



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 03:27 PM UTC

PDB ID : 1ESM / pdb_00001esm
Title : STRUCTURAL BASIS FOR THE FEEDBACK REGULATION OF ES-
CHERICHIA COLI PANTOTHENATE KINASE BY COENZYME A
Authors : Yun, M.; Park, C.G.; Kim, J.Y.; Rock, C.O.; Jackowski, S.; Park, H.W.
Deposited on : 2000-04-10
Resolution : 2.50 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

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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

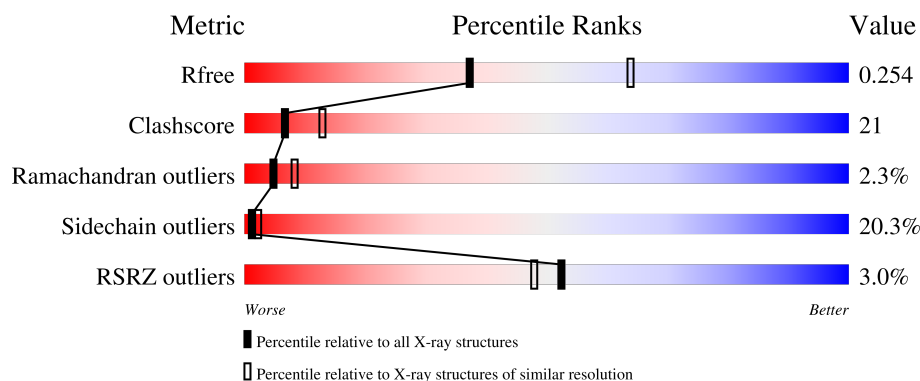
1 Overall quality at a glance

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	316	
1	B	316	
1	C	316	
1	D	316	

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 10473 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 PANTOTHENATE KINASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	311	Total	C	N	O	Se	0	0	0
			2528	1623	434	465	6			
1	B	307	Total	C	N	O	Se	0	0	0
			2495	1603	427	459	6			
1	C	307	Total	C	N	O	Se	0	0	0
			2491	1599	428	458	6			
1	D	303	Total	C	N	O	Se	0	0	0
			2466	1588	421	451	6			

There are 24 discrepancies between the modelled and reference sequences:

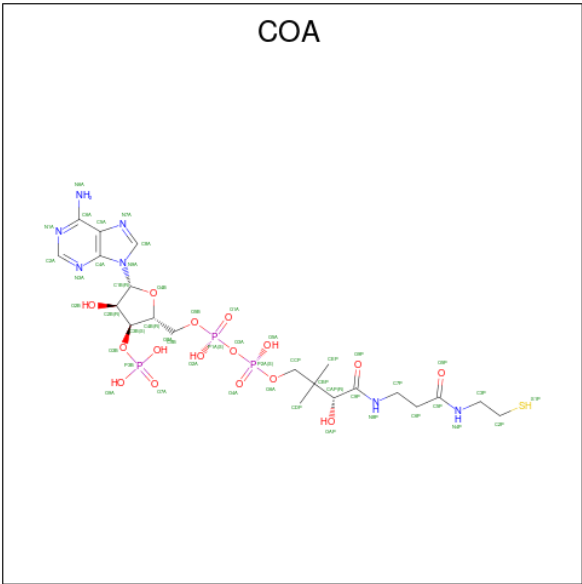
Chain	Residue	Modelled	Actual	Comment	Reference
A	9	MSE	MET	modified residue	UNP P0A6I3
A	29	MSE	MET	modified residue	UNP P0A6I3
A	142	MSE	MET	modified residue	UNP P0A6I3
A	153	MSE	MET	modified residue	UNP P0A6I3
A	208	MSE	MET	modified residue	UNP P0A6I3
A	275	MSE	MET	modified residue	UNP P0A6I3
B	9	MSE	MET	modified residue	UNP P0A6I3
B	29	MSE	MET	modified residue	UNP P0A6I3
B	142	MSE	MET	modified residue	UNP P0A6I3
B	153	MSE	MET	modified residue	UNP P0A6I3
B	208	MSE	MET	modified residue	UNP P0A6I3
B	275	MSE	MET	modified residue	UNP P0A6I3
C	9	MSE	MET	modified residue	UNP P0A6I3
C	29	MSE	MET	modified residue	UNP P0A6I3
C	142	MSE	MET	modified residue	UNP P0A6I3
C	153	MSE	MET	modified residue	UNP P0A6I3
C	208	MSE	MET	modified residue	UNP P0A6I3
C	275	MSE	MET	modified residue	UNP P0A6I3
D	9	MSE	MET	modified residue	UNP P0A6I3
D	29	MSE	MET	modified residue	UNP P0A6I3
D	142	MSE	MET	modified residue	UNP P0A6I3

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Chain	Residue	Modelled	Actual	Comment	Reference
D	153	MSE	MET	modified residue	UNP P0A6I3
D	208	MSE	MET	modified residue	UNP P0A6I3
D	275	MSE	MET	modified residue	UNP P0A6I3

- Molecule 2 is COENZYME A (CCD ID: COA) (formula: C₂₁H₃₆N₇O₁₆P₃S).



Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
2	A	1	Total	C	N	O	P	S	0	0
			48	21	7	16	3	1		
2	B	1	Total	C	N	O	P	S	0	0
			48	21	7	16	3	1		
2	C	1	Total	C	N	O	P	S	0	0
			48	21	7	16	3	1		
2	D	1	Total	C	N	O	P	S	0	0
			48	21	7	16	3	1		

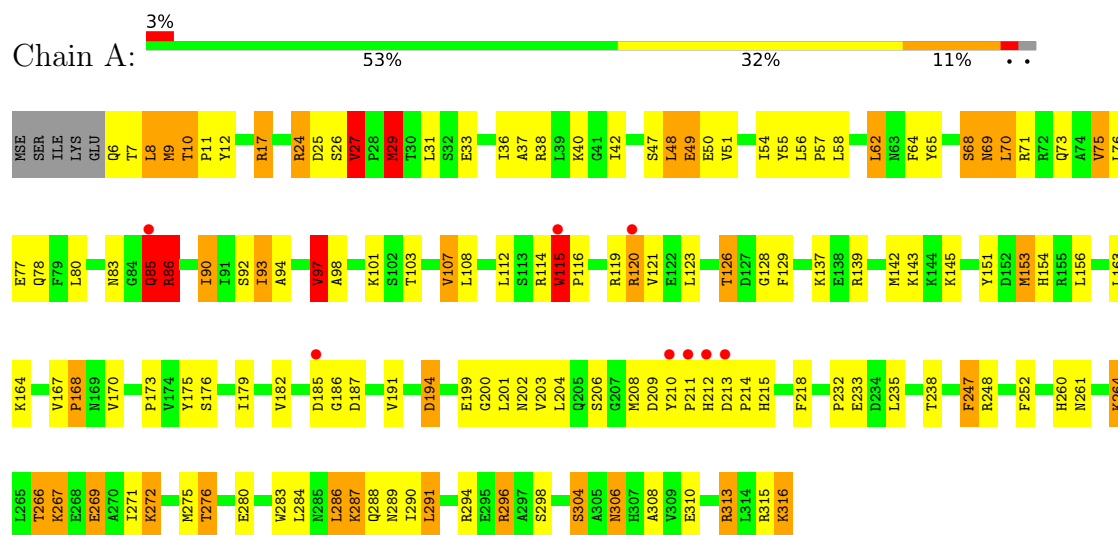
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	67	Total	O	0	0
			67	67		
3	B	78	Total	O	0	0
			78	78		
3	C	72	Total	O	0	0
			72	72		
3	D	84	Total	O	0	0
			84	84		

