	TRP	2.2
1	A	66	GLY	2.2
1	A	379	TYR	2.2
1	C	229	TYR	2.2
2	D	342	ALA	2.2
1	C	283	SER	2.2
2	D	11	SER	2.2
2	D	92	SER	2.2
1	A	228	ASP	2.2
1	C	123	ILE	2.2
1	C	178	ILE	2.2
1	C	204	ASP	2.2
1	C	199	ASN	2.2
1	A	26	LYS	2.2
1	A	174	LEU	2.2
1	A	272	LEU	2.2
2	B	521	LEU	2.2
2	B	128	GLN	2.2
1	C	456	PHE	2.2
1	C	459	PHE	2.2
1	C	168	LYS	2.2
2	B	26	LYS	2.2
2	B	171	LYS	2.2
1	C	169	VAL	2.2

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Mol	Chain	Res	Type	RSRZ
1	A	15	GLU	2.2
2	B	178	GLU	2.2
1	A	275	CYS	2.2
1	C	33	ALA	2.2
1	C	63	ALA	2.2
1	A	20	TYR	2.2
1	A	125	PHE	2.2
1	A	231	ILE	2.2
1	C	361	ARG	2.2
1	A	363	VAL	2.2
1	C	413	VAL	2.2
1	C	317	ASP	2.2
2	D	2	SER	2.2
1	A	406	GLY	2.2
1	C	131	LEU	2.2
1	A	340	ALA	2.2
1	C	51	LYS	2.2
1	C	83	HIS	2.1
1	A	10	GLU	2.1
2	D	165	PHE	2.1
1	C	379	TYR	2.1
1	A	156	ILE	2.1
1	C	390	THR	2.1
2	D	29	ASP	2.1
2	D	126	GLY	2.1
2	B	138	CYS	2.1
1	C	12	LEU	2.1
1	C	187	ARG	2.1
1	C	309	LEU	2.1
2	D	36	PRO	2.1
2	B	131	MET	2.1
1	C	337	ALA	2.1
1	C	477	ALA	2.1
1	A	381	PHE	2.1
1	A	226	ILE	2.1
1	A	229	TYR	2.1
2	D	8	ILE	2.1
1	C	161	ASP	2.1
1	C	211	ASP	2.1
1	A	377	THR	2.1
1	C	115	THR	2.1
1	C	335	TRP	2.1

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Mol	Chain	Res	Type	RSRZ
2	D	169	SER	2.1
1	A	413	VAL	2.1
2	D	7	LYS	2.1
2	B	60	GLU	2.1
1	A	54	PRO	2.1
1	A	309	LEU	2.1
1	C	432	GLN	2.1
2	B	75	ALA	2.1
2	B	140	ALA	2.1
1	A	416	ILE	2.1
1	C	128	ASP	2.1
1	C	281	TYR	2.1
2	B	35	TYR	2.1
2	B	92	SER	2.1
1	A	86	VAL	2.1
1	C	29	ASN	2.1
1	C	86	VAL	2.1
1	C	106	VAL	2.1
2	D	96	VAL	2.1
1	A	399	LEU	2.1
1	C	224	ALA	2.1
1	C	340	ALA	2.1
1	C	403	ASP	2.1
1	A	146	LYS	2.0
1	A	431	PHE	2.0
1	C	216	PHE	2.0
1	C	306	ILE	2.0
2	D	31	PHE	2.0
1	C	276	TYR	2.0
1	A	112	MET	2.0
1	A	279	MET	2.0
1	C	255	GLY	2.0
2	D	130	ASN	2.0
1	C	375	VAL	2.0
2	B	522	VAL	2.0
1	C	399	LEU	2.0
2	D	162	LEU	2.0
2	D	430	LEU	2.0
2	D	97	ALA	2.0
1	A	129	LYS	2.0
1	C	195	HIS	2.0
1	C	259	ILE	2.0

