



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 07:29 AM GMT

PDB ID : 3AYZ
Title : Membrane-bound respiratory [NiFe] hydrogenase from *Hydrogenovibrio marinus* in an air-oxidized condition
Authors : Shomura, Y.; Yoon, K.S.; Nishihara, H.; Higuchi, Y.
Deposited on : 2011-05-20
Resolution : 1.22 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
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467
Mogul : 1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026688
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

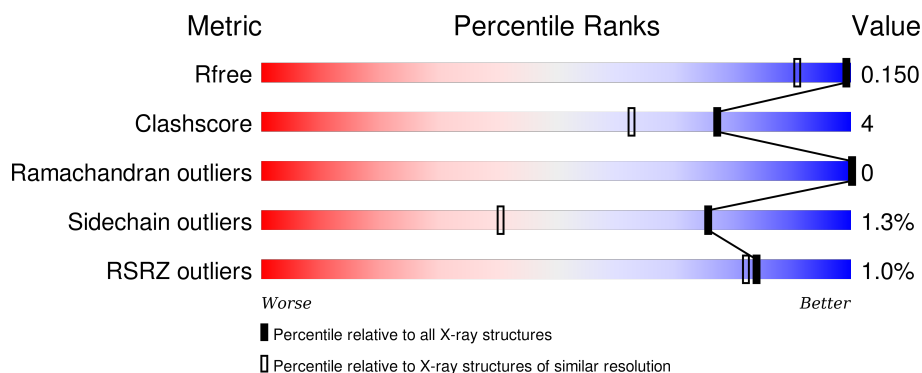
1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.22 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}	91344	1197 (1.26-1.18)
Clashscore	102246	1295 (1.26-1.18)
Ramachandran outliers	100387	1239 (1.26-1.18)
Sidechain outliers	100360	1237 (1.26-1.18)
RSRZ outliers	91569	1201 (1.26-1.18)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. 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	596	<div> <div></div> <div>86%12% .</div> </div>
1	C	596	<div> <div>%</div> <div>85%13% .</div> </div>
2	B	283	<div> <div>2%</div> <div>81%14% . .</div> </div>
2	D	283	<div> <div>%</div> <div>81%12% . 6%</div> </div>

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
6	CYN	A	605	-	-	-	X
7	O	A	607	-	-	X	-
7	O	A	608	-	-	-	X
7	O	A	609	-	-	-	X
7	O	A	610	-	-	-	X
7	O	C	606	-	-	-	X
7	O	C	607	-	-	X	X
7	O	C	609	-	-	-	X
8	GOL	A	702	-	-	-	X
8	GOL	A	703	-	-	-	X
8	GOL	C	702	-	-	-	X
8	GOL	C	703	-	-	-	X

2 Entry composition [i](#)

There are 14 unique types of molecules in this entry. The entry contains 15529 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 Membrane-bound hydrogenase large subunit.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	595	Total	C	N	O	S	0	19	0
			4770	3030	831	884	25			
1	C	595	Total	C	N	O	S	0	15	0
			4750	3014	829	882	25			

- Molecule 2 is a protein called Membrane-bound hydrogenase small subunit.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	273	Total	C	N	O	S	0	8	0
			2159	1370	369	399	21			
2	D	267	Total	C	N	O	S	0	8	0
			2109	1341	358	390	20			

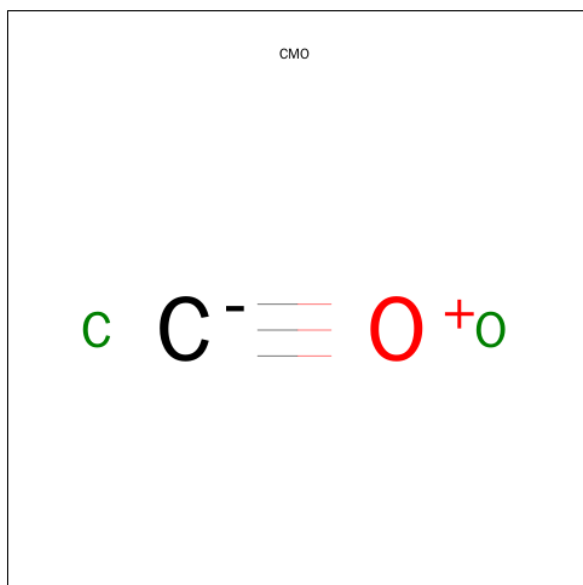
- Molecule 3 is FE (II) ION (three-letter code: FE2) (formula: Fe).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	1	Total	Fe	0	0
			1	1		
3	C	1	Total	Fe	0	0
			1	1		

- Molecule 4 is NICKEL (III) ION (three-letter code: 3NI) (formula: Ni).

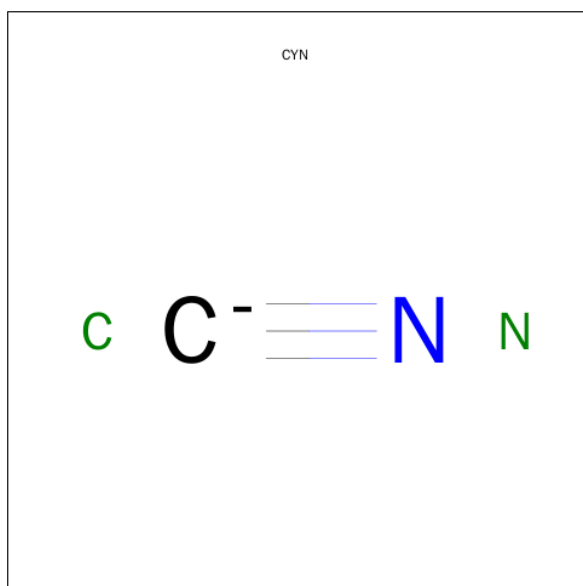
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	1	Total	Ni	0	0
			1	1		
4	C	1	Total	Ni	0	0
			1	1		

- Molecule 5 is CARBON MONOXIDE (three-letter code: CMO) (formula: CO).



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

- Molecule 6 is CYANIDE ION (three-letter code: CYN) (formula: CN).



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

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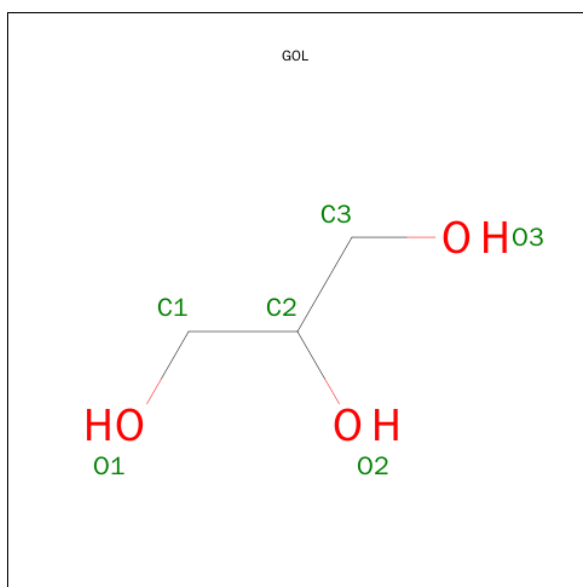
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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	C	1	Total	C	N	0	0
			2	1	1		
6	C	1	Total	C	N	0	0
			2	1	1		

- Molecule 7 is OXYGEN ATOM (three-letter code: O) (formula: O).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	5	Total	O	0	0
			5	5		
7	C	5	Total	O	0	0
			5	5		

- Molecule 8 is GLYCEROL (three-letter code: GOL) (formula: C₃H₈O₃).

