



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 07:19 AM UTC

PDB ID : 3ZX0 / pdb_00003zx0
Title : NTPDase1 in complex with Heptamolybdate
Authors : Zebisch, M.; Schaefer, P.; Straeter, N.
Deposited on : 2011-08-04
Resolution : 2.50 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

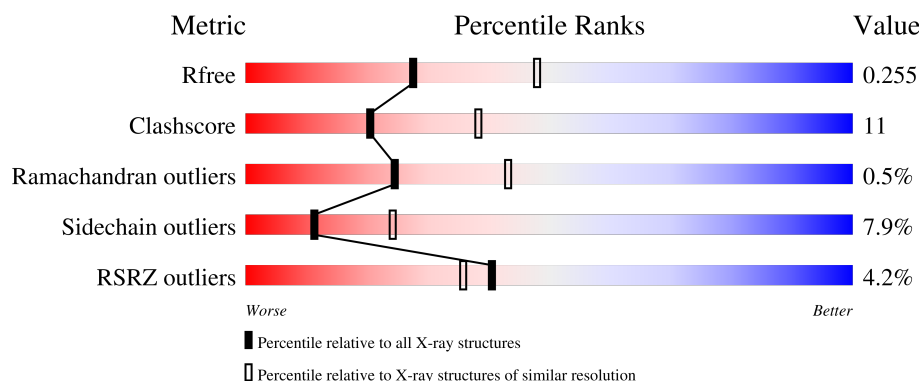
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.50 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	5829 (2.50-2.50)
Clashscore	190562	6492 (2.50-2.50)
Ramachandran outliers	187476	6378 (2.50-2.50)
Sidechain outliers	187428	6380 (2.50-2.50)
RSRZ outliers	180081	5833 (2.50-2.50)

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	452	7% 61% 21% • 15%
1	B	452	4% 63% 21% • 15%
1	C	452	• 61% 22% • 13%
1	D	452	2% 65% 20% • 12%

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

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

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	ACY	A	511	-	-	X	-
3	ACY	C	511	-	-	X	-
4	MO7	B	531[A]	-	-	X	-
4	MO7	C	531[B]	-	-	X	-

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 12434 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 ECTONUCLEOSIDE TRIPHOSPHATE DIPHOSPHOHYDROLASE 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	385	Total	C	N	O	S	0	2	0
			3026	1958	486	562	20			
1	B	386	Total	C	N	O	S	0	1	0
			2994	1935	482	558	19			
1	C	393	Total	C	N	O	S	0	2	0
			3115	2020	499	576	20			
1	D	397	Total	C	N	O	S	0	3	0
			3121	2021	504	576	20			

There are 132 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	15	MET	-	expression tag	UNP P97687
A	16	ALA	-	expression tag	UNP P97687
A	17	HIS	-	expression tag	UNP P97687
A	18	HIS	-	expression tag	UNP P97687
A	19	HIS	-	expression tag	UNP P97687
A	20	HIS	-	expression tag	UNP P97687
A	21	HIS	-	expression tag	UNP P97687
A	22	HIS	-	expression tag	UNP P97687
A	23	VAL	-	expression tag	UNP P97687
A	24	GLY	-	expression tag	UNP P97687
A	25	THR	-	expression tag	UNP P97687
A	26	GLY	-	expression tag	UNP P97687
A	27	SER	-	expression tag	UNP P97687
A	28	ASN	-	expression tag	UNP P97687
A	29	ASP	-	expression tag	UNP P97687
A	30	ASP	-	expression tag	UNP P97687
A	31	ASP	-	expression tag	UNP P97687
A	32	ASP	-	expression tag	UNP P97687
A	33	LYS	-	expression tag	UNP P97687
A	34	SER	-	expression tag	UNP P97687

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Chain	Residue	Modelled	Actual	Comment	Reference
A	35	PRO	-	expression tag	UNP P97687
A	36	ASP	-	expression tag	UNP P97687
A	37	PRO	-	expression tag	UNP P97687
A	80	GLN	LEU	SEE REMARK 999	UNP P97687
A	190	LYS	-	linker	UNP P97687
A	191	THR	-	linker	UNP P97687
A	192	PRO	-	linker	UNP P97687
A	204	GLY	-	linker	UNP P97687
A	205	GLY	-	linker	UNP P97687
A	206	SER	-	linker	UNP P97687
A	220	ILE	VAL	SEE REMARK 999	UNP P97687
A	227	SER	GLN	SEE REMARK 999	UNP P97687
A	331	ILE	PHE	conflict	UNP P97687
B	15	MET	-	expression tag	UNP P97687
B	16	ALA	-	expression tag	UNP P97687
B	17	HIS	-	expression tag	UNP P97687
B	18	HIS	-	expression tag	UNP P97687
B	19	HIS	-	expression tag	UNP P97687
B	20	HIS	-	expression tag	UNP P97687
B	21	HIS	-	expression tag	UNP P97687
B	22	HIS	-	expression tag	UNP P97687
B	23	VAL	-	expression tag	UNP P97687
B	24	GLY	-	expression tag	UNP P97687
B	25	THR	-	expression tag	UNP P97687
B	26	GLY	-	expression tag	UNP P97687
B	27	SER	-	expression tag	UNP P97687
B	28	ASN	-	expression tag	UNP P97687
B	29	ASP	-	expression tag	UNP P97687
B	30	ASP	-	expression tag	UNP P97687
B	31	ASP	-	expression tag	UNP P97687
B	32	ASP	-	expression tag	UNP P97687
B	33	LYS	-	expression tag	UNP P97687
B	34	SER	-	expression tag	UNP P97687
B	35	PRO	-	expression tag	UNP P97687
B	36	ASP	-	expression tag	UNP P97687
B	37	PRO	-	expression tag	UNP P97687
B	80	GLN	LEU	SEE REMARK 999	UNP P97687
B	190	LYS	-	linker	UNP P97687
B	191	THR	-	linker	UNP P97687
B	192	PRO	-	linker	UNP P97687
B	204	GLY	-	linker	UNP P97687
B	205	GLY	-	linker	UNP P97687

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Chain	Residue	Modelled	Actual	Comment	Reference
B	206	SER	-	linker	UNP P97687
B	220	ILE	VAL	SEE REMARK 999	UNP P97687
B	227	SER	GLN	SEE REMARK 999	UNP P97687
B	331	ILE	PHE	conflict	UNP P97687
C	15	MET	-	expression tag	UNP P97687
C	16	ALA	-	expression tag	UNP P97687
C	17	HIS	-	expression tag	UNP P97687
C	18	HIS	-	expression tag	UNP P97687
C	19	HIS	-	expression tag	UNP P97687
C	20	HIS	-	expression tag	UNP P97687
C	21	HIS	-	expression tag	UNP P97687
C	22	HIS	-	expression tag	UNP P97687
C	23	VAL	-	expression tag	UNP P97687
C	24	GLY	-	expression tag	UNP P97687
C	25	THR	-	expression tag	UNP P97687
C	26	GLY	-	expression tag	UNP P97687
C	27	SER	-	expression tag	UNP P97687
C	28	ASN	-	expression tag	UNP P97687
C	29	ASP	-	expression tag	UNP P97687
C	30	ASP	-	expression tag	UNP P97687
C	31	ASP	-	expression tag	UNP P97687
C	32	ASP	-	expression tag	UNP P97687
C	33	LYS	-	expression tag	UNP P97687
C	34	SER	-	expression tag	UNP P97687
C	35	PRO	-	expression tag	UNP P97687
C	36	ASP	-	expression tag	UNP P97687
C	37	PRO	-	expression tag	UNP P97687
C	80	GLN	LEU	SEE REMARK 999	UNP P97687
C	190	LYS	-	linker	UNP P97687
C	191	THR	-	linker	UNP P97687
C	192	PRO	-	linker	UNP P97687
C	204	GLY	-	linker	UNP P97687
C	205	GLY	-	linker	UNP P97687
C	206	SER	-	linker	UNP P97687
C	220	ILE	VAL	SEE REMARK 999	UNP P97687
C	227	SER	GLN	SEE REMARK 999	UNP P97687
C	331	ILE	PHE	conflict	UNP P97687
D	15	MET	-	expression tag	UNP P97687
D	16	ALA	-	expression tag	UNP P97687
D	17	HIS	-	expression tag	UNP P97687
D	18	HIS	-	expression tag	UNP P97687
D	19	HIS	-	expression tag	UNP P97687

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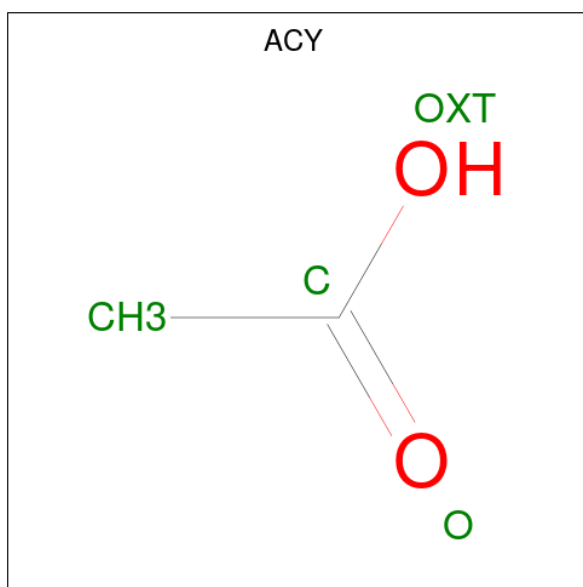
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Chain	Residue	Modelled	Actual	Comment	Reference
D	20	HIS	-	expression tag	UNP P97687
D	21	HIS	-	expression tag	UNP P97687
D	22	HIS	-	expression tag	UNP P97687
D	23	VAL	-	expression tag	UNP P97687
D	24	GLY	-	expression tag	UNP P97687
D	25	THR	-	expression tag	UNP P97687
D	26	GLY	-	expression tag	UNP P97687
D	27	SER	-	expression tag	UNP P97687
D	28	ASN	-	expression tag	UNP P97687
D	29	ASP	-	expression tag	UNP P97687
D	30	ASP	-	expression tag	UNP P97687
D	31	ASP	-	expression tag	UNP P97687
D	32	ASP	-	expression tag	UNP P97687
D	33	LYS	-	expression tag	UNP P97687
D	34	SER	-	expression tag	UNP P97687
D	35	PRO	-	expression tag	UNP P97687
D	36	ASP	-	expression tag	UNP P97687
D	37	PRO	-	expression tag	UNP P97687
D	80	GLN	LEU	SEE REMARK 999	UNP P97687
D	190	LYS	-	linker	UNP P97687
D	191	THR	-	linker	UNP P97687
D	192	PRO	-	linker	UNP P97687
D	204	GLY	-	linker	UNP P97687
D	205	GLY	-	linker	UNP P97687
D	206	SER	-	linker	UNP P97687
D	220	ILE	VAL	SEE REMARK 999	UNP P97687
D	227	SER	GLN	SEE REMARK 999	UNP P97687
D	331	ILE	PHE	conflict	UNP P97687

- Molecule 2 is CHLORIDE ION (CCD ID: CL) (formula: Cl).

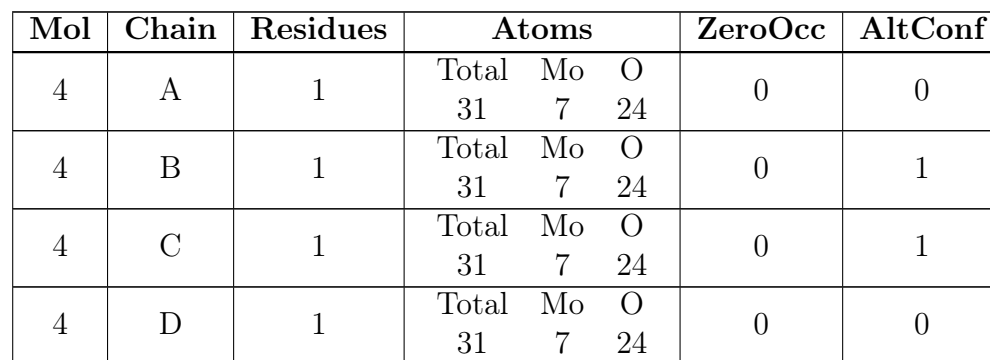
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	4	Total Cl 4 4	0	0
2	B	5	Total Cl 5 5	0	0
2	C	5	Total Cl 5 5	0	0
2	D	8	Total Cl 8 8	0	0

- Molecule 3 is ACETIC ACID (CCD ID: ACY) (formula: C₂H₄O₂).