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Mol	Chain	Res	Type	RSRZ
1	A	29	ASN	2.0
1	A	435	GLY	2.0
1	C	378	GLY	2.0
2	D	85	THR	2.0
1	C	401	TYR	2.0
2	B	421	VAL	2.0
2	D	89	VAL	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
8	TRS	D	602	8/8	0.72	0.17	52,60,65,66	0
8	TRS	B	604	8/8	0.73	0.19	53,60,71,72	0
5	GOL	C	508	6/6	0.73	0.26	54,63,70,81	0
5	GOL	B	608	6/6	0.76	0.28	24,35,53,63	0
5	GOL	A	503	6/6	0.76	0.18	39,42,44,44	0
5	GOL	C	503	6/6	0.77	0.14	48,58,61,63	0
5	GOL	C	507	6/6	0.78	0.17	49,52,57,59	0
5	GOL	C	506	6/6	0.78	0.26	57,72,80,83	0
5	GOL	C	505	6/6	0.80	0.21	34,43,48,52	0
5	GOL	B	602	6/6	0.81	0.19	40,48,53,55	0
5	GOL	C	504	6/6	0.84	0.17	42,51,56,58	0
5	GOL	D	603	6/6	0.85	0.12	39,48,53,54	0
5	GOL	B	603	6/6	0.86	0.12	37,38,40,46	0
5	GOL	B	606	6/6	0.86	0.18	47,53,57,69	0
3	HCA	C	501	14/14	0.88	0.11	28,34,39,39	0
5	GOL	B	607	6/6	0.89	0.11	35,45,51,52	0

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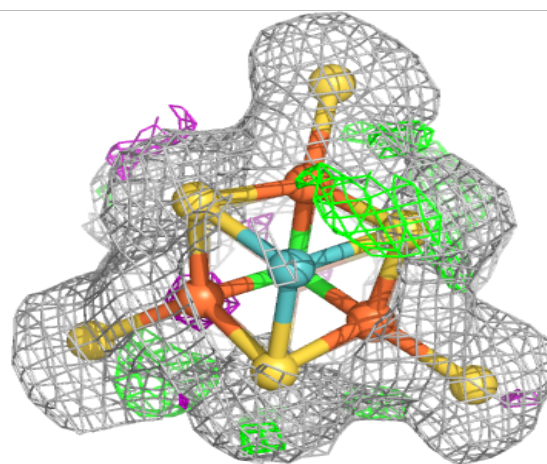
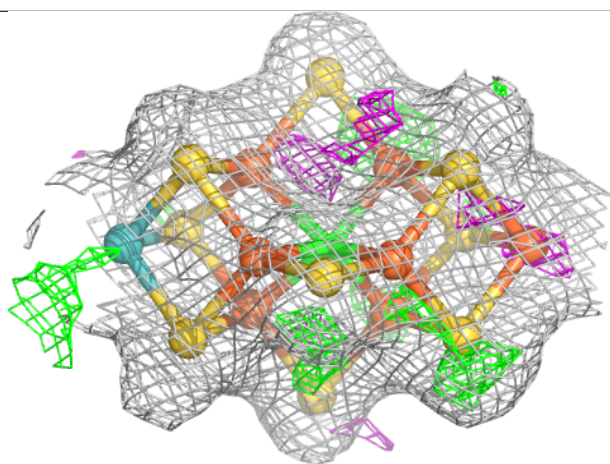
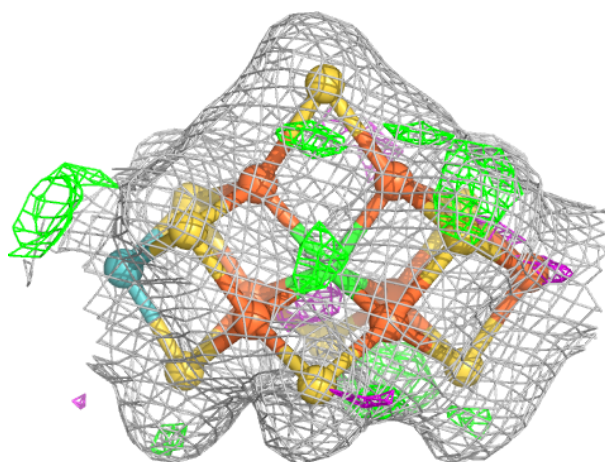
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
5	GOL	B	605	6/6	0.90	0.12	37,46,53,53	0
3	HCA	A	501	14/14	0.90	0.10	27,30,39,39	0
5	GOL	D	601	6/6	0.90	0.11	54,57,59,65	0
6	1CL	A	504	15/15	0.94	0.09	26,30,37,41	15
6	1CL	C	509	15/15	0.95	0.08	28,31,40,42	0
4	ICS	C	502	18/18	0.98	0.05	28,33,39,40	0
4	ICS	A	502	18/18	0.98	0.06	25,32,35,37	0
7	CA	B	601	1/1	0.99	0.04	41,41,41,41	0
7	CA	B	609	1/1	0.99	0.07	42,42,42,42	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.