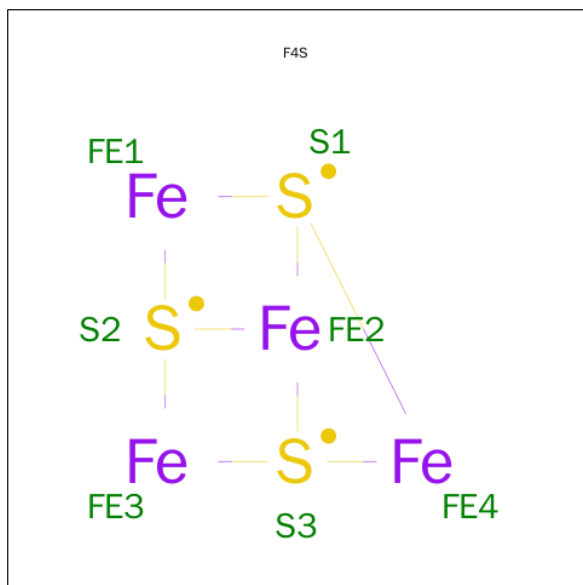


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
8	A	1	Total	C	O	0	0
			6	3	3		
8	A	1	Total	C	O	0	0
			6	3	3		
8	C	1	Total	C	O	0	0
			6	3	3		
8	C	1	Total	C	O	0	0
			6	3	3		

- Molecule 9 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

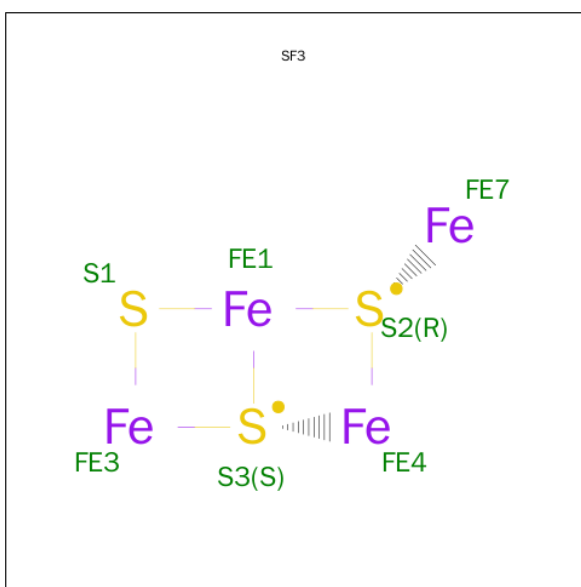
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
9	A	1	Total	Mg	0	0
			1	1		
9	C	1	Total	Mg	0	0
			1	1		

- Molecule 10 is FE4-S3 CLUSTER (three-letter code: F4S) (formula: Fe_4S_3).



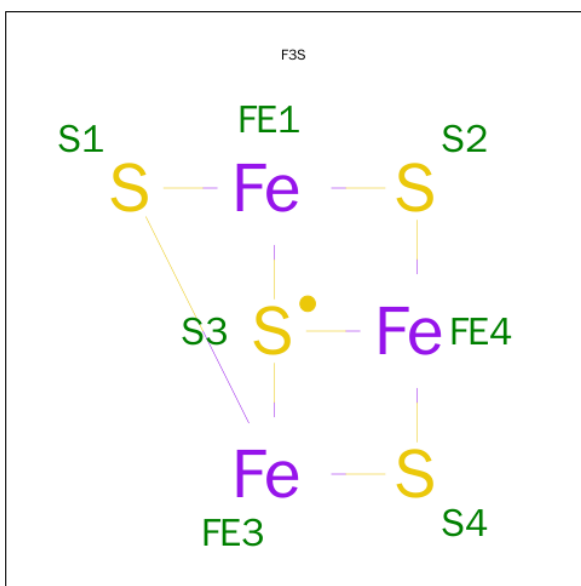
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
10	B	1	Total	Fe	S	0	1
			7	4	3		
10	D	1	Total	Fe	S	0	1
			7	4	3		

- Molecule 11 is FE4-S3 CLUSTER (three-letter code: SF3) (formula: Fe_4S_3).



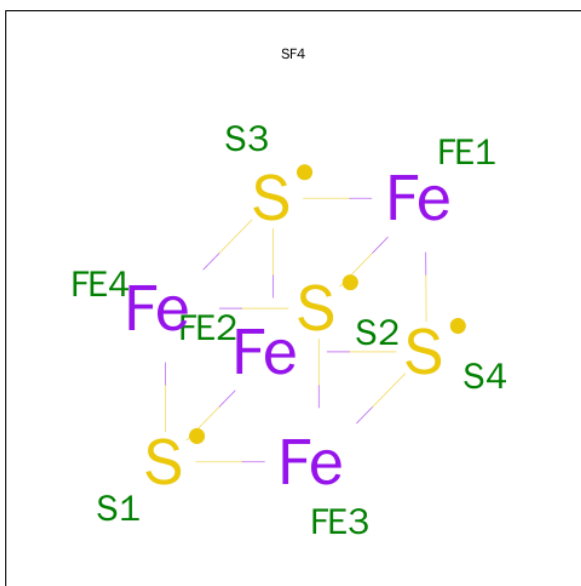
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
11	B	1	Total	Fe	S	0	1
			7	4	3		
11	D	1	Total	Fe	S	0	1
			7	4	3		

- Molecule 12 is FE3-S4 CLUSTER (three-letter code: F3S) (formula: Fe_3S_4).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
12	B	1	Total	Fe	S	0	0
			7	3	4		
12	D	1	Total	Fe	S	0	0
			7	3	4		

- Molecule 13 is IRON/SULFUR CLUSTER (three-letter code: SF4) (formula: Fe_4S_4).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
13	B	1	Total	Fe	S	0	0
			8	4	4		
13	D	1	Total	Fe	S	0	0
			8	4	4		

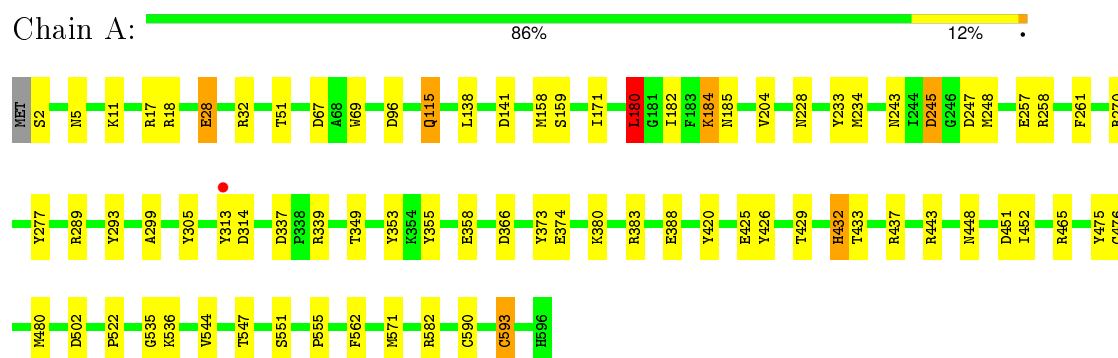
- Molecule 14 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
14	A	622	Total	O	0	0
			622	622		
14	B	253	Total	O	0	0
			253	253		
14	C	532	Total	O	0	0
			532	532		
14	D	224	Total	O	0	0
			224	224		