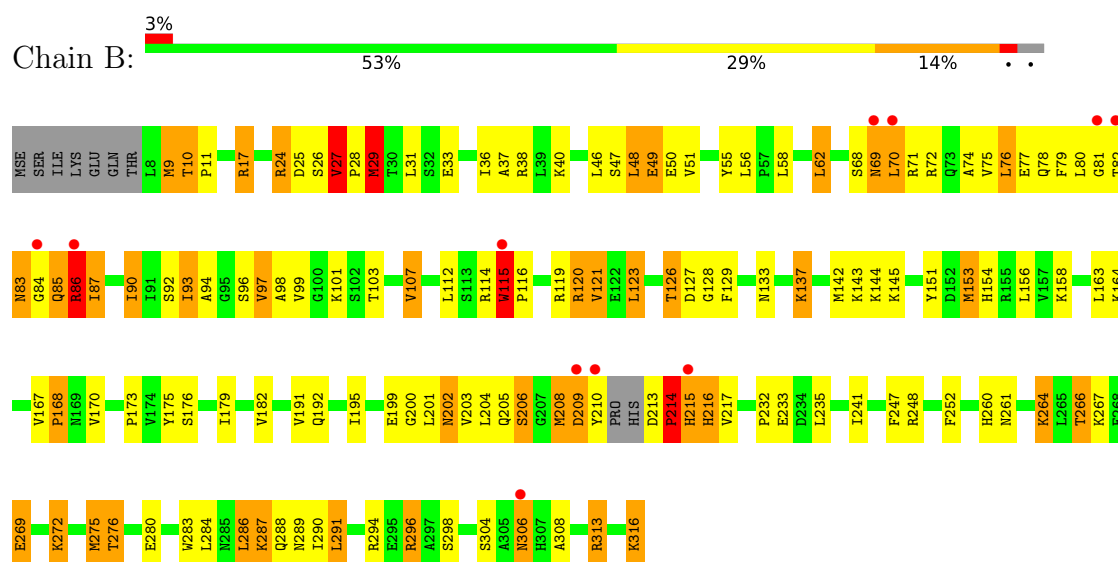
3 Residue-property plots

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: PANTOTHENATE KINASE

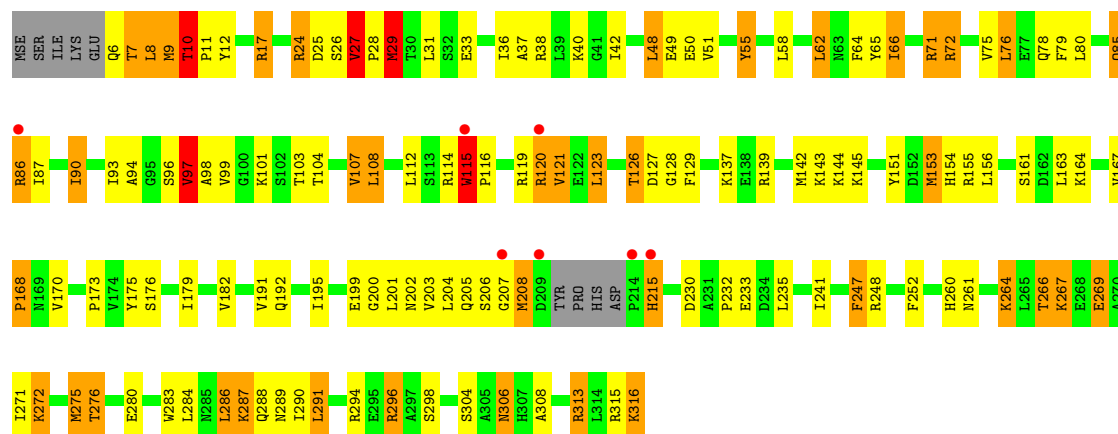


• Molecule 1: PANTOTHENATE KINASE

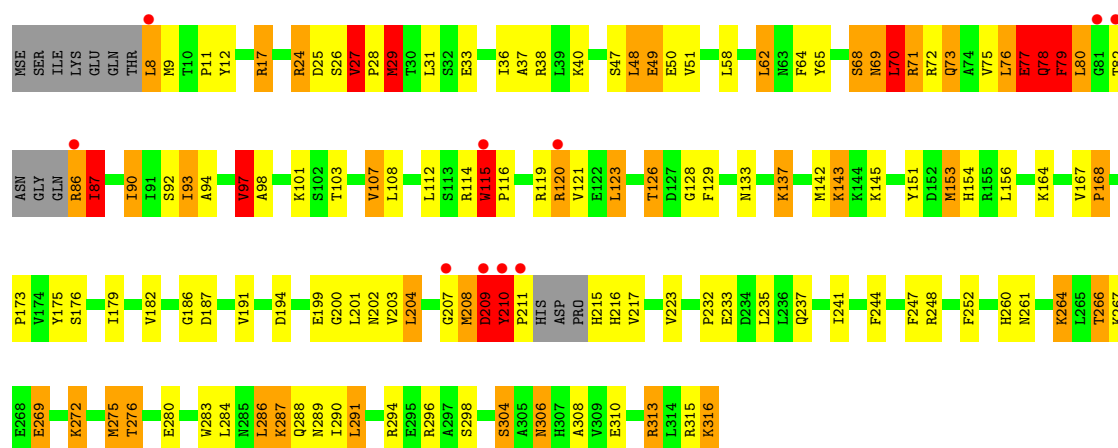


• Molecule 1: PANTOTHENATE KINASE





● Molecule 1: PANTOTHENATE KINASE



4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	62.00Å 71.24Å 87.68Å 102.44° 89.48° 93.23°	Depositor
Resolution (Å)	50.00 – 2.50 50.00 – 2.50	Depositor EDS
% Data completeness (in resolution range)	81.4 (50.00-2.50) 81.4 (50.00-2.50)	Depositor EDS
R_{merge}	0.04	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.93 (at 2.51Å)	Xtriage
Refinement program	X-PLOR	Depositor
R, R_{free}	0.201 , 0.259 0.202 , 0.254	Depositor DCC
R_{free} test set	2175 reflections (5.04%)	wwPDB-VP
Wilson B-factor (Å ²)	29.2	Xtriage
Anisotropy	0.232	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 59.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	10473	wwPDB-VP
Average B, all atoms (Å ²)	32.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.08% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: COA