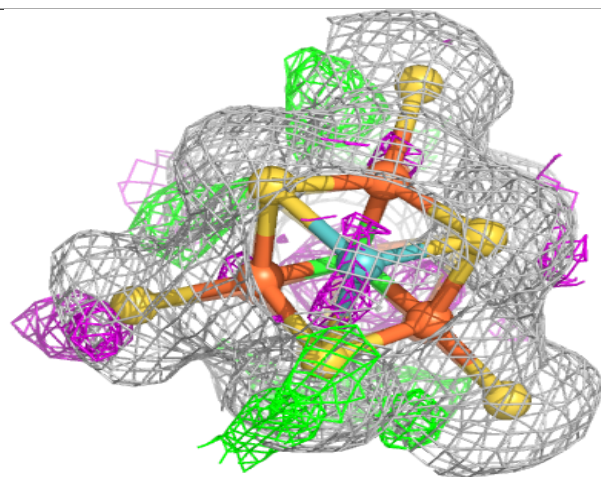
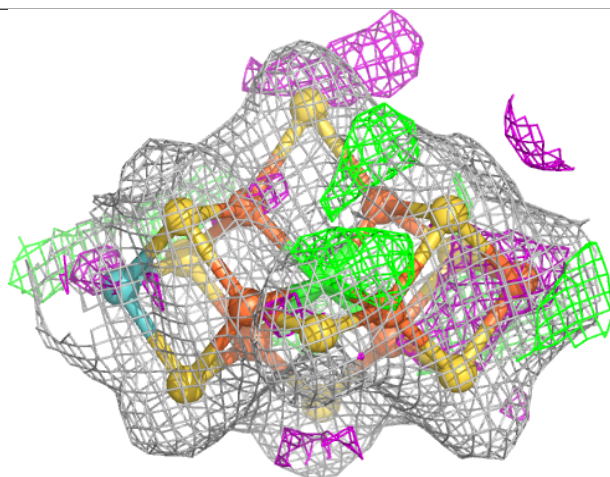
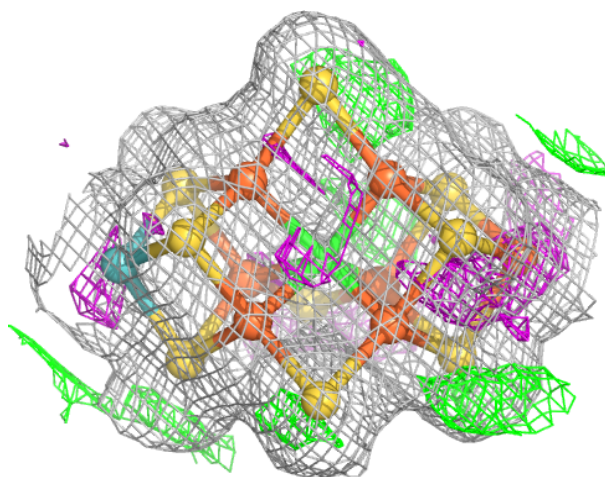
Electron density around ICS C 502:

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 ICS A 502:

$2mF_o-DF_c$ (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.