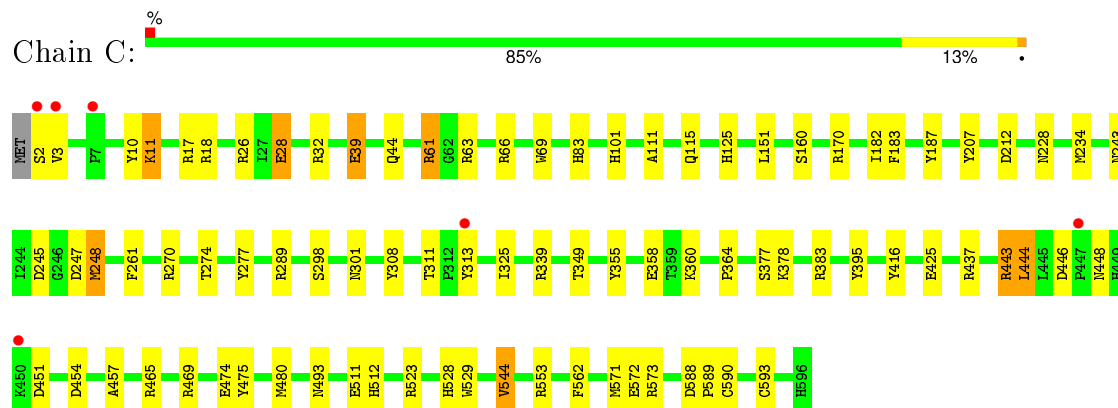
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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.

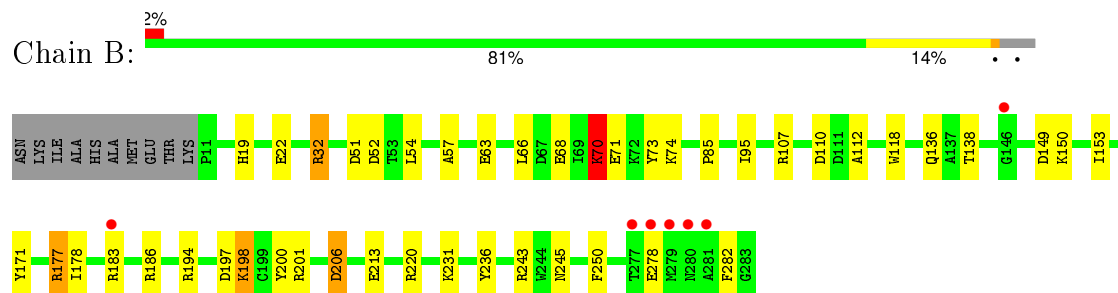
- Molecule 1: Membrane-bound hydrogenase large subunit



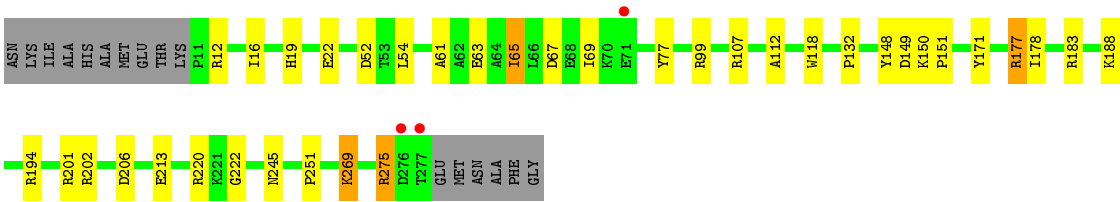
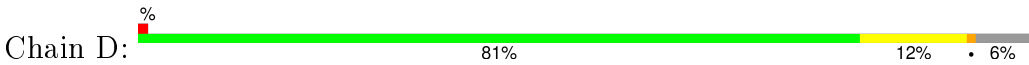
- Molecule 1: Membrane-bound hydrogenase large subunit



- Molecule 2: Membrane-bound hydrogenase small subunit



- Molecule 2: Membrane-bound hydrogenase small subunit



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	75.65Å 116.66Å 113.61Å 90.00° 91.34° 90.00°	Depositor
Resolution (Å)	20.00 – 1.22 19.95 – 1.22	Depositor EDS
% Data completeness (in resolution range)	100.0 (20.00-1.22) 95.0 (19.95-1.22)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.44 (at 1.22Å)	Xtriage
Refinement program	SHELXL-97	Depositor
R, R_{free}	0.139 , 0.171 0.129 , 0.150	Depositor DCC
R_{free} test set	28834 reflections (5.72%)	DCC
Wilson B-factor (Å ²)	11.0	Xtriage
Anisotropy	0.200	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	(Not available) , (Not available)	EDS
Estimated twinning fraction	0.006 for -h,-l,-k 0.000 for -h,l,k 0.087 for h,-k,-l	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.34$	Xtriage
Outliers	0 of 1088205 reflections	Xtriage
F_o, F_c correlation	0.98	EDS
Total number of atoms	15529	wwPDB-VP
Average B, all atoms (Å ²)	15.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.01% 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, 0.375 respectively for untwinned datasets, and 0.333, 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: CMO, GOL, MG, SF4, SF3, O, 3NI, F4S, F3S, FE2, CYN

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	0.92	6/4952 (0.1%)	1.36	61/6739 (0.9%)
1	C	0.87	2/4919 (0.0%)	1.41	71/6698 (1.1%)
2	B	0.90	0/2241	1.54	44/3032 (1.5%)
2	D	0.86	0/2190	1.44	33/2966 (1.1%)
All	All	0.89	8/14302 (0.1%)	1.42	209/19435 (1.1%)

All (8) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	28	GLU	CD-OE2	7.55	1.33	1.25
1	A	383	ARG	CD-NE	7.04	1.58	1.46
1	A	28	GLU	CD-OE1	6.38	1.32	1.25
1	A	593	CYS	CB-SG	-6.36	1.71	1.82
1	A	374	GLU	CD-OE1	-6.18	1.18	1.25
1	A	383	ARG	CZ-NH1	5.57	1.40	1.33
1	A	257	GLU	CD-OE2	-5.08	1.20	1.25
1	C	101	HIS	CB-CG	5.03	1.59	1.50