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

- Molecule 4 is bis(mu4-oxo)-bis(mu3-oxo)-octakis(mu2-oxo)-dodecaoxo-heptamolybdenum (VI) (CCD ID: MO7) (formula: Mo₇O₂₄).

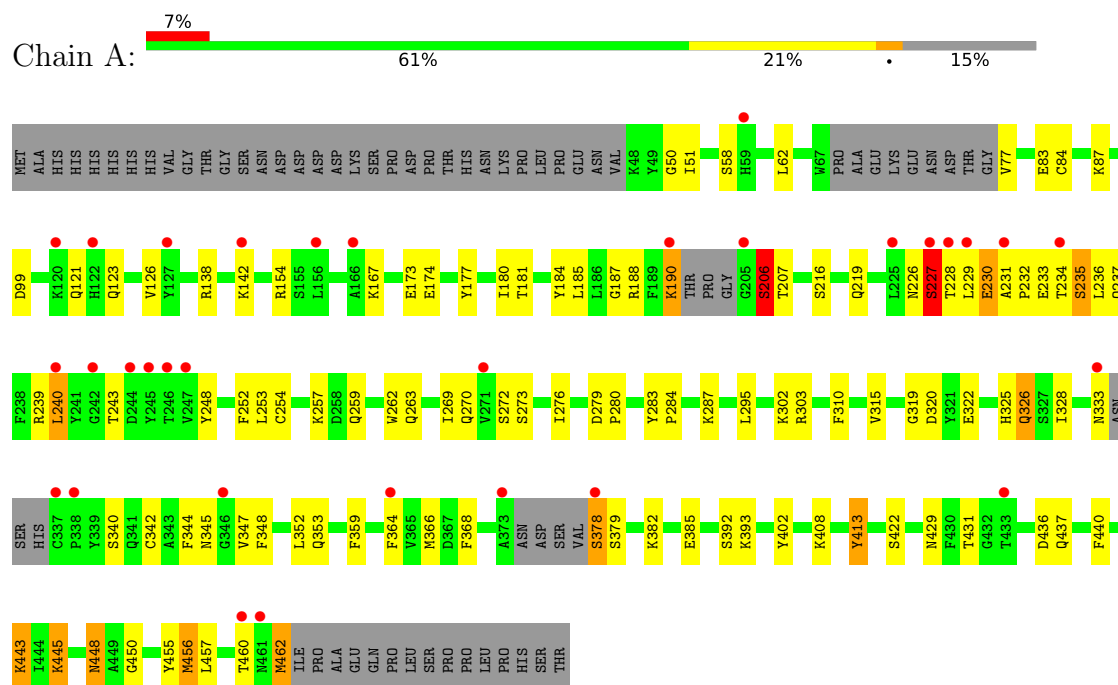


- | Mol | Chain | Residues | Atoms | ZeroOcc | AltConf |
|-----|-------|----------|-----------------|---------|---------|
| 5 | B | 1 | Total Na
1 1 | 0 | 0 |
| 5 | C | 2 | Total Na
2 2 | 0 | 0 |
| 5 | D | 1 | Total Na
1 1 | 0 | 0 |

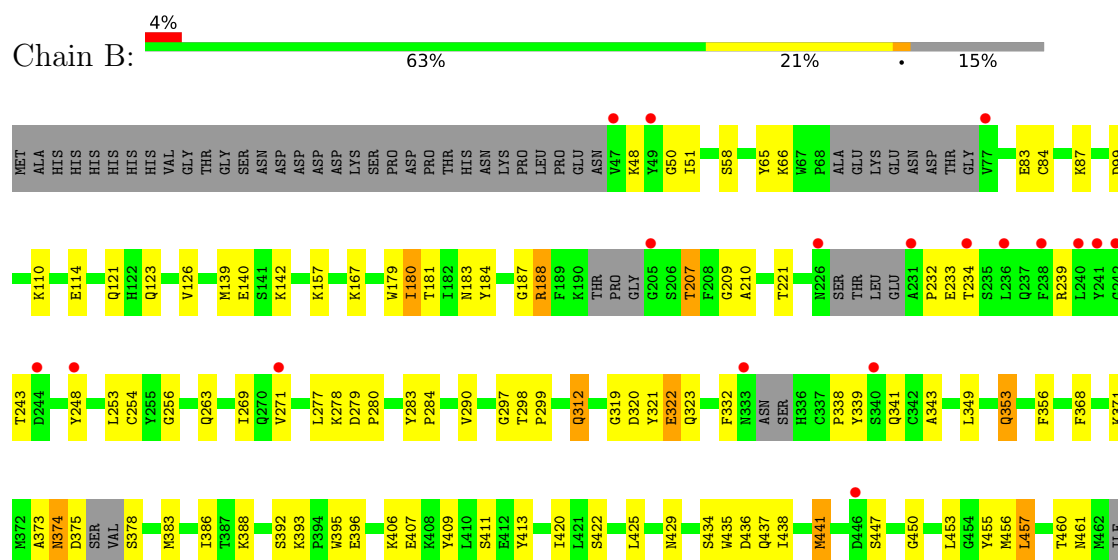
3 Residue-property plots

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

• Molecule 1: ECTONUCLEOSIDE TRIPHOSPHATE DIPHOSPHOHYDROLASE 1

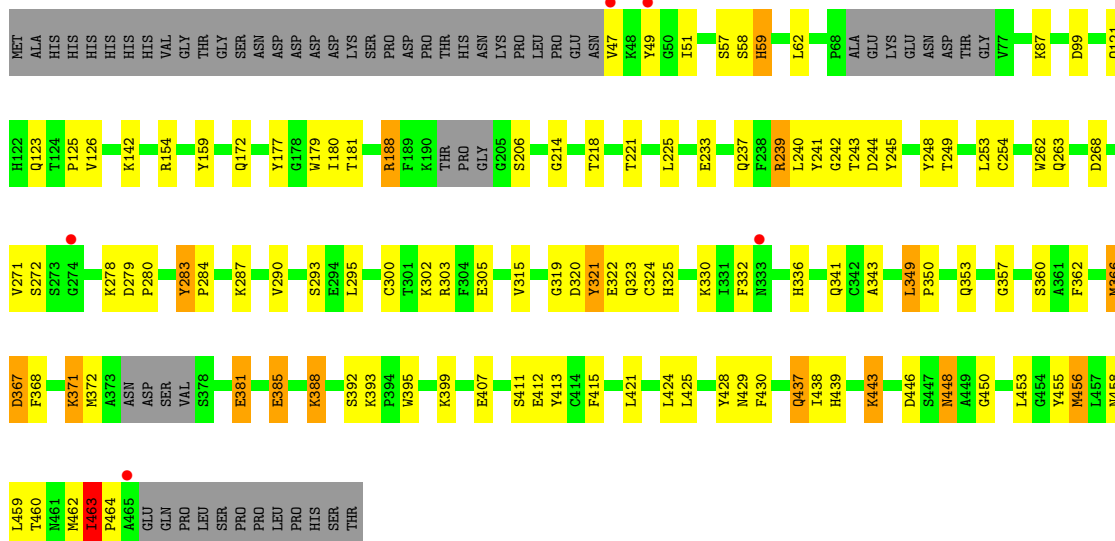


• Molecule 1: ECTONUCLEOSIDE TRIPHOSPHATE DIPHOSPHOHYDROLASE 1

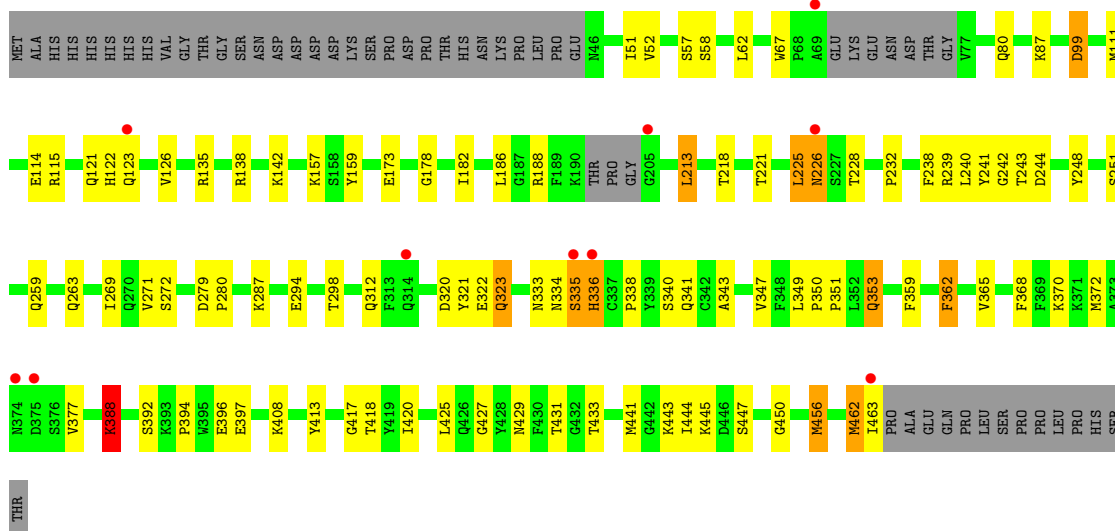


PRO
ALA
GLU
GLN
PRO
LEU
SER
PRO
PRO
LEU
PRO
HIS
SER
THR

• Molecule 1: ECTONUCLEOSIDE TRIPHOSPHATE DIPHOSPHOHYDROLASE 1



• Molecule 1: ECTONUCLEOSIDE TRIPHOSPHATE DIPHOSPHOHYDROLASE 1



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	163.81Å 80.27Å 164.92Å 90.00° 117.92° 90.00°	Depositor
Resolution (Å)	145.73 – 2.50 145.72 – 2.50	Depositor EDS
% Data completeness (in resolution range)	87.6 (145.73-2.50) 87.9 (145.72-2.50)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.21 (at 2.51Å)	Xtriage
Refinement program	REFMAC 5.6.0117	Depositor
R, R_{free}	0.213 , 0.257 0.213 , 0.255	Depositor DCC
R_{free} test set	1157 reflections (1.87%)	wwPDB-VP
Wilson B-factor (Å ²)	57.4	Xtriage
Anisotropy	0.043	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 56.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.007 for h,-k,-h-l	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	12434	wwPDB-VP
Average B, all atoms (Å ²)	72.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.75% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: MO7, NA, CL, ACY

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	1.00	0/3110	1.19	18/4203 (0.4%)
1	B	0.98	1/3073 (0.0%)	1.10	8/4158 (0.2%)
1	C	1.09	5/3204 (0.2%)	1.26	24/4334 (0.6%)
1	D	1.14	5/3213 (0.2%)	1.25	26/4351 (0.6%)
All	All	1.06	11/12600 (0.1%)	1.20	76/17046 (0.4%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1

All (11) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	135	ARG	CZ-NH1	-7.43	1.22	1.32
1	D	135	ARG	CZ-NH2	-7.07	1.24	1.33
1	C	59	HIS	CG-CD2	6.53	1.43	1.35
1	C	59	HIS	ND1-CE1	5.65	1.38	1.32
1	D	336	HIS	CG-CD2	5.54	1.42	1.35
1	C	237	GLN	CA-C	-5.43	1.46	1.52
1	D	213	LEU	CA-C	-5.28	1.46	1.52
1	D	122	HIS	CG-CD2	5.13	1.41	1.35
1	C	336	HIS	CG-CD2	5.08	1.41	1.35
1	C	283	TYR	CA-C	-5.04	1.47	1.53
1	B	395	TRP	C-O	5.00	1.30	1.24