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	0.60	5/2581 (0.2%)	1.06	18/3494 (0.5%)
1	B	0.65	6/2545 (0.2%)	1.12	23/3442 (0.7%)
1	C	0.61	6/2540 (0.2%)	1.08	22/3434 (0.6%)
1	D	0.63	5/2515 (0.2%)	1.13	24/3400 (0.7%)
All	All	0.62	22/10181 (0.2%)	1.10	87/13770 (0.6%)

All (22) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	153	MSE	CG-SE	-7.27	1.73	1.95
1	C	153	MSE	CG-SE	-7.05	1.74	1.95
1	D	153	MSE	CG-SE	-6.99	1.74	1.95
1	B	29	MSE	CG-SE	-6.87	1.74	1.95
1	C	29	MSE	CG-SE	-6.77	1.75	1.95
1	A	153	MSE	CG-SE	-6.76	1.75	1.95
1	D	29	MSE	CG-SE	-6.61	1.75	1.95
1	B	208	MSE	CG-SE	-6.41	1.76	1.95
1	A	29	MSE	CG-SE	-6.29	1.76	1.95
1	D	208	MSE	CG-SE	-6.18	1.76	1.95
1	A	9	MSE	CG-SE	-5.82	1.77	1.95
1	D	275	MSE	CG-SE	-5.76	1.78	1.95
1	C	208	MSE	CG-SE	-5.72	1.78	1.95
1	A	275	MSE	CG-SE	-5.65	1.78	1.95
1	C	9	MSE	CG-SE	-5.54	1.78	1.95
1	D	142	MSE	CG-SE	-5.53	1.78	1.95
1	C	275	MSE	CG-SE	-5.46	1.79	1.95
1	A	208	MSE	CG-SE	-5.44	1.79	1.95
1	B	275	MSE	CG-SE	-5.44	1.79	1.95
1	B	142	MSE	CG-SE	-5.44	1.79	1.95
1	B	9	MSE	CG-SE	-5.35	1.79	1.95
1	C	142	MSE	CG-SE	-5.33	1.79	1.95

All (87) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	143	LYS	N-CA-C	-15.31	92.78	113.30
1	C	143	LYS	N-CA-C	-15.28	92.83	113.30
1	D	143	LYS	N-CA-C	-15.02	93.18	113.30
1	B	143	LYS	N-CA-C	-14.85	93.41	113.30
1	C	10	THR	N-CA-C	-11.52	90.96	109.40
1	D	208	MSE	N-CA-C	11.13	123.94	110.91
1	D	142	MSE	N-CA-C	9.85	123.70	112.57
1	B	142	MSE	N-CA-C	9.74	123.57	112.57
1	D	78	GLN	N-CA-C	-9.54	95.12	110.20
1	A	142	MSE	N-CA-C	9.20	122.97	112.57
1	C	154	HIS	N-CA-C	-9.06	101.40	111.28
1	C	142	MSE	N-CA-C	9.05	122.79	112.57
1	A	154	HIS	N-CA-C	-8.69	101.81	111.28
1	B	154	HIS	N-CA-C	-8.63	101.87	111.28
1	A	9	MSE	N-CA-C	8.50	123.15	107.60
1	D	154	HIS	N-CA-C	-8.47	102.05	111.28
1	C	7	THR	N-CA-C	-8.34	101.98	112.90
1	B	85	GLN	CB-CA-C	-8.07	107.27	116.63
1	A	10	THR	N-CA-C	-7.85	88.62	108.40
1	C	10	THR	CA-C-N	-7.41	112.17	119.87
1	C	10	THR	C-N-CA	-7.41	112.17	119.87
1	B	86	ARG	N-CA-C	-7.27	103.45	113.56
1	C	288	GLN	N-CA-C	7.07	118.77	111.14
1	C	9	MSE	N-CA-C	6.92	122.85	108.53
1	A	288	GLN	N-CA-C	6.83	118.52	111.14
1	D	115	TRP	CA-C-N	-6.66	111.51	119.84
1	D	115	TRP	C-N-CA	-6.66	111.51	119.84
1	D	288	GLN	N-CA-C	6.59	118.26	111.14
1	D	208	MSE	CA-CB-CG	-6.43	101.25	114.10
1	B	153	MSE	N-CA-C	6.42	120.95	113.18
1	B	214	PRO	CA-C-N	-6.40	109.32	121.54
1	B	214	PRO	C-N-CA	-6.40	109.32	121.54
1	A	153	MSE	N-CA-C	6.34	120.85	113.18
1	C	115	TRP	CA-C-N	-6.29	111.97	119.84
1	C	115	TRP	C-N-CA	-6.29	111.97	119.84
1	D	77	GLU	N-CA-C	-6.23	104.18	110.97
1	B	209	ASP	N-CA-C	-6.22	97.55	110.80
1	B	29	MSE	CB-CG-SE	-6.20	94.12	112.70
1	D	153	MSE	N-CA-C	6.19	120.67	113.18
1	D	87	ILE	CA-C-N	6.15	126.17	119.89
1	D	87	ILE	C-N-CA	6.15	126.17	119.89
1	A	55	TYR	N-CA-C	6.12	120.01	112.54