All (209) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	194	ARG	NE-CZ-NH2	-14.12	113.24	120.30
1	C	170	ARG	NE-CZ-NH2	-13.89	113.36	120.30
1	C	573	ARG	NE-CZ-NH1	13.80	127.20	120.30
1	A	18	ARG	NE-CZ-NH2	13.32	126.96	120.30
2	D	275	ARG	CD-NE-CZ	12.98	141.77	123.60
2	B	32	ARG	NE-CZ-NH2	12.76	126.68	120.30
2	B	177	ARG	CG-CD-NE	-11.98	86.64	111.80
1	C	248	MET	CG-SD-CE	-11.87	81.20	100.20
1	A	443	ARG	NE-CZ-NH1	11.72	126.16	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	248	MET	CG-SD-CE	-11.71	81.47	100.20
1	C	465	ARG	NE-CZ-NH1	11.39	125.99	120.30
1	C	66	ARG	NE-CZ-NH2	-11.33	114.64	120.30
1	A	339	ARG	NE-CZ-NH2	-11.28	114.66	120.30
1	C	26	ARG	NE-CZ-NH1	11.02	125.81	120.30
1	C	443	ARG	NE-CZ-NH2	-10.98	114.81	120.30
2	B	177	ARG	CD-NE-CZ	10.51	138.31	123.60
1	A	443	ARG	NE-CZ-NH2	-10.32	115.14	120.30
2	B	194	ARG	NE-CZ-NH2	-10.17	115.22	120.30
2	B	206	ASP	CB-CG-OD2	-9.92	109.37	118.30
1	A	32	ARG	NE-CZ-NH1	9.88	125.24	120.30
1	A	17	ARG	NE-CZ-NH1	9.71	125.16	120.30
1	C	69	TRP	CZ3-CH2-CZ2	9.70	133.24	121.60
2	B	186	ARG	NE-CZ-NH2	9.61	125.11	120.30
1	C	28	GLU	CG-CD-OE1	9.55	137.41	118.30
2	D	275	ARG	NE-CZ-NH1	9.55	125.08	120.30
2	B	282	PHE	CB-CG-CD2	9.47	127.43	120.80
1	C	277	TYR	CB-CG-CD1	9.42	126.65	121.00
1	C	63	ARG	NE-CZ-NH1	9.31	124.96	120.30
2	B	52	ASP	CB-CG-OD2	9.18	126.56	118.30
1	A	358	GLU	OE1-CD-OE2	9.15	134.28	123.30
1	C	17	ARG	NE-CZ-NH1	-8.87	115.87	120.30
1	A	437	ARG	NE-CZ-NH1	-8.67	115.96	120.30
2	D	183	ARG	NE-CZ-NH1	8.66	124.63	120.30
2	B	54	LEU	O-C-N	-8.49	109.12	122.70
2	D	99	ARG	CD-NE-CZ	8.48	135.48	123.60
1	A	28	GLU	CG-CD-OE2	8.45	135.19	118.30
2	B	194	ARG	CD-NE-CZ	8.42	135.39	123.60
1	A	69	TRP	CZ3-CH2-CZ2	8.33	131.60	121.60
1	A	355	TYR	CB-CG-CD1	8.30	125.98	121.00
2	B	282	PHE	CB-CG-CD1	-8.21	115.06	120.80
1	A	582	ARG	NE-CZ-NH1	8.17	124.39	120.30
1	C	313	TYR	CB-CG-CD2	8.00	125.80	121.00
1	C	339	ARG	NE-CZ-NH2	-7.99	116.31	120.30
1	C	277	TYR	CB-CG-CD2	-7.85	116.29	121.00
2	B	177	ARG	NE-CZ-NH2	-7.76	116.42	120.30
1	C	18	ARG	NE-CZ-NH1	7.76	124.18	120.30
1	A	305	TYR	CB-CG-CD1	7.72	125.64	121.00
1	C	245[A]	ASP	CB-CG-OD1	7.71	125.23	118.30
1	C	245[B]	ASP	CB-CG-OD1	7.71	125.23	118.30
1	A	245[A]	ASP	CB-CG-OD1	7.66	125.20	118.30
1	A	245[B]	ASP	CB-CG-OD1	7.66	125.20	118.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	366	ASP	CB-CG-OD1	-7.63	111.43	118.30
1	A	465	ARG	NE-CZ-NH1	7.61	124.11	120.30
1	C	544[A]	VAL	CA-CB-CG1	7.53	122.20	110.90
1	C	544[B]	VAL	CA-CB-CG1	7.53	122.20	110.90
1	A	277	TYR	CB-CG-CD1	7.50	125.50	121.00
1	C	28	GLU	OE1-CD-OE2	-7.50	114.30	123.30
2	D	213	GLU	OE1-CD-OE2	7.45	132.24	123.30
2	B	243	ARG	NE-CZ-NH2	-7.42	116.59	120.30
1	C	289	ARG	NE-CZ-NH1	7.35	123.98	120.30
1	C	437	ARG	NE-CZ-NH2	7.35	123.97	120.30
1	C	358	GLU	CG-CD-OE2	-7.31	103.68	118.30
2	B	73	TYR	CG-CD2-CE2	7.25	127.10	121.30
2	B	73	TYR	CB-CG-CD2	7.25	125.35	121.00
1	A	18	ARG	NH1-CZ-NH2	-7.23	111.44	119.40
1	A	562	PHE	CB-CG-CD1	7.22	125.85	120.80
1	A	28	GLU	CG-CD-OE1	-7.17	103.95	118.30
1	C	475	TYR	CB-CG-CD1	7.15	125.29	121.00
2	D	52[A]	ASP	CB-CG-OD1	7.13	124.72	118.30
2	D	52[B]	ASP	CB-CG-OD1	7.13	124.72	118.30
1	C	383	ARG	NE-CZ-NH1	-7.13	116.74	120.30
1	A	258	ARG	NE-CZ-NH2	-7.12	116.74	120.30
2	B	206	ASP	CB-CG-OD1	7.09	124.68	118.30
1	C	437	ARG	NE-CZ-NH1	-7.09	116.75	120.30
2	D	194	ARG	NH1-CZ-NH2	7.07	127.17	119.40
1	A	270	ARG	NE-CZ-NH1	7.06	123.83	120.30
1	C	69	TRP	CH2-CZ2-CE2	-7.00	110.40	117.40
1	A	383	ARG	NE-CZ-NH2	6.99	123.80	120.30
2	B	197	ASP	CB-CG-OD1	-6.99	112.01	118.30
1	C	562	PHE	CB-CG-CD1	6.96	125.67	120.80
1	C	61[A]	ARG	NE-CZ-NH1	-6.95	116.82	120.30
1	C	61[B]	ARG	NE-CZ-NH1	-6.95	116.82	120.30
2	D	54	LEU	O-C-N	-6.91	111.64	122.70
1	C	298	SER	C-N-CA	-6.82	104.65	121.70
2	D	220	ARG	NE-CZ-NH2	-6.76	116.92	120.30
1	C	289	ARG	NE-CZ-NH2	-6.75	116.92	120.30
2	B	201	ARG	NE-CZ-NH2	6.70	123.65	120.30
1	C	69	TRP	CE3-CZ3-CH2	-6.67	113.86	121.20
1	A	339	ARG	NE-CZ-NH1	6.63	123.62	120.30
2	D	201	ARG	NE-CZ-NH1	6.58	123.59	120.30
2	B	197	ASP	CB-CG-OD2	6.57	124.21	118.30
1	A	314	ASP	CB-CG-OD1	6.56	124.21	118.30
1	A	425	GLU	OE1-CD-OE2	-6.54	115.45	123.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	553	ARG	NE-CZ-NH1	6.51	123.55	120.30
1	A	562	PHE	CB-CG-CD2	-6.39	116.32	120.80
1	A	234	MET	CA-CB-CG	-6.34	102.51	113.30
1	A	358	GLU	CG-CD-OE2	-6.29	105.73	118.30
2	B	278	GLU	CA-C-O	6.23	133.19	120.10
2	D	99	ARG	NE-CZ-NH2	-6.21	117.19	120.30
1	A	571	MET	CG-SD-CE	-6.19	90.30	100.20
1	C	465	ARG	NE-CZ-NH2	-6.18	117.21	120.30
1	A	289	ARG	NE-CZ-NH1	-6.18	117.21	120.30
2	B	110	ASP	CB-CG-OD1	6.17	123.86	118.30