All (76) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	135	ARG	NH1-CZ-NH2	-8.38	108.40	119.30
1	C	360	SER	CB-CA-C	-8.21	107.10	116.54
1	C	121	GLN	N-CA-C	8.02	119.80	111.14
1	A	207	THR	N-CA-C	7.63	121.49	109.81
1	D	67	TRP	N-CA-C	7.21	114.70	108.22
1	A	234	THR	N-CA-C	-7.12	104.48	113.02
1	D	135	ARG	NE-CZ-NH2	7.07	125.56	119.20
1	A	413	TYR	N-CA-C	6.99	118.89	111.28
1	C	413	TYR	N-CA-C	6.98	119.74	111.71
1	B	121	GLN	N-CA-C	6.98	118.96	111.36
1	C	180	ILE	N-CA-C	6.81	117.51	110.36
1	C	321	TYR	N-CA-C	6.71	119.16	111.11
1	A	359	PHE	N-CA-C	6.71	117.33	108.07
1	A	448	ASN	N-CA-C	6.54	119.97	110.28
1	B	411	SER	N-CA-C	6.40	119.07	111.71
1	D	138	ARG	CD-NE-CZ	6.25	133.15	124.40
1	A	393	LYS	CA-C-N	-6.23	113.25	119.92
1	A	393	LYS	C-N-CA	-6.23	113.25	119.92
1	C	350	PRO	CA-C-N	-6.19	113.40	119.78
1	C	350	PRO	C-N-CA	-6.19	113.40	119.78
1	D	362	PHE	N-CA-C	-6.18	104.55	111.28
1	D	294	GLU	N-CA-C	-6.17	104.48	111.14
1	A	121	GLN	N-CA-C	6.13	118.04	111.36
1	A	276	ILE	CB-CA-C	-6.12	100.60	110.28
1	A	138	ARG	NE-CZ-NH2	-5.99	113.81	119.20
1	C	366	MET	N-CA-C	-5.97	104.90	111.82
1	A	364	PHE	N-CA-CB	5.87	119.27	110.22
1	C	450	GLY	N-CA-C	-5.84	99.34	113.18
1	D	159	TYR	CA-C-N	-5.80	112.58	119.84
1	D	159	TYR	C-N-CA	-5.80	112.58	119.84
1	C	367	ASP	N-CA-C	5.80	117.60	111.28
1	D	121	GLN	N-CA-C	5.80	118.82	111.69
1	B	450	GLY	N-CA-C	-5.76	102.83	111.19
1	D	226	ASN	N-CA-C	5.72	122.98	110.80
1	B	207	THR	N-CA-C	5.67	118.03	109.41
1	A	379	SER	N-CA-C	5.66	117.37	110.41
1	D	450	GLY	N-CA-C	-5.65	102.50	110.75
1	C	448	ASN	N-CA-C	5.54	118.26	110.23
1	A	180	ILE	CB-CA-C	-5.53	104.89	111.97
1	B	438	ILE	CB-CA-C	-5.51	104.30	110.96
1	D	340	SER	N-CA-C	-5.49	105.38	111.36
1	C	268	ASP	N-CA-C	5.49	117.34	111.36
1	D	287	LYS	CA-CB-CG	5.48	125.06	114.10

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	138	ARG	NE-CZ-NH1	5.44	126.94	121.50
1	D	418	THR	N-CA-C	-5.43	105.44	111.36
1	C	324	CYS	N-CA-C	-5.41	105.07	110.97
1	C	425	LEU	N-CA-C	5.40	116.97	111.14
1	D	388	LYS	N-CA-C	-5.39	105.30	111.07
1	C	206	SER	N-CA-C	5.38	117.03	108.79
1	D	114	GLU	N-CA-C	-5.38	106.56	113.23
1	A	345	ASN	N-CA-C	5.35	118.81	111.54
1	D	80	GLN	N-CA-C	-5.34	101.28	109.76
1	A	310	PHE	CA-C-N	5.33	127.85	120.29
1	A	310	PHE	C-N-CA	5.33	127.85	120.29
1	D	138	ARG	NE-CZ-NH2	-5.32	114.42	119.20
1	C	362	PHE	N-CA-C	-5.31	105.57	111.36
1	D	251	SER	CA-CB-OG	-5.31	100.49	111.10
1	D	347	VAL	N-CA-C	5.30	115.93	109.30
1	C	349	LEU	CA-C-N	-5.28	114.94	120.38
1	C	349	LEU	C-N-CA	-5.28	114.94	120.38
1	B	256	GLY	N-CA-C	-5.27	105.79	112.54
1	C	159	TYR	CA-C-N	-5.26	113.26	119.84
1	C	159	TYR	C-N-CA	-5.26	113.26	119.84
1	D	67	TRP	CA-C-N	-5.21	114.55	119.76
1	D	67	TRP	C-N-CA	-5.21	114.55	119.76
1	A	138	ARG	CD-NE-CZ	5.20	131.68	124.40
1	C	412	GLU	CB-CA-C	-5.18	99.78	109.72
1	C	463	ILE	CA-C-N	-5.16	115.26	120.31
1	C	463	ILE	C-N-CA	-5.16	115.26	120.31
1	D	372	MET	CB-CG-SD	-5.15	97.25	112.70
1	D	173	GLU	CA-C-N	-5.10	113.05	120.29
1	D	173	GLU	C-N-CA	-5.10	113.05	120.29
1	B	187	GLY	N-CA-C	-5.09	108.80	115.47
1	A	364	PHE	N-CA-C	5.09	117.57	111.71
1	B	435	TRP	N-CA-C	5.02	117.40	111.33
1	C	424	LEU	N-CA-C	5.02	116.83	111.36

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	206	SER	Peptide

5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3026	0	2900	80	0
1	B	2994	0	2847	79	0
1	C	3115	0	3024	61	0
1	D	3121	0	3007	47	0
2	A	4	0	0	1	0
2	B	5	0	0	1	0
2	C	5	0	0	3	0
2	D	8	0	0	3	0
3	A	4	0	3	3	0
3	B	8	0	6	1	0
3	C	8	0	6	3	0
3	D	8	0	6	2	0
4	A	31	0	0	1	0
4	B	31	0	0	8	0
4	C	31	0	0	13	0
4	D	31	0	0	1	0
5	B	1	0	0	0	0
5	C	2	0	0	0	0
5	D	1	0	0	0	0
All	All	12434	0	11799	271	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 11.

All (271) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:230:GLU:C	1:A:232:PRO:HD3	1.53	1.33
1:D:225:LEU:HD13	1:D:353:GLN:NE2	1.56	1.20
1:A:167:LYS:HD2	1:B:232:PRO:HG2	1.15	1.14
1:D:225:LEU:HD13	1:D:353:GLN:HE21	0.98	1.12
1:B:50:GLY:HA3	1:B:456:MET:HE1	1.30	1.07
1:A:231:ALA:N	1:A:232:PRO:HD3	1.71	1.04
1:A:366:MET:HE2	3:A:511:ACY:H1	1.42	1.00
1:A:50:GLY:HA3	1:A:456:MET:CE	1.93	0.97