1	A	451	ASP	CB-CG-OD2	-6.16	112.76	118.30
2	B	278	GLU	O-C-N	-6.13	112.89	122.70
1	C	480	MET	CG-SD-CE	-6.12	90.41	100.20
2	D	269	LYS	O-C-N	-6.11	112.82	123.20
1	A	17	ARG	NE-CZ-NH2	-6.10	117.25	120.30
1	C	32	ARG	NE-CZ-NH2	-6.09	117.25	120.30
2	B	63[A]	GLU	OE1-CD-OE2	6.06	130.57	123.30
2	B	63[B]	GLU	OE1-CD-OE2	6.06	130.57	123.30
1	C	28	GLU	CG-CD-OE2	-6.05	106.20	118.30
1	A	475	TYR	CB-CG-CD1	6.05	124.63	121.00
2	B	51	ASP	CB-CG-OD2	-6.05	112.86	118.30
2	B	220	ARG	NE-CZ-NH1	-6.04	117.28	120.30
1	A	69	TRP	CH2-CZ2-CE2	-6.04	111.36	117.40
1	C	170	ARG	NE-CZ-NH1	6.02	123.31	120.30
2	B	236	TYR	CB-CG-CD2	6.02	124.61	121.00
2	D	148	TYR	CB-CG-CD1	-6.00	117.40	121.00
1	C	187	TYR	CB-CG-CD1	5.98	124.59	121.00
1	A	293	TYR	CB-CG-CD2	5.93	124.56	121.00
1	C	572	GLU	OE1-CD-OE2	5.93	130.42	123.30
2	D	107	ARG	NE-CZ-NH2	-5.92	117.34	120.30
2	D	177	ARG	CA-CB-CG	5.92	126.42	113.40
1	C	355	TYR	CB-CG-CD1	5.91	124.55	121.00
2	D	213	GLU	CG-CD-OE1	-5.89	106.52	118.30
2	D	202	ARG	NE-CZ-NH2	5.89	123.24	120.30
1	A	233	TYR	CB-CG-CD1	5.87	124.52	121.00
1	C	377[A]	SER	CB-CA-C	5.87	121.25	110.10
1	C	377[B]	SER	CB-CA-C	5.87	121.25	110.10
2	B	198[A]	LYS	CD-CE-NZ	5.87	125.19	111.70
2	B	198[B]	LYS	CD-CE-NZ	5.87	125.19	111.70
1	A	502	ASP	CB-CG-OD1	5.83	123.55	118.30
1	A	180	LEU	CB-CG-CD2	5.81	120.88	111.00
2	B	197	ASP	CA-CB-CG	5.80	126.17	113.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	416	TYR	CA-CB-CG	-5.77	102.43	113.40
1	C	457	ALA	N-CA-CB	5.76	118.17	110.10
1	A	67	ASP	CB-CG-OD2	5.76	123.49	118.30
2	B	201	ARG	NE-CZ-NH1	-5.76	117.42	120.30
2	B	213	GLU	OE1-CD-OE2	5.73	130.18	123.30
1	C	571	MET	CG-SD-CE	-5.70	91.09	100.20
2	B	32	ARG	NE-CZ-NH1	-5.69	117.45	120.30
1	A	96[A]	ASP	CB-CG-OD1	5.67	123.40	118.30
1	A	96[B]	ASP	CB-CG-OD1	5.67	123.40	118.30
1	A	480	MET	CG-SD-CE	-5.66	91.14	100.20
2	D	177	ARG	CD-NE-CZ	5.65	131.51	123.60
1	C	183	PHE	CB-CG-CD1	-5.62	116.86	120.80
1	C	553	ARG	NE-CZ-NH2	-5.59	117.50	120.30
1	C	395	TYR	CA-CB-CG	5.58	124.00	113.40
1	C	425	GLU	OE1-CD-OE2	-5.57	116.62	123.30
2	D	67	ASP	CB-CG-OD1	-5.55	113.31	118.30
1	C	234	MET	CA-CB-CG	-5.52	103.92	113.30
1	C	469	ARG	NE-CZ-NH1	5.52	123.06	120.30
1	C	454	ASP	CB-CG-OD1	5.52	123.27	118.30
1	C	313	TYR	CG-CD1-CE1	5.50	125.70	121.30
1	A	313	TYR	CG-CD2-CE2	5.49	125.69	121.30
1	C	454	ASP	CB-CG-OD2	-5.47	113.38	118.30
2	B	107	ARG	NE-CZ-NH1	5.45	123.02	120.30
2	D	275	ARG	CG-CD-NE	5.45	123.23	111.80
1	A	451	ASP	O-C-N	-5.44	113.99	122.70
2	D	171	TYR	CB-CG-CD2	5.44	124.27	121.00
2	B	250	PHE	CB-CG-CD1	5.44	124.61	120.80
2	B	149	ASP	CB-CG-OD1	5.43	123.19	118.30
2	B	171	TYR	CB-CG-CD2	5.42	124.25	121.00
2	D	177	ARG	NE-CZ-NH2	-5.41	117.60	120.30
1	C	183	PHE	CB-CG-CD2	5.40	124.58	120.80
1	C	562	PHE	CB-CG-CD2	-5.40	117.02	120.80
1	C	358	GLU	CG-CD-OE1	5.39	129.08	118.30
1	C	44	GLN	CG-CD-OE1	5.31	132.22	121.60
1	C	212	ASP	CB-CG-OD1	5.29	123.06	118.30
2	B	194	ARG	NH1-CZ-NH2	5.28	125.21	119.40
2	D	118	TRP	CA-CB-CG	5.28	123.73	113.70
1	A	432	HIS	CA-CB-CG	-5.26	104.65	113.60
1	C	573	ARG	NH1-CZ-NH2	-5.25	113.62	119.40
1	A	448	ASN	CB-CG-ND2	-5.25	104.10	116.70
2	D	52[A]	ASP	O-C-N	-5.24	114.32	122.70
2	D	52[B]	ASP	O-C-N	-5.24	114.32	122.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	269	LYS	CA-C-N	5.24	126.67	116.20
2	B	200	TYR	CG-CD1-CE1	5.21	125.47	121.30
1	C	270	ARG	NE-CZ-NH1	5.21	122.91	120.30
2	B	118	TRP	CA-CB-CG	5.19	123.56	113.70
1	A	141	ASP	CB-CG-OD2	5.18	122.96	118.30
1	C	378	LYS	CD-CE-NZ	5.18	123.61	111.70
2	B	70	LYS	CD-CE-NZ	5.17	123.58	111.70
2	D	12	ARG	CD-NE-CZ	5.15	130.81	123.60
2	D	77	TYR	CB-CG-CD1	5.14	124.09	121.00
1	C	523	ARG	NE-CZ-NH2	-5.14	117.73	120.30
2	B	32	ARG	CD-NE-CZ	5.13	130.78	123.60
2	D	149	ASP	CB-CG-OD1	5.13	122.92	118.30
1	A	353	TYR	CB-CG-CD2	-5.13	117.92	121.00
1	A	448	ASN	CB-CG-OD1	5.12	131.84	121.60
1	A	437	ARG	CD-NE-CZ	5.11	130.75	123.60
1	C	248	MET	CB-CG-SD	-5.10	97.10	112.40
1	A	337	ASP	CB-CG-OD2	-5.10	113.71	118.30
1	A	383	ARG	CA-CB-CG	5.09	124.61	113.40
1	A	299	ALA	N-CA-CB	-5.08	102.98	110.10
1	C	10	TYR	CD1-CE1-CZ	5.08	124.37	119.80
1	C	311	THR	O-C-N	5.07	130.74	121.10
1	A	69	TRP	CE3-CZ3-CH2	-5.07	115.62	121.20
1	C	308	TYR	CB-CG-CD2	-5.07	117.96	121.00
2	D	52[A]	ASP	CB-CG-OD2	-5.06	113.74	118.30
2	D	52[B]	ASP	CB-CG-OD2	-5.06	113.74	118.30
1	A	184[A]	LYS	CG-CD-CE	5.06	127.07	111.90
1	A	184[B]	LYS	CG-CD-CE	5.06	127.07	111.90
2	B	250	PHE	CG-CD1-CE1	5.05	126.35	120.80
1	A	426	TYR	CG-CD2-CE2	5.04	125.33	121.30
1	C	187	TYR	CG-CD1-CE1	5.02	125.32	121.30
1	A	373	TYR	CB-CG-CD1	5.02	124.01	121.00
2	B	278	GLU	CB-CA-C	5.01	120.42	110.40

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	4770	0	4704	48	0
1	C	4750	0	4668	32	0
2	B	2159	0	2102	17	0
2	D	2109	0	2058	12	0
3	A	1	0	0	0	0
3	C	1	0	0	0	0
4	A	1	0	0	0	0
4	C	1	0	0	0	0
5	A	2	0	0	0	0
5	C	2	0	0	0	0
6	A	4	0	0	0	0
6	C	4	0	0	0	0
7	A	5	0	0	6	0
7	C	5	0	0	5	0
8	A	12	0	15	2	0
8	C	12	0	14	1	0
9	A	1	0	0	0	0
9	C	1	0	0	0	0
10	B	7	0	0	0	0
10	D	7	0	0	0	0
11	B	7	0	0	0	0
11	D	7	0	0	0	0
12	B	7	0	0	0	0
12	D	7	0	0	0	0
13	B	8	0	0	0	0
13	D	8	0	0	0	0
14	A	622	0	0	10	0
14	B	253	0	0	6	0
14	C	532	0	0	8	0
14	D	224	0	0	2	0
All	All	15529	0	13561	101	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 4.

All (101) 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:593:CYS:CB	7:C:607:O:O	2.13	0.95
1:A:593:CYS:CB	7:A:607:O:O	2.20	0.89
1:C:593:CYS:HB2	7:C:607:O:O	1.75	0.86
2:B:198[B]:LYS:HE3	14:B:1051:HOH:O	1.81	0.79