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:167:LYS:CD	1:B:232:PRO:HG2	1.94	0.95
4:C:531[B]:MO7:O21	4:C:531[B]:MO7:O17	1.86	0.92
1:C:225:LEU:HG	1:C:353:GLN:NE2	1.86	0.91
1:A:230:GLU:C	1:A:232:PRO:CD	2.45	0.88
1:A:167:LYS:HD2	1:B:232:PRO:CG	2.04	0.87
1:D:225:LEU:CD1	1:D:353:GLN:NE2	2.39	0.85
1:A:226:ASN:O	1:A:227:SER:OG	1.95	0.84
1:C:262[B]:TRP:HE3	1:C:295:LEU:HD12	1.44	0.82
1:A:366:MET:CE	3:A:511:ACY:H1	2.09	0.82
1:B:322:GLU:HA	1:B:322:GLU:OE1	1.79	0.80
1:C:407:GLU:O	1:C:411:SER:HB2	1.82	0.80
1:B:407:GLU:HG3	4:C:531[B]:MO7:O18	1.82	0.79
4:C:531[B]:MO7:O21	4:C:531[B]:MO7:O18	2.01	0.79
4:B:531[A]:MO7:O22	4:B:531[A]:MO7:O6	2.02	0.78
1:D:52:VAL:HG23	1:D:456:MET:HE3	1.67	0.77
1:A:231:ALA:N	1:A:232:PRO:CD	2.49	0.74
1:C:233:GLU:HG2	2:C:506:CL:CL	2.26	0.73
1:C:279:ASP:OD1	1:C:280:PRO:HD2	1.89	0.72
1:C:188:ARG:CG	1:C:188:ARG:HH11	2.03	0.71
1:D:239:ARG:HE	1:D:242:GLY:HA2	1.55	0.71
1:A:50:GLY:HA3	1:A:456:MET:HE3	1.73	0.70
1:B:140:GLU:OE2	1:B:297:GLY:O	2.09	0.70
1:B:65:TYR:HB2	1:B:456:MET:HE2	1.74	0.70
1:B:406:LYS:HG2	4:B:531[A]:MO7:O4	1.92	0.70
1:B:434:SER:O	1:B:437:GLN:HG2	1.93	0.68
1:A:177:TYR:CE1	1:A:455:TYR:HA	2.30	0.67
4:C:531[B]:MO7:O22	4:C:531[B]:MO7:O24	2.13	0.67
1:A:50:GLY:HA3	1:A:456:MET:HE1	1.77	0.67
1:B:290:VAL:O	1:B:312:GLN:HB2	1.95	0.67
1:B:368:PHE:CG	1:B:413:TYR:CE2	2.83	0.67
1:C:366:MET:CE	3:C:511:ACY:H1	2.25	0.66
1:B:368:PHE:CB	1:B:413:TYR:HE2	2.09	0.66
1:C:172:GLN:HG2	1:C:249:THR:HG23	1.78	0.65
1:C:262[B]:TRP:CE3	1:C:295:LEU:HD12	2.29	0.65
1:D:462:MET:O	1:D:463:ILE:CB	2.44	0.65
1:D:239:ARG:NE	1:D:242:GLY:HA2	2.12	0.65
1:B:341:GLN:NE2	1:B:349:LEU:O	2.23	0.64
1:C:283:TYR:HB3	1:C:393:LYS:O	1.96	0.64
1:B:253:LEU:O	1:B:254:CYS:HB2	1.96	0.64
1:D:365:VAL:HG11	1:D:420[A]:ILE:HD12	1.78	0.64
1:A:287:LYS:HA	1:A:315:VAL:O	1.98	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:50:GLY:CA	1:B:456:MET:HE1	2.17	0.64
1:B:50:GLY:HA3	1:B:456:MET:CE	2.19	0.63
1:A:366:MET:HE2	3:A:511:ACY:CH3	2.25	0.63
1:A:408:LYS:HD3	4:A:531:MO7:O19	1.98	0.63
1:B:409:TYR:HB3	1:B:413:TYR:HE1	1.63	0.63
1:A:378:SER:HB2	1:A:382:LYS:HE3	1.81	0.63
1:B:368:PHE:CG	1:B:413:TYR:HE2	2.16	0.63
1:A:174:GLU:OE2	1:A:219:GLN:NE2	2.32	0.62
1:A:279:ASP:OD1	1:A:280:PRO:HD2	1.97	0.62
1:D:239:ARG:HA	1:D:243:THR:O	1.99	0.62
1:C:181:THR:HG23	1:C:453:LEU:HB3	1.82	0.62
1:D:279:ASP:OD1	1:D:280:PRO:HD2	1.99	0.62
4:C:531[B]:MO7:O21	4:C:531[B]:MO7:MO6	1.70	0.62
1:C:51:ILE:HB	1:C:126:VAL:HG22	1.83	0.61
1:C:225:LEU:HG	1:C:353:GLN:HE21	1.60	0.61
4:C:531[B]:MO7:O11	4:C:531[B]:MO7:O14	2.17	0.61
4:C:531[B]:MO7:MO7	4:C:531[B]:MO7:O23	1.71	0.61
4:B:531[A]:MO7:MO7	4:B:531[A]:MO7:O23	1.71	0.61
1:A:173:GLU:OE1	1:B:233:GLU:HB2	2.00	0.61
1:A:262[B]:TRP:HE3	1:A:295:LEU:HD13	1.65	0.61
1:D:408:LYS:NZ	4:D:531:MO7:O23	2.34	0.61
1:B:209:GLY:HA3	1:B:356:PHE:CD2	2.36	0.61
1:B:184:TYR:CD2	1:B:457:LEU:HD21	2.35	0.60
1:B:409:TYR:O	1:B:413:TYR:HD1	1.84	0.60
1:C:188:ARG:HH11	1:C:188:ARG:HG2	1.66	0.60
1:A:284:PRO:HD3	1:A:319:GLY:HA3	1.83	0.60
1:C:57:SER:HA	2:C:503:CL:CL	2.38	0.60
4:B:531[A]:MO7:O22	4:B:531[A]:MO7:MO6	1.72	0.60
1:C:367:ASP:OD2	1:C:371:LYS:HE3	2.00	0.60
1:D:320:ASP:HB3	1:D:323:GLN:NE2	2.17	0.60
4:B:531[A]:MO7:MO6	4:B:531[A]:MO7:O18	1.72	0.60
4:C:531[B]:MO7:O14	4:C:531[B]:MO7:MO4	1.73	0.60
4:C:531[B]:MO7:O6	4:C:531[B]:MO7:MO2	1.73	0.60
1:A:174:GLU:OE2	1:A:219:GLN:CD	2.44	0.60
1:C:366:MET:HE2	3:C:511:ACY:H1	1.82	0.59
1:C:239:ARG:NH1	1:C:242:GLY:HA2	2.16	0.59
1:C:239:ARG:HA	1:C:243:THR:O	2.03	0.59
1:D:52:VAL:CG2	1:D:456:MET:HE3	2.32	0.59
1:D:186:LEU:HB2	1:D:188:ARG:HG2	1.85	0.59
4:B:531[A]:MO7:O11	4:B:531[A]:MO7:MO3	1.73	0.59
4:B:531[A]:MO7:O14	4:B:531[A]:MO7:MO4	1.72	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:225:LEU:HG	1:C:353:GLN:HE22	1.62	0.59
1:B:409:TYR:O	1:B:413:TYR:CD1	2.56	0.58
1:D:396:GLU:HG2	2:D:508:CL:CL	2.40	0.58
1:A:262[B]:TRP:HE3	1:A:295:LEU:CD1	2.15	0.58
1:B:368:PHE:CD1	1:B:413:TYR:CD2	2.91	0.58
1:B:321:TYR:HB3	1:B:388:LYS:HG3	1.85	0.58
1:A:187:GLY:O	1:A:190:LYS:HD2	2.04	0.57
1:A:248:TYR:CD1	1:A:248:TYR:C	2.83	0.57
1:C:303:ARG:HD3	1:D:338:PRO:O	2.04	0.57
1:B:407:GLU:OE2	4:C:531[B]:MO7:O21	2.21	0.57
1:A:270:GLN:O	1:A:273:SER:OG	2.12	0.57
1:D:321:TYR:HB3	1:D:388:LYS:HG2	1.85	0.57
1:A:230:GLU:HB3	1:A:232:PRO:CD	2.34	0.57
1:B:453:LEU:O	1:B:456:MET:HB3	2.05	0.56
1:C:177:TYR:OH	1:C:458:ASN:ND2	2.32	0.56
1:C:381:GLU:O	1:C:385:GLU:HG2	2.07	0.55
1:B:341:GLN:HG2	1:B:349:LEU:O	2.06	0.55
1:C:253:LEU:O	1:C:254:CYS:HB2	2.08	0.54
1:B:407:GLU:CG	4:C:531[B]:MO7:O21	2.56	0.54
1:A:320:ASP:OD1	1:A:322:GLU:HB2	2.07	0.54
1:B:425:LEU:O	1:B:429:ASN:HA	2.07	0.54
1:C:368:PHE:CE2	1:C:372:MET:CE	2.91	0.54
1:A:326:GLN:OE1	1:A:326:GLN:HA	2.07	0.54
1:D:232:PRO:HD2	2:D:507:CL:CL	2.45	0.54
1:A:263:GLN:OE1	1:A:303:ARG:NH1	2.42	0.53
1:C:395:TRP:CE2	1:C:399:LYS:HE2	2.44	0.53
1:D:228:THR:HB	1:D:351:PRO:HD2	1.91	0.53
1:B:320:ASP:HB3	1:B:323:GLN:NE2	2.24	0.53
1:C:428:TYR:O	1:C:429:ASN:HB2	2.09	0.52
1:A:216:SER:HA	1:A:259:GLN:HG2	1.90	0.52
1:D:259:GLN:O	1:D:263:GLN:HG3	2.09	0.52
1:B:368:PHE:CD1	1:B:413:TYR:HD2	2.28	0.52
1:C:320:ASP:HB3	1:C:323:GLN:HE21	1.76	0.51
1:A:230:GLU:HA	1:A:230:GLU:OE1	2.10	0.51
1:B:338:PRO:HG2	1:B:339:TYR:CE2	2.46	0.51
1:A:253:LEU:O	1:A:254:CYS:HB2	2.11	0.51
1:C:458:ASN:HA	1:C:463:ILE:HD11	1.92	0.51
1:A:230:GLU:HB3	1:A:232:PRO:HD3	1.91	0.50
1:A:230:GLU:O	1:A:232:PRO:HD3	2.01	0.50
1:D:429:ASN:C	1:D:431:THR:H	2.19	0.50
1:C:284:PRO:HD3	1:C:319:GLY:HA3	1.92	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:99:ASP:OD1	1:A:99:ASP:N	2.42	0.50
1:A:83:GLU:HG2	1:A:84:CYS:N	2.27	0.50
1:A:177:TYR:CE2	1:A:455:TYR:HD2	2.30	0.49
1:A:322:GLU:OE1	1:A:322:GLU:HA	2.11	0.49
1:D:370:LYS:HE2	1:D:377:VAL:CB	2.43	0.49
1:C:188:ARG:CG	1:C:188:ARG:NH1	2.65	0.49
1:D:225:LEU:CD1	1:D:353:GLN:HE21	1.93	0.49
1:B:239:ARG:HA	1:B:243:THR:O	2.13	0.49
1:D:240:LEU:O	1:D:241:TYR:HB2	2.13	0.49
1:A:235:SER:O	1:A:236:LEU:HD23	2.12	0.49
1:C:357:GLY:HA2	1:C:439:HIS:O	2.13	0.49
1:A:283:TYR:O	1:A:284:PRO:C	2.56	0.48
1:B:283:TYR:O	1:B:284:PRO:C	2.56	0.48
1:D:417:GLY:O	3:D:511:ACY:H3	2.14	0.48
1:A:228:THR:CB	1:B:139:MET:HG2	2.43	0.48
1:B:407:GLU:HG3	4:C:531[B]:MO7:O21	2.14	0.48
1:C:395:TRP:NE1	1:C:399:LYS:HE2	2.28	0.48
1:D:368:PHE:CD2	1:D:413:TYR:CD2	3.02	0.48
1:D:87:LYS:HB2	1:D:87:LYS:HE3	1.65	0.48
1:A:228:THR:CB	1:B:139:MET:CG	2.92	0.47
1:B:460:THR:O	1:B:461:ASN:HB2	2.13	0.47
1:D:157:LYS:HB3	1:D:157:LYS:HE2	1.47	0.47
1:B:284:PRO:HD3	1:B:319:GLY:HA3	1.95	0.47
1:D:99:ASP:OD1	1:D:99:ASP:N	2.44	0.47
1:D:178:GLY:O	1:D:182:ILE:HG23	2.14	0.47
1:A:342:CYS:HB3	1:A:347:VAL:O	2.13	0.47
1:C:240:LEU:HB2	1:C:245:TYR:CE2	2.50	0.47
1:C:248:TYR:CD1	1:C:248:TYR:C	2.91	0.47
1:B:353:GLN:O	1:B:353:GLN:HG3	2.15	0.47
1:A:77:VAL:HA	1:A:184:TYR:OH	2.15	0.47
1:C:188:ARG:NH1	1:C:188:ARG:HG3	2.29	0.47
4:C:531[B]:MO7:O6	4:C:531[B]:MO7:O16	2.32	0.47
1:C:287:LYS:HA	1:C:315:VAL:O	2.14	0.47
1:B:51:ILE:HB	1:B:126:VAL:HG22	1.96	0.47
1:B:221:THR:HA	1:B:248:TYR:O	2.15	0.47
1:B:140:GLU:HG3	1:B:299:PRO:HG3	1.96	0.47
1:B:167:LYS:HE2	1:B:455:TYR:OH	2.14	0.47
1:B:434:SER:O	1:B:437:GLN:CG	2.62	0.46
1:B:373:ALA:HB2	1:B:386:ILE:CD1	2.45	0.46
1:A:230:GLU:HB2	1:A:348:PHE:CZ	2.50	0.46
1:B:65:TYR:CE1	1:B:453:LEU:HD13	2.51	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:167:LYS:NZ	1:B:232:PRO:HB2	2.31	0.46
1:C:214:GLY:HA3	2:C:501:CL:CL	2.53	0.46
1:A:368:PHE:CE2	1:A:413:TYR:HD2	2.34	0.46
1:D:425:LEU:O	1:D:431:THR:HG23	2.16	0.46
1:A:232:PRO:O	1:A:233:GLU:CB	2.64	0.46
1:A:62:LEU:C	1:A:62:LEU:HD23	2.41	0.45
1:A:51:ILE:HB	1:A:126:VAL:HG22	1.98	0.45
1:A:167:LYS:HZ2	1:B:232:PRO:HB2	1.82	0.45
1:B:254:CYS:O	1:B:263:GLN:NE2	2.49	0.45
1:C:240:LEU:HB2	1:C:245:TYR:HE2	1.81	0.45
1:D:341:GLN:HG2	1:D:349:LEU:O	2.15	0.45
1:C:322:GLU:O	1:C:325:HIS:HB3	2.16	0.45
1:B:183:ASN:OD1	1:B:207:THR:HB	2.17	0.45
1:C:99:ASP:OD1	1:C:99:ASP:N	2.44	0.45
1:A:269:ILE:O	1:A:269:ILE:HG23	2.16	0.45
1:B:110:LYS:HZ2	1:B:114:GLU:HG2	1.82	0.45
1:A:231:ALA:CB	1:B:139:MET:SD	3.06	0.44
1:A:443:LYS:HE2	1:A:448:ASN:OD1	2.17	0.44
1:C:320:ASP:HB3	1:C:323:GLN:NE2	2.32	0.44
1:C:455:TYR:CE1	1:C:459:LEU:HD11	2.52	0.44
1:C:188:ARG:HD2	1:C:188:ARG:HA	1.72	0.44
1:C:456:MET:HE2	1:C:456:MET:HB3	1.55	0.44
1:A:402:TYR:HA	2:A:505:CL:CL	2.55	0.44
1:C:332:PHE:CZ	3:C:512:ACY:H2	2.52	0.44
1:D:51:ILE:HB	1:D:126:VAL:HG22	2.00	0.44
1:C:87:LYS:HB2	1:C:87:LYS:HE3	1.74	0.44
1:B:87:LYS:HE3	1:B:87:LYS:HB2	1.70	0.44
1:B:374:ASN:O	1:B:375:ASP:C	2.61	0.44
1:C:321:TYR:HB2	1:C:388:LYS:HA	2.00	0.44
1:B:269:ILE:HG23	1:B:269:ILE:O	2.17	0.44
1:C:302:LYS:HA	1:C:305:GLU:HG3	1.99	0.44
1:C:460:THR:OG1	1:C:462:MET:HG3	2.18	0.44
1:D:394:PRO:O	1:D:397:GLU:HB3	2.18	0.44
1:A:230:GLU:O	1:A:232:PRO:CD	2.62	0.44
1:B:338:PRO:HG2	1:B:339:TYR:CD2	2.53	0.44
1:B:409:TYR:HB3	1:B:413:TYR:CE1	2.49	0.44
1:A:240:LEU:HD23	1:A:240:LEU:HA	1.52	0.43
1:B:99:ASP:OD1	1:B:99:ASP:N	2.49	0.43
1:C:49:TYR:O	1:C:125:PRO:HD2	2.18	0.43
1:B:279:ASP:OD1	1:B:280:PRO:HD2	2.18	0.43
1:A:429:ASN:C	1:A:431:THR:H	2.26	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:396:GLU:HG2	2:B:506:CL:CL	2.55	0.43
1:C:415:PHE:CD1	1:C:415:PHE:C	2.97	0.43
1:D:111:MET:O	1:D:115:ARG:HB2	2.19	0.43
1:A:457:LEU:H	1:A:457:LEU:HG	1.68	0.43
1:A:368:PHE:CD2	1:A:413:TYR:CD2	3.07	0.43
1:B:209:GLY:HA3	1:B:356:PHE:CE2	2.54	0.43
1:B:320:ASP:OD1	1:B:322:GLU:HB2	2.18	0.43
4:B:531[A]:MO7:O18	4:B:531[A]:MO7:O20	2.37	0.43
1:C:437:GLN:HE21	1:C:437:GLN:HB3	1.66	0.43
1:A:325:HIS:O	1:A:326:GLN:C	2.59	0.42
1:A:252:PHE:CD2	1:A:344:PHE:CZ	3.07	0.42
1:B:277:LEU:HA	1:B:277:LEU:HD12	1.81	0.42
1:B:441:MET:HE2	1:B:441:MET:HB3	1.77	0.42
1:B:323:GLN:HE21	1:B:323:GLN:HB2	1.55	0.42
1:C:241:TYR:CE2	1:C:464:PRO:HD2	2.55	0.42
1:A:368:PHE:CD2	1:A:413:TYR:HD2	2.37	0.42
1:B:179:TRP:HA	1:B:210:ALA:HB2	2.01	0.42
1:C:443:LYS:HE3	1:C:446:ASP:HA	2.02	0.42
1:A:185:LEU:O	1:A:445:LYS:HD2	2.20	0.41
1:A:269:ILE:O	1:A:269:ILE:CG2	2.68	0.41
1:C:341:GLN:HG2	1:C:349:LEU:O	2.20	0.41
1:D:213:LEU:HD12	1:D:218:THR:HB	2.02	0.41
1:D:443:LYS:HA	1:D:447:SER:O	2.20	0.41
1:A:188:ARG:NH2	1:A:206:SER:O	2.54	0.41
1:D:225:LEU:HA	1:D:225:LEU:HD12	1.78	0.41
1:D:269:ILE:HD12	1:D:269:ILE:HA	1.91	0.41
1:D:335:SER:HB3	1:D:336:HIS:CD2	2.55	0.41
1:B:320:ASP:HB3	1:B:323:GLN:HE21	1.84	0.41
1:A:87:LYS:HE3	1:A:87:LYS:HB2	1.76	0.41
1:A:177:TYR:CE2	1:A:455:TYR:CD2	3.09	0.41
1:A:462:MET:HE2	1:A:462:MET:HA	2.02	0.41
1:D:57:SER:HA	2:D:503:CL:CL	2.58	0.41
1:A:181:THR:HG21	1:A:450:GLY:O	2.21	0.41
1:A:230:GLU:OE1	1:A:230:GLU:CA	2.69	0.41
1:B:180:ILE:O	1:B:181:THR:C	2.64	0.41
1:B:253:LEU:O	1:B:254:CYS:CB	2.66	0.41
1:C:263:GLN:HG2	1:C:300:CYS:O	2.21	0.41
1:A:440:PHE:CD1	1:A:440:PHE:N	2.88	0.40
1:C:430:PHE:CG	1:C:438:ILE:HD11	2.56	0.40
1:B:83:GLU:HG2	1:B:84:CYS:N	2.37	0.40
1:B:283:TYR:HB3	1:B:393:LYS:O	2.22	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:221:THR:HA	1:D:248:TYR:O	2.22	0.40
1:A:239:ARG:HA	1:A:243:THR:O	2.21	0.40
1:B:48:LYS:O	1:B:66:LYS:HA	2.21	0.40
1:A:352:LEU:HD23	1:A:352:LEU:HA	1.80	0.40
1:B:332:PHE:CZ	3:B:512:ACY:H3	2.56	0.40
1:C:421:LEU:HD23	1:C:421:LEU:HA	1.91	0.40
1:D:248:TYR:CE2	1:D:350:PRO:HD3	2.56	0.40
1:D:334:ASN:OD1	3:D:512:ACY:O	2.40	0.40
1:D:359:PHE:O	1:D:362:PHE:HB2	2.21	0.40
1:A:228:THR:CB	1:B:139:MET:HG3	2.51	0.40
1:A:231:ALA:HB1	1:B:139:MET:SD	2.62	0.40
1:A:262[B]:TRP:CE3	1:A:295:LEU:CD1	3.01	0.40
1:B:248:TYR:CD1	1:B:248:TYR:C	2.99	0.40
1:C:62:LEU:HD23	1:C:62:LEU:C	2.46	0.40
1:C:179:TRP:HB2	1:C:221:THR:HG21	2.04	0.40
1:D:62:LEU:HD23	1:D:62:LEU:C	2.47	0.40
1:D:444:ILE:O	1:D:445:LYS:C	2.64	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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	377/452 (83%)	348 (92%)	27 (7%)	2 (0%)	24	43
1	B	375/452 (83%)	347 (92%)	26 (7%)	2 (0%)	24	43
1	C	387/452 (86%)	374 (97%)	12 (3%)	1 (0%)	36	55
1	D	394/452 (87%)	370 (94%)	21 (5%)	3 (1%)	16	31
All	All	1533/1808 (85%)	1439 (94%)	86 (6%)	8 (0%)	24	43