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:180:LEU:HG	14:A:1377:HOH:O	1.82	0.79
1:A:184[A]:LYS:HD2	14:B:971:HOH:O	1.83	0.78
1:A:184[A]:LYS:HE3	14:A:914:HOH:O	1.83	0.77
1:A:593:CYS:HB2	7:A:607:O:O	1.86	0.75
1:C:274[A]:THR:HG22	1:C:474:GLU:OE2	1.87	0.74
14:A:1620:HOH:O	2:B:57:ALA:HA	1.88	0.73
1:A:5:ASN:HD21	1:A:11:LYS:NZ	1.88	0.71
2:B:112:ALA:O	2:B:150:LYS:HD2	1.95	0.67
1:C:151[A]:LEU:HD11	1:C:444:LEU:HD23	1.76	0.67
1:C:590:CYS:CB	7:C:606:O:O	2.43	0.66
1:A:555:PRO:HA	14:A:1041:HOH:O	1.94	0.66
1:C:593:CYS:N	7:C:607:O:O	2.30	0.65
1:C:444:LEU:HD13	14:C:1032:HOH:O	1.96	0.64
1:A:171[B]:ILE:HD11	1:A:204:VAL:HG11	1.78	0.64
1:A:593:CYS:N	7:A:607:O:O	2.31	0.63
1:A:535:GLY:O	1:A:536[B]:LYS:HE3	1.99	0.62
1:C:83:HIS:HD2	1:C:528:HIS:NE2	1.98	0.62
1:A:158[B]:MET:HE1	14:A:821:HOH:O	2.00	0.61
1:C:182:ILE:HG22	14:D:1308:HOH:O	1.99	0.61
1:A:590:CYS:CB	7:A:606:O:O	2.49	0.60
1:A:115[B]:GLN:OE1	1:A:522:PRO:HG3	2.02	0.59
1:A:547:THR:O	1:A:551[B]:SER:HB3	2.01	0.59
1:C:349:THR:HB	14:C:1597:HOH:O	2.03	0.57
1:C:243:ASN:OD1	8:C:703:GOL:H31	2.04	0.57
1:A:228:ASN:HD21	2:B:32:ARG:HH21	1.53	0.57
1:A:349:THR:HG21	1:A:555:PRO:HG3	1.86	0.56
1:A:180:LEU:HD12	14:A:959:HOH:O	2.05	0.56
1:C:446:ASP:OD1	1:C:448:ASN:HB2	2.07	0.55
1:C:228:ASN:H	2:D:245:ASN:HD21	1.55	0.54
1:C:28:GLU:OE2	7:C:608:O:O	2.25	0.54
1:C:111:ALA:O	1:C:115[B]:GLN:HG2	2.07	0.54
2:B:206:ASP:OD2	2:D:206:ASP:OD2	2.27	0.52
2:B:183[A]:ARG:HG3	14:B:1223:HOH:O	2.09	0.51
2:D:61:ALA:O	2:D:65[A]:ILE:HD12	2.10	0.51
1:A:184[B]:LYS:HG3	1:A:185:ASN:N	2.25	0.51
1:A:544[B]:VAL:HG11	1:A:593:CYS:HB3	1.92	0.51
1:A:228:ASN:H	2:B:245:ASN:HD21	1.59	0.51
2:D:63:GLU:HG2	14:D:1273:HOH:O	2.11	0.51
1:C:83:HIS:HE1	1:C:593:CYS:SG	2.35	0.50
2:D:16:ILE:HD11	2:D:69:ILE:HG21	1.94	0.49
1:A:243:ASN:OD1	8:A:703:GOL:H31	2.13	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:182:ILE:HG22	14:B:584:HOH:O	2.12	0.48
1:C:247[B]:ASP:OD1	1:C:248:MET:HG2	2.14	0.48
1:A:544[A]:VAL:HG21	1:A:593:CYS:HB3	1.95	0.48
1:C:39:GLU:H	1:C:39:GLU:CD	2.16	0.48
1:A:247[B]:ASP:OD2	2:D:188:LYS:HD3	2.14	0.47
1:A:159:SER:HG	1:C:160[B]:SER:HB3	1.80	0.47
1:C:3:VAL:CG1	1:C:11:LYS:HG3	2.45	0.47
2:B:198[A]:LYS:CE	14:C:1560:HOH:O	2.63	0.47
1:A:536[B]:LYS:HE3	14:A:767:HOH:O	2.15	0.47
2:B:198[A]:LYS:HE3	14:C:1560:HOH:O	2.14	0.47
8:A:703:GOL:H12	14:A:1319:HOH:O	2.15	0.46
1:A:536[B]:LYS:HD2	14:A:962:HOH:O	2.15	0.46
1:A:184[A]:LYS:HE2	2:B:68:GLU:OE1	2.15	0.46
1:C:61[B]:ARG:NH2	14:C:764:HOH:O	2.49	0.46
1:C:151[A]:LEU:CD1	1:C:444:LEU:HD23	2.45	0.46
1:C:443:ARG:NH1	1:C:451:ASP:OD1	2.48	0.46
1:A:28:GLU:OE1	7:A:608:O:O	2.34	0.46
2:B:136[A]:GLN:NE2	14:B:293:HOH:O	2.49	0.45
1:A:245[A]:ASP:OD1	2:D:177:ARG:NH1	2.47	0.45
1:C:443:ARG:NH2	1:C:451:ASP:OD1	2.50	0.45
2:D:112:ALA:O	2:D:150:LYS:HD2	2.16	0.45
1:A:5:ASN:ND2	1:A:11:LYS:NZ	2.61	0.45
1:C:511:GLU:HG2	1:C:512:HIS:CD2	2.52	0.44
1:A:2:SER:N	14:A:908:HOH:O	2.49	0.44
2:B:70:LYS:NZ	14:B:1093:HOH:O	2.51	0.44
1:A:380:LYS:NZ	1:A:388:GLU:OE1	2.50	0.44
1:A:171[B]:ILE:CD1	1:A:204:VAL:HG11	2.46	0.44
1:C:2:SER:N	14:C:1592:HOH:O	2.50	0.44
2:B:70:LYS:O	2:B:70:LYS:HG3	2.11	0.44
14:C:1560:HOH:O	2:D:222:GLY:HA3	2.18	0.43
1:A:5:ASN:HD21	1:A:11:LYS:CE	2.30	0.43
1:A:5:ASN:HD21	1:A:11:LYS:HZ3	1.66	0.43
1:C:125:HIS:HE1	1:C:207:TYR:O	2.00	0.43
1:A:349:THR:CG2	1:A:555:PRO:HG3	2.48	0.43
1:C:588:ASP:N	1:C:589:PRO:HD3	2.34	0.43
1:A:544[B]:VAL:CG1	1:A:593:CYS:HB3	2.49	0.43
1:A:138:LEU:HD21	1:A:171[B]:ILE:HG22	2.00	0.43
2:D:151:PRO:HG2	2:D:178[B]:ILE:CD1	2.49	0.43
1:C:364:PRO:HB2	1:C:529:TRP:CD2	2.54	0.42
1:C:544[B]:VAL:HG21	1:C:593:CYS:HB3	2.01	0.42
1:A:452:ILE:HD13	1:A:452:ILE:HA	1.77	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:19:HIS:HD1	2:D:22[A]:GLU:CD	2.23	0.42
1:A:429:THR:O	1:A:433[A]:THR:HG23	2.20	0.42
1:C:301:ASN:HA	1:C:325:ILE:O	2.20	0.41
1:A:51:THR:HB	2:B:95:ILE:HB	2.02	0.41
2:B:153:ILE:HD11	2:B:178[A]:ILE:HD12	2.02	0.41
2:B:19:HIS:HD1	2:B:22[B]:GLU:CD	2.23	0.41
1:A:115[B]:GLN:HG3	1:A:476:CYS:SG	2.61	0.41
1:A:115[A]:GLN:NE2	1:A:522:PRO:HA	2.35	0.41
1:A:420:TYR:OH	1:A:432:HIS:HE1	2.04	0.41
2:B:85:PRO:HD2	2:B:138:THR:O	2.21	0.40
1:A:544[A]:VAL:HG22	1:A:547:THR:OG1	2.21	0.40
1:A:593:CYS:CA	7:A:607:O:O	2.68	0.40
1:C:493:ASN:HB2	14:C:1409:HOH:O	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	612/596 (103%)	599 (98%)	13 (2%)	0	100	100
1	C	608/596 (102%)	595 (98%)	13 (2%)	0	100	100
2	B	279/283 (99%)	269 (96%)	10 (4%)	0	100	100
2	D	273/283 (96%)	262 (96%)	11 (4%)	0	100	100
All	All	1772/1758 (101%)	1725 (97%)	47 (3%)	0	100	100

There are no Ramachandran outliers to report.

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	523/505 (104%)	519 (99%)	4 (1%)	86	62
1	C	519/505 (103%)	514 (99%)	5 (1%)	82	53
2	B	233/233 (100%)	227 (97%)	6 (3%)	54	12
2	D	229/233 (98%)	223 (97%)	6 (3%)	54	12
All	All	1504/1476 (102%)	1483 (99%)	21 (1%)	76	38

All (21) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	115[A]	GLN
1	A	115[B]	GLN
1	A	180	LEU
1	A	261	PHE
2	B	66	LEU
2	B	70	LYS
2	B	71	GLU
2	B	74	LYS
2	B	177	ARG
2	B	231	LYS
1	C	11	LYS
1	C	39	GLU
1	C	261	PHE
1	C	360	LYS
1	C	444	LEU
2	D	65[A]	ILE
2	D	65[B]	ILE
2	D	132	PRO
2	D	251	PRO
2	D	269	LYS
2	D	275	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (22) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	5	ASN
1	A	36	ASN
1	A	41	ASN
1	A	168	GLN
1	A	185	ASN
1	A	228	ASN
1	A	232	ASN
1	A	273	ASN
1	A	432	HIS
1	A	439	ASN
1	A	493	ASN
2	B	245	ASN
1	C	41	ASN
1	C	83	HIS
1	C	125	HIS
1	C	168	GLN
1	C	232	ASN
1	C	273	ASN
1	C	432	HIS
1	C	439	ASN
1	C	558	ASN
2	D	245	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 carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 34 ligands modelled in this entry, 16 are monoatomic - leaving 18 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
5	CMO	A	603	-	0,1,1	0.00	-	0,0,0	0.00	-
6	CYN	A	604	-	0,1,1	0.00	-	0,0,0	0.00	-
6	CYN	A	605	-	0,1,1	0.00	-	0,0,0	0.00	-
8	GOL	A	702	-	5,5,5	0.95	0	5,5,5	1.83	2 (40%)
8	GOL	A	703	-	5,5,5	0.84	0	5,5,5	4.09	5 (100%)
10	F4S	B	301[A]	2	0,9,9	0.00	-	0,15,15	0.00	-
11	SF3	B	302[B]	2	0,8,8	0.00	-	0,12,12	0.00	-
12	F3S	B	308	2	0,9,9	0.00	-	0,15,15	0.00	-
13	SF4	B	309	2	0,12,12	0.00	-	0,24,24	0.00	-
5	CMO	C	603	-	0,1,1	0.00	-	0,0,0	0.00	-
6	CYN	C	604	-	0,1,1	0.00	-	0,0,0	0.00	-
6	CYN	C	605	-	0,1,1	0.00	-	0,0,0	0.00	-
8	GOL	C	702	-	5,5,5	0.64	0	5,5,5	3.47	3 (60%)
8	GOL	C	703	-	5,5,5	1.28	0	5,5,5	2.34	2 (40%)
10	F4S	D	301[A]	2	0,9,9	0.00	-	0,15,15	0.00	-
11	SF3	D	302[B]	2	0,8,8	0.00	-	0,12,12	0.00	-
12	F3S	D	308	2	0,9,9	0.00	-	0,15,15	0.00	-
13	SF4	D	309	2	0,12,12	0.00	-	0,24,24	0.00	-