All (8) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	343	ALA
1	D	226	ASN
1	A	229	LEU
1	D	343	ALA
1	A	227	SER
1	B	188	ARG
1	C	343	ALA
1	D	427	GLY

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	318/390 (82%)	288 (91%)	30 (9%)	8	18
1	B	312/390 (80%)	288 (92%)	24 (8%)	12	25
1	C	334/390 (86%)	308 (92%)	26 (8%)	11	24
1	D	330/390 (85%)	308 (93%)	22 (7%)	15	31
All	All	1294/1560 (83%)	1192 (92%)	102 (8%)	11	24

All (102) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	58	SER
1	A	123	GLN
1	A	142	LYS
1	A	154	ARG
1	A	190	LYS
1	A	206	SER
1	A	227	SER
1	A	230	GLU
1	A	235	SER
1	A	237	GLN
1	A	240	LEU
1	A	257	LYS
1	A	272	SER
1	A	302	LYS

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Mol	Chain	Res	Type
1	A	326	GLN
1	A	328	ILE
1	A	333	ASN
1	A	340	SER
1	A	353	GLN
1	A	378	SER
1	A	385	GLU
1	A	392	SER
1	A	422	SER
1	A	436	ASP
1	A	437	GLN
1	A	443	LYS
1	A	445	LYS
1	A	456	MET
1	A	460	THR
1	A	462	MET
1	B	58	SER
1	B	123	GLN
1	B	142	LYS
1	B	157	LYS
1	B	180	ILE
1	B	188	ARG
1	B	234	THR
1	B	271	VAL
1	B	278	LYS
1	B	298	THR
1	B	312	GLN
1	B	322	GLU
1	B	353	GLN
1	B	371	LYS
1	B	374	ASN
1	B	378	SER
1	B	383	MET
1	B	392	SER
1	B	420	ILE
1	B	422	SER
1	B	436	ASP
1	B	441	MET
1	B	447	SER
1	B	457	LEU
1	C	47	VAL
1	C	58	SER

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Mol	Chain	Res	Type
1	C	59	HIS
1	C	123	GLN
1	C	142	LYS
1	C	154	ARG
1	C	188	ARG
1	C	218	THR
1	C	239	ARG
1	C	244	ASP
1	C	271	VAL
1	C	272	SER
1	C	278	LYS
1	C	290	VAL
1	C	293	SER
1	C	330	LYS
1	C	371	LYS
1	C	381	GLU
1	C	385	GLU
1	C	388	LYS
1	C	392	SER
1	C	437	GLN
1	C	443	LYS
1	C	448	ASN
1	C	456	MET
1	C	463	ILE
1	D	58	SER
1	D	99	ASP
1	D	123	GLN
1	D	142	LYS
1	D	225	LEU
1	D	238	PHE
1	D	244	ASP
1	D	271	VAL
1	D	272	SER
1	D	298	THR
1	D	312	GLN
1	D	322	GLU
1	D	323	GLN
1	D	333	ASN
1	D	335	SER
1	D	353	GLN
1	D	388	LYS
1	D	392	SER

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Mol	Chain	Res	Type
1	D	433	THR
1	D	441	MET
1	D	456	MET
1	D	462	MET

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (44) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	61	ASN
1	A	123	GLN
1	A	164	GLN
1	A	172	GLN
1	A	226	ASN
1	A	237	GLN
1	A	250	HIS
1	A	259	GLN
1	A	267	GLN
1	A	270	GLN
1	A	311	ASN
1	A	323	GLN
1	A	426	GLN
1	A	429	ASN
1	B	61	ASN
1	B	123	GLN
1	B	164	GLN
1	B	250	HIS
1	B	314	GLN
1	B	316	GLN
1	B	323	GLN
1	B	325	HIS
1	B	353	GLN
1	B	374	ASN
1	B	439	HIS
1	C	59	HIS
1	C	61	ASN
1	C	123	GLN
1	C	164	GLN
1	C	250	HIS
1	C	323	GLN
1	C	326	GLN
1	C	336	HIS
1	C	353	GLN

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Mol	Chain	Res	Type
1	C	437	GLN
1	C	458	ASN
1	D	61	ASN
1	D	122	HIS
1	D	123	GLN
1	D	164	GLN
1	D	237	GLN
1	D	323	GLN
1	D	336	HIS
1	D	353	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](#)

Of 37 ligands modelled in this entry, 26 are monoatomic - leaving 11 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	$\# Z > 2$
3	ACY	A	511	-	3,3,3	1.20	0	3,3,3	0.73	0
3	ACY	D	511	-	3,3,3	0.93	0	3,3,3	0.37	0
3	ACY	B	511	-	3,3,3	1.17	0	3,3,3	0.10	0
4	MO7	D	531	-	24,42,42	3.04	5 (20%)	-		

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	ACY	D	512	-	3,3,3	0.96	0	3,3,3	0.61	0
4	MO7	A	531	-	24,42,42	1.54	4 (16%)	-		
4	MO7	C	531[B]	1	24,42,42	39.10	4 (16%)	-		
4	MO7	B	531[A]	-	24,42,42	2.76	3 (12%)	-		
3	ACY	C	512	-	3,3,3	1.00	0	3,3,3	1.06	0
3	ACY	C	511	-	3,3,3	1.46	1 (33%)	3,3,3	0.86	0
3	ACY	B	512	-	3,3,3	0.76	0	3,3,3	1.53	1 (33%)

All (17) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	C	531[B]	MO7	O22-MO6	191.02	5.85	1.71
4	C	531[B]	MO7	O13-MO4	12.33	1.98	1.71
4	D	531	MO7	O13-MO4	12.17	1.97	1.71
4	B	531[A]	MO7	O13-MO4	11.68	1.96	1.71
4	D	531	MO7	O15-MO5	5.06	1.76	1.68
4	D	531	MO7	O8-MO2	5.00	1.76	1.68
4	B	531[A]	MO7	O15-MO5	4.81	1.76	1.68
4	C	531[B]	MO7	O8-MO2	4.46	1.75	1.68
4	A	531	MO7	O15-MO5	3.72	1.74	1.68
4	A	531	MO7	O8-MO2	3.72	1.74	1.68
4	B	531[A]	MO7	O8-MO2	3.58	1.74	1.68
4	C	531[B]	MO7	O15-MO5	3.55	1.74	1.68
4	A	531	MO7	O5-MO1	-2.94	2.16	2.28
4	A	531	MO7	O13-MO4	2.67	1.77	1.71
4	D	531	MO7	O2-MO1	-2.57	2.18	2.28
4	D	531	MO7	O5-MO1	-2.55	2.18	2.28
3	C	511	ACY	O-C	2.34	1.32	1.22

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	512	ACY	O-C-CH3	-2.10	113.90	122.53

There are no chirality outliers.