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	CMO	A	603	-	-	0/0/0/0	0/0/0/0
6	CYN	A	604	-	-	0/0/0/0	0/0/0/0
6	CYN	A	605	-	-	0/0/0/0	0/0/0/0
8	GOL	A	702	-	-	0/4/4/4	0/0/0/0
8	GOL	A	703	-	-	0/4/4/4	0/0/0/0
10	F4S	B	301[A]	2	-	0/0/24/24	0/0/3/3
11	SF3	B	302[B]	2	-	0/0/17/17	0/2/2/2
12	F3S	B	308	2	-	0/0/24/24	0/0/3/3
13	SF4	B	309	2	-	0/0/48/48	0/6/5/5
5	CMO	C	603	-	-	0/0/0/0	0/0/0/0
6	CYN	C	604	-	-	0/0/0/0	0/0/0/0

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
6	CYN	C	605	-	-	0/0/0/0	0/0/0/0
8	GOL	C	702	-	-	0/4/4/4	0/0/0/0
8	GOL	C	703	-	-	0/4/4/4	0/0/0/0
10	F4S	D	301[A]	2	-	0/0/24/24	0/0/3/3
11	SF3	D	302[B]	2	-	0/0/17/17	0/2/2/2
12	F3S	D	308	2	-	0/0/24/24	0/0/3/3
13	SF4	D	309	2	-	0/0/48/48	0/6/5/5

There are no bond length outliers.

All (12) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	C	702	GOL	C3-C2-C1	-6.41	85.97	111.12
8	A	703	GOL	C3-C2-C1	-5.36	90.09	111.12
8	A	703	GOL	O3-C3-C2	-3.32	94.06	110.18
8	C	702	GOL	O3-C3-C2	-2.86	96.31	110.18
8	C	702	GOL	O2-C2-C3	-2.64	96.54	108.65
8	A	702	GOL	O1-C1-C2	2.04	120.08	110.18
8	A	703	GOL	O1-C1-C2	2.53	122.48	110.18
8	A	702	GOL	O2-C2-C1	2.71	121.06	108.65
8	C	703	GOL	O2-C2-C3	3.10	122.87	108.65
8	C	703	GOL	O2-C2-C1	4.08	127.35	108.65
8	A	703	GOL	O2-C2-C1	4.09	127.38	108.65
8	A	703	GOL	O2-C2-C3	4.55	129.50	108.65

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
8	A	703	GOL	2	0
8	C	703	GOL	1	0

5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

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	595/596 (99%)	-0.67	1 (0%) 95 95	5, 10, 26, 58	0
1	C	595/596 (99%)	-0.54	6 (1%) 84 82	5, 13, 33, 63	0
2	B	273/283 (96%)	-0.54	7 (2%) 59 55	5, 10, 32, 59	0
2	D	267/283 (94%)	-0.47	3 (1%) 82 80	6, 11, 34, 64	0
All	All	1730/1758 (98%)	-0.57	17 (0%) 84 82	5, 11, 31, 64	0

All (17) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	D	277	THR	8.4
2	B	281	ALA	4.8
1	C	450	LYS	3.1
1	C	3	VAL	3.1
1	A	313	TYR	2.8
2	B	279	MET	2.7
2	B	146	GLY	2.7
2	B	183[A]	ARG	2.4
2	B	278	GLU	2.4
2	D	276	ASP	2.3
1	C	2	SER	2.2
1	C	7	PRO	2.2
1	C	447	PRO	2.1
2	B	280	ASN	2.1
1	C	313	TYR	2.1
2	D	71	GLU	2.1
2	B	277	THR	2.0

6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

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

6.3 Carbohydrates ⓘ

There are no carbohydrates in this entry.

6.4 Ligands ⓘ

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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	LLDF	B-factors(Å ²)	Q<0.9
7	O	A	609	1/1	0.96	0.22	17.07	7,7,7,7	1
7	O	C	609	1/1	0.98	0.16	8.91	8,8,8,8	1
7	O	A	610	1/1	0.98	0.22	6.46	8,8,8,8	1
7	O	C	606	1/1	0.96	0.09	6.14	14,14,14,14	0
8	GOL	C	702	6/6	0.89	0.13	5.86	21,23,30,43	0
8	GOL	A	702	6/6	0.94	0.10	4.86	19,22,26,29	0
8	GOL	A	703	6/6	0.96	0.12	4.63	18,28,34,35	0
6	CYN	A	605	2/2	0.99	0.07	4.58	6,6,6,6	0
7	O	A	608	1/1	0.98	0.17	4.13	9,9,9,9	1
8	GOL	C	703	6/6	0.91	0.16	3.97	18,25,29,34	0
7	O	C	607	1/1	0.90	0.12	2.39	8,8,8,8	1
7	O	C	610	1/1	0.98	0.12	1.87	7,7,7,7	1
7	O	A	607	1/1	0.96	0.10	1.72	8,8,8,8	1
6	CYN	A	604	2/2	0.99	0.05	1.57	6,6,6,7	0
6	CYN	C	605	2/2	0.99	0.07	0.94	8,8,8,8	0
4	3NI	C	602	1/1	1.00	0.08	0.59	15,15,15,15	0
7	O	C	608	1/1	0.96	0.07	0.44	9,9,9,9	1
6	CYN	C	604	2/2	0.99	0.04	0.02	9,9,9,9	0
4	3NI	A	602	1/1	0.99	0.06	-0.01	12,12,12,12	0
9	MG	C	701	1/1	1.00	0.04	-0.58	8,8,8,8	0
5	CMO	C	603	2/2	0.99	0.04	-0.59	8,8,8,10	0
3	FE2	C	601	1/1	1.00	0.02	-1.83	8,8,8,8	0
5	CMO	A	603	2/2	0.99	0.03	-1.89	6,6,6,7	0
13	SF4	B	309	8/8	1.00	0.02	-1.99	6,6,7,7	0
12	F3S	D	308	7/7	1.00	0.02	-2.30	6,6,7,7	0
13	SF4	D	309	8/8	1.00	0.02	-2.48	7,7,7,7	0
12	F3S	B	308	7/7	1.00	0.02	-2.58	5,5,5,6	0
9	MG	A	701	1/1	1.00	0.03	-3.10	6,6,6,6	0
10	F4S	D	301[A]	7/7	1.00	0.02	-3.10	7,8,9,9	7
11	SF3	D	302[B]	7/7	1.00	0.02	-3.17	7,8,9,11	7

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
10	F4S	B	301[A]	7/7	1.00	0.02	-3.19	6,6,7,7	7
3	FE2	A	601	1/1	1.00	0.02	-3.41	6,6,6,6	0
11	SF3	B	302[B]	7/7	1.00	0.02	-3.42	6,6,7,10	7
7	O	A	606	1/1	0.95	0.08	-	12,12,12,12	0

6.5 Other polymers [i](#)

There are no such residues in this entry.