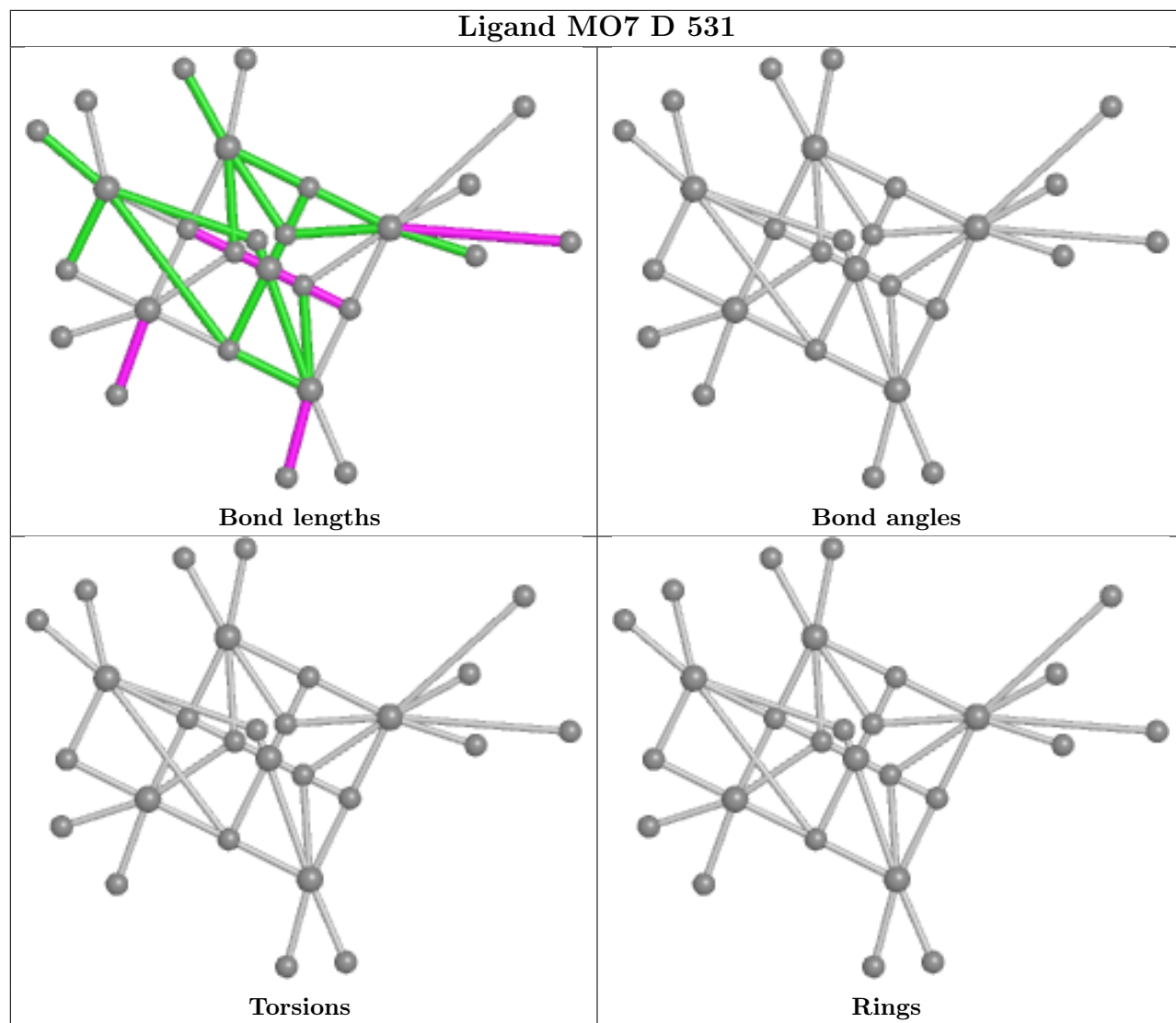
There are no torsion outliers.

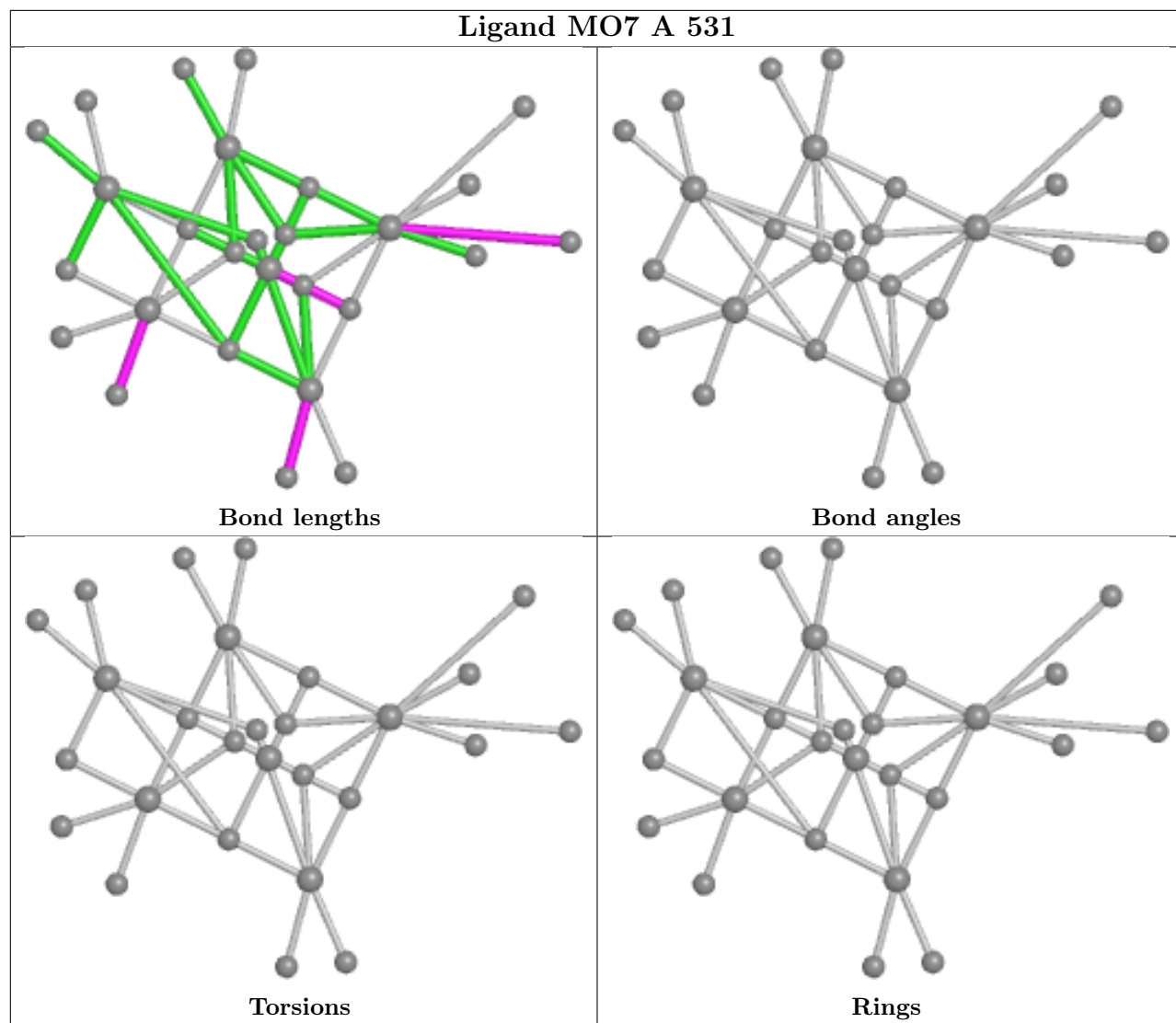
There are no ring outliers.

10 monomers are involved in 32 short contacts:

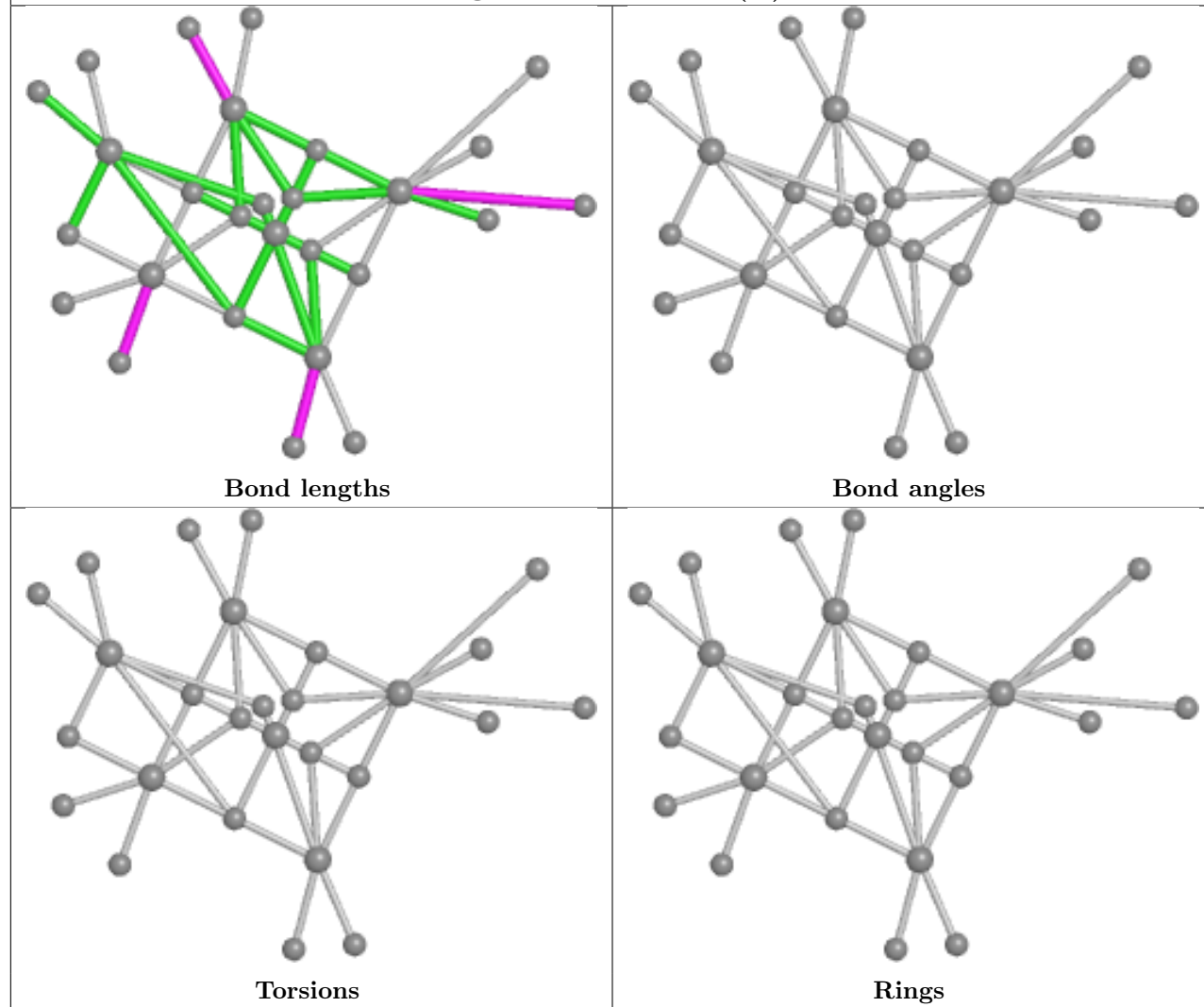
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	511	ACY	3	0
3	D	511	ACY	1	0
4	D	531	MO7	1	0
3	D	512	ACY	1	0
4	A	531	MO7	1	0
4	C	531[B]	MO7	13	0
4	B	531[A]	MO7	8	0
3	C	512	ACY	1	0
3	C	511	ACY	2	0
3	B	512	ACY	1	0

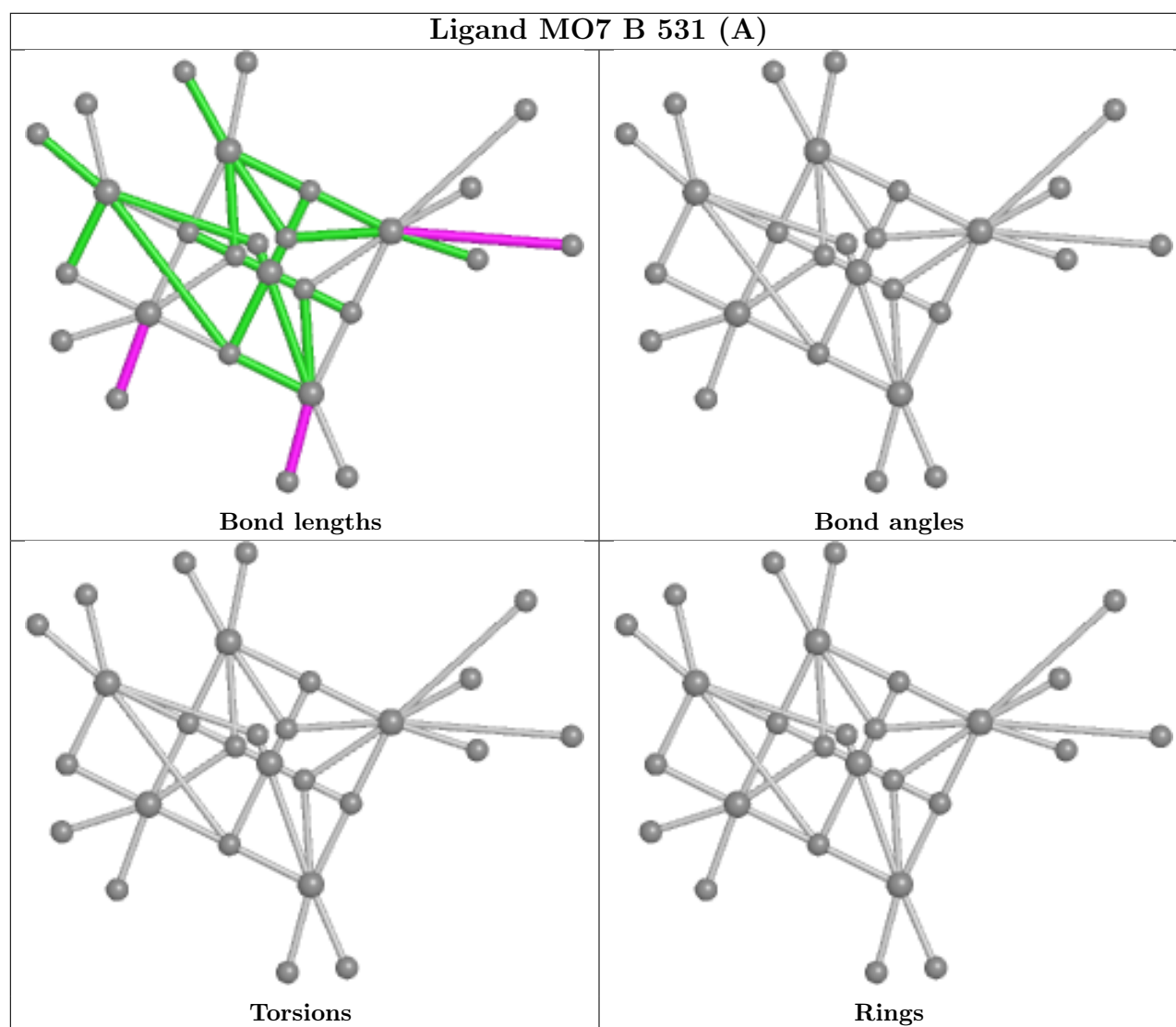
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.





Ligand MO7 C 531 (B)





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	385/452 (85%)	0.40	32 (8%)	17 15	30, 79, 132, 158	2 (0%)
1	B	386/452 (85%)	0.34	18 (4%)	36 32	36, 79, 128, 162	1 (0%)
1	C	393/452 (86%)	-0.17	5 (1%)	75 71	27, 63, 103, 128	2 (0%)
1	D	397/452 (87%)	-0.18	10 (2%)	58 54	25, 58, 92, 114	3 (0%)
All	All	1561/1808 (86%)	0.10	65 (4%)	40 36	25, 70, 118, 162	8 (0%)

All (65) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	205	GLY	4.8
1	C	465	ALA	4.6
1	A	229	LEU	4.2
1	B	226	ASN	3.9
1	A	234	THR	3.9
1	A	333	ASN	3.6
1	A	461	ASN	3.5
1	B	244	ASP	3.4
1	B	234	THR	3.3
1	B	77	VAL	3.2
1	B	205	GLY	3.1
1	B	47	VAL	3.1
1	D	374	ASN	3.1
1	A	231	ALA	3.0
1	A	338	PRO	3.0
1	A	244	ASP	3.0
1	A	378	SER	2.9
1	B	231	ALA	2.8
1	A	190	LYS	2.8
1	A	247	VAL	2.8
1	A	433	THR	2.8

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Mol	Chain	Res	Type	RSRZ
1	A	364	PHE	2.8
1	A	373	ALA	2.8
1	D	205	GLY	2.7
1	A	245	TYR	2.7
1	A	240	LEU	2.7
1	A	227	SER	2.7
1	B	236	LEU	2.6
1	B	340	SER	2.6
1	A	59[A]	HIS	2.6
1	D	336	HIS	2.6
1	C	274	GLY	2.6
1	A	225	LEU	2.6
1	A	142	LYS	2.6
1	B	242	GLY	2.5
1	D	335	SER	2.5
1	A	122	HIS	2.5
1	A	166	ALA	2.5
1	A	346	GLY	2.4
1	D	123	GLN	2.4
1	A	246	THR	2.4
1	D	69	ALA	2.4
1	B	271	VAL	2.4
1	D	463	ILE	2.4
1	A	127	TYR	2.4
1	B	241	TYR	2.3
1	C	47	VAL	2.3
1	A	120	LYS	2.2
1	A	156	LEU	2.2
1	B	240	LEU	2.2
1	B	333	ASN	2.2
1	A	337	CYS	2.2
1	B	248	TYR	2.2
1	A	242	GLY	2.2
1	A	271	VAL	2.1
1	A	228	THR	2.1
1	C	49	TYR	2.1
1	A	460	THR	2.1
1	B	446	ASP	2.1
1	D	375	ASP	2.0
1	D	314	GLN	2.0
1	B	238	PHE	2.0
1	C	333	ASN	2.0

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Mol	Chain	Res	Type	RSRZ
1	D	226	ASN	2.0
1	B	49	TYR	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
5	NA	C	521	1/1	0.81	0.09	58,58,58,58	0
5	NA	D	521	1/1	0.85	0.07	48,48,48,48	0
3	ACY	A	511	4/4	0.90	0.12	48,54,59,61	0
2	CL	B	501	1/1	0.91	0.11	63,63,63,63	0
3	ACY	B	512	4/4	0.91	0.30	61,66,67,67	0
3	ACY	B	511	4/4	0.94	0.13	45,55,58,59	0
3	ACY	C	512	4/4	0.94	0.17	33,45,47,49	0
2	CL	D	508	1/1	0.95	0.12	69,69,69,69	0
4	MO7	B	531[A]	31/31	0.95	0.08	43,64,82,94	31
3	ACY	C	511	4/4	0.96	0.10	29,38,41,45	0
2	CL	A	501	1/1	0.96	0.06	56,56,56,56	0
2	CL	B	503	1/1	0.96	0.06	65,65,65,65	0
5	NA	B	521	1/1	0.96	0.03	56,56,56,56	0
2	CL	D	501	1/1	0.96	0.05	41,41,41,41	0
2	CL	D	506	1/1	0.96	0.10	58,58,58,58	0
2	CL	D	505	1/1	0.97	0.05	58,58,58,58	0
4	MO7	C	531[B]	31/31	0.97	0.07	47,61,73,84	31
2	CL	B	506	1/1	0.97	0.11	67,67,67,67	0
2	CL	C	503	1/1	0.97	0.07	63,63,63,63	0
2	CL	B	502	1/1	0.97	0.10	60,60,60,60	0
2	CL	A	503	1/1	0.98	0.09	60,60,60,60	0

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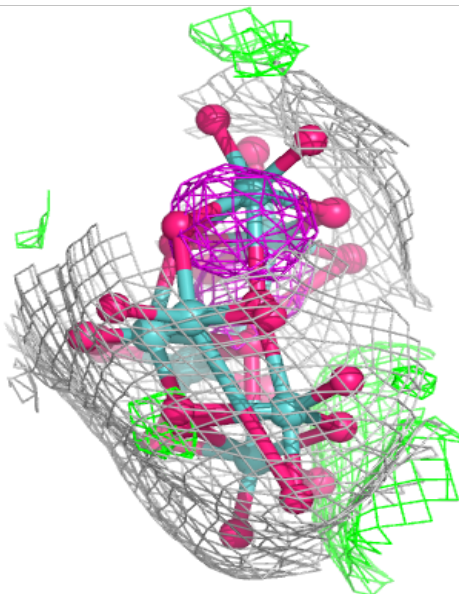
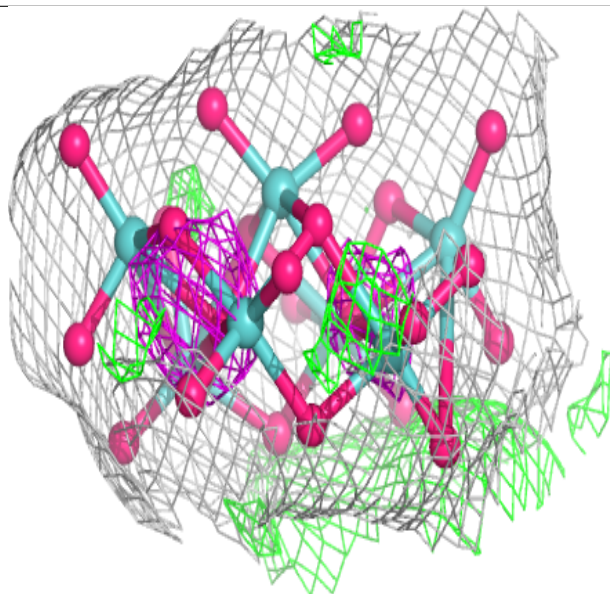
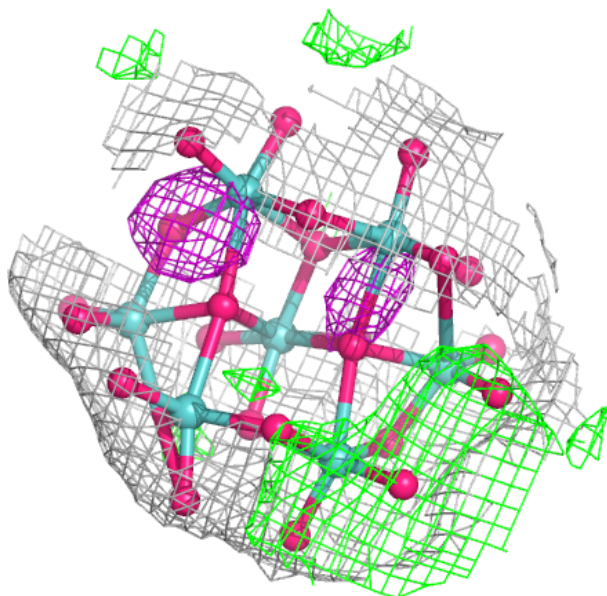
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	CL	C	501	1/1	0.98	0.04	39,39,39,39	0
3	ACY	D	511	4/4	0.98	0.07	45,46,46,52	0
3	ACY	D	512	4/4	0.98	0.08	42,42,42,43	0
2	CL	D	507	1/1	0.98	0.03	52,52,52,52	0
2	CL	C	502	1/1	0.98	0.12	54,54,54,54	0
2	CL	A	502	1/1	0.98	0.20	60,60,60,60	0
2	CL	C	506	1/1	0.98	0.05	43,43,43,43	0
5	NA	C	522	1/1	0.98	0.03	42,42,42,42	0
2	CL	B	505	1/1	0.98	0.04	58,58,58,58	0
2	CL	D	502	1/1	0.99	0.16	52,52,52,52	0
2	CL	D	503	1/1	0.99	0.07	44,44,44,44	0
4	MO7	D	531	31/31	0.99	0.05	29,41,54,55	31
2	CL	D	509	1/1	0.99	0.22	42,42,42,42	1
2	CL	A	505	1/1	0.99	0.09	56,56,56,56	0
2	CL	C	505	1/1	0.99	0.07	50,50,50,50	0
4	MO7	A	531	31/31	0.99	0.05	30,43,52,60	31

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.

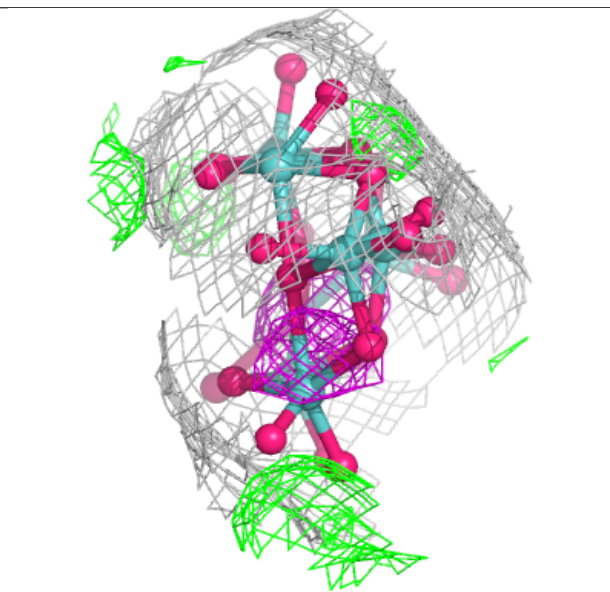
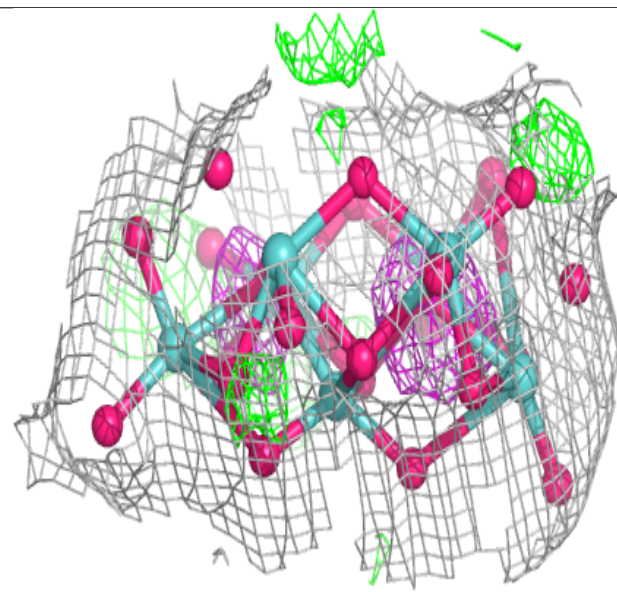
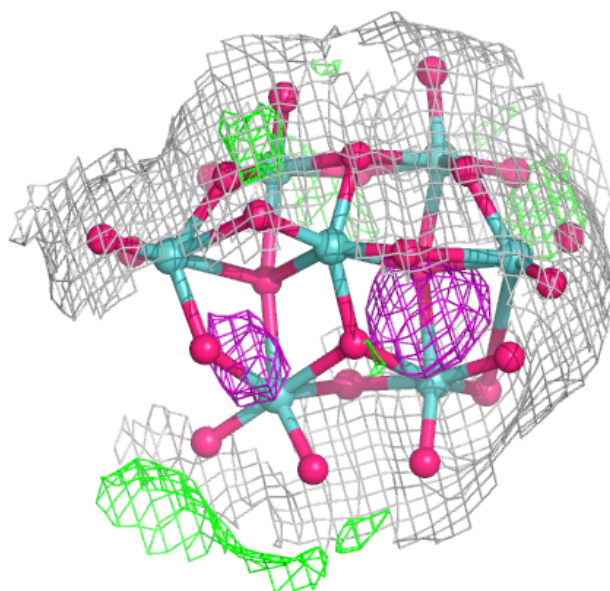
Electron density around MO7 B 531 (A):

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



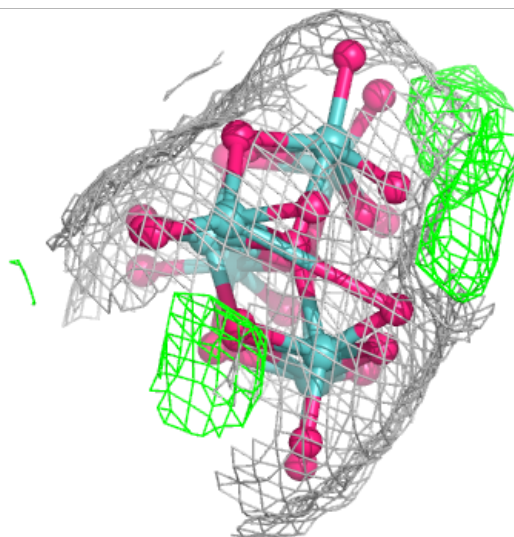
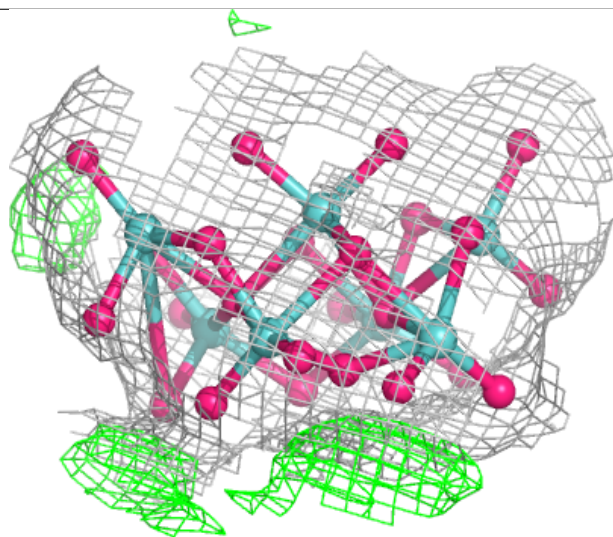
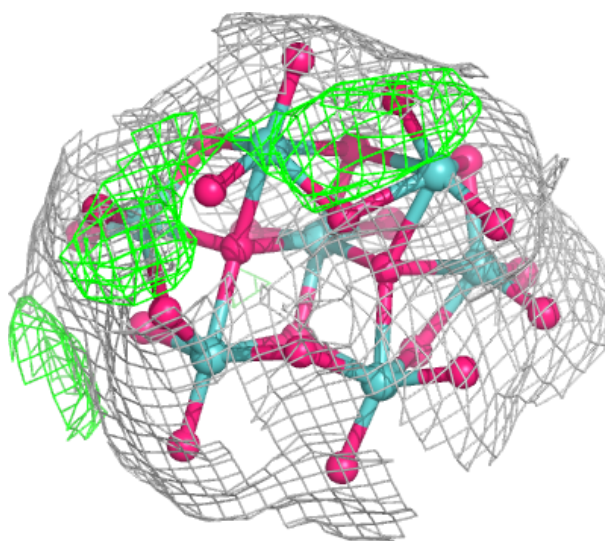
Electron density around MO7 C 531 (B):

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



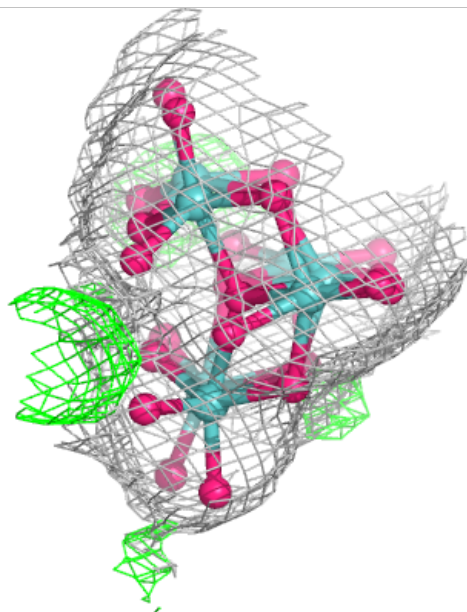
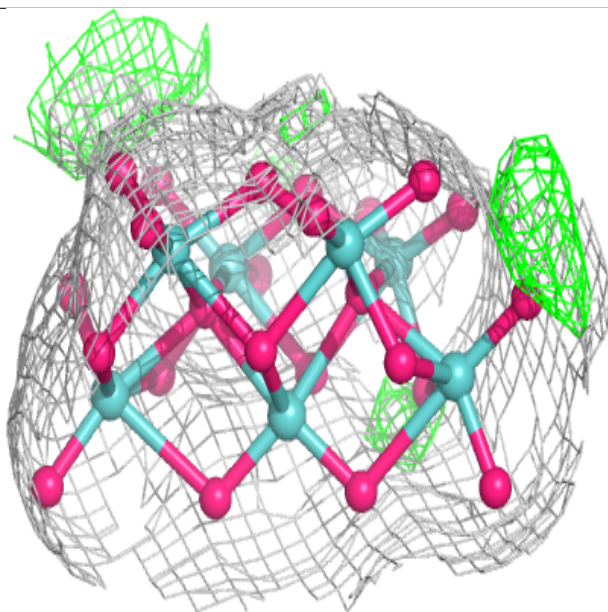
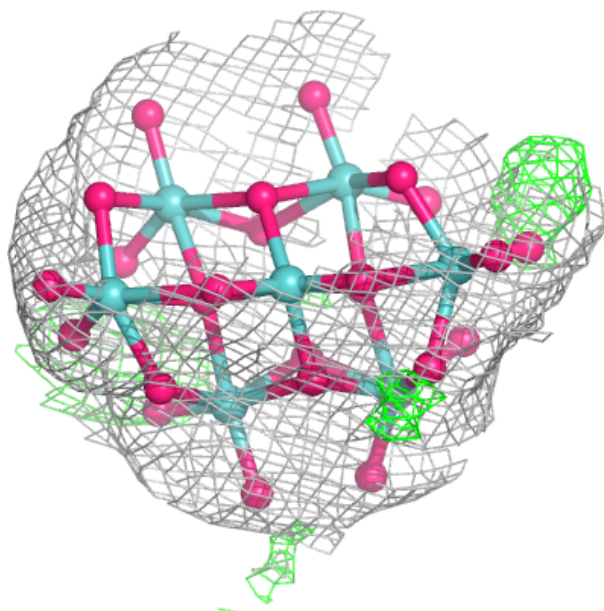
Electron density around MO7 D 531:

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



Electron density around MO7 A 531:

$2mF_o-DF_c$ (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.