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	115	TRP	CA-C-N	-6.12	112.19	119.84
1	B	115	TRP	C-N-CA	-6.12	112.19	119.84
1	A	115	TRP	CA-C-N	-6.11	112.20	119.84
1	A	115	TRP	C-N-CA	-6.11	112.20	119.84
1	B	10	THR	CA-C-N	6.10	126.21	119.87
1	B	10	THR	C-N-CA	6.10	126.21	119.87
1	B	288	GLN	N-CA-C	6.09	117.72	111.14
1	A	266	THR	N-CA-C	-6.00	103.03	110.41
1	D	142	MSE	CB-CG-SE	-5.94	94.88	112.70
1	B	87	ILE	N-CA-C	5.88	115.37	108.96
1	A	27	VAL	N-CA-C	-5.88	102.55	108.96
1	C	153	MSE	N-CA-C	5.82	120.38	113.28
1	D	266	THR	N-CA-C	-5.79	103.28	110.41
1	D	97	VAL	N-CA-C	-5.78	102.12	109.58
1	C	29	MSE	CB-CG-SE	-5.76	95.42	112.70
1	D	29	MSE	CB-CG-SE	-5.74	95.48	112.70
1	B	153	MSE	CA-CB-CG	-5.72	102.66	114.10
1	C	27	VAL	N-CA-C	-5.67	102.77	108.96
1	A	29	MSE	N-CA-C	5.67	119.05	109.76
1	C	230	ASP	N-CA-C	5.63	118.72	109.72
1	A	247	PHE	N-CA-C	-5.60	105.25	111.36
1	A	97	VAL	N-CA-C	-5.58	102.38	109.58
1	C	29	MSE	N-CA-C	5.57	118.89	109.76
1	B	142	MSE	CB-CG-SE	-5.53	96.11	112.70
1	C	153	MSE	CA-CB-CG	-5.52	103.07	114.10
1	B	247	PHE	N-CA-C	-5.49	105.30	111.28
1	A	194	ASP	N-CA-C	-5.49	105.71	112.90
1	B	266	THR	N-CA-C	-5.49	103.66	110.41
1	D	194	ASP	N-CA-C	-5.47	105.74	112.90
1	D	247	PHE	N-CA-C	-5.46	105.33	111.28
1	B	27	VAL	N-CA-C	-5.42	103.05	108.96
1	D	79	PHE	N-CA-CB	5.41	119.63	110.49
1	C	266	THR	N-CA-C	-5.41	103.76	110.41
1	C	55	TYR	N-CA-C	5.38	119.56	112.89
1	D	27	VAL	N-CA-C	-5.36	103.12	108.96
1	D	153	MSE	CA-CB-CG	-5.33	103.43	114.10
1	C	142	MSE	CB-CG-SE	-5.33	96.72	112.70
1	A	29	MSE	CB-CG-SE	-5.29	96.81	112.70
1	C	97	VAL	N-CA-C	-5.21	102.86	109.58
1	D	208	MSE	CA-C-N	5.16	131.40	121.54
1	D	208	MSE	C-N-CA	5.16	131.40	121.54
1	C	247	PHE	N-CA-C	-5.16	105.73	111.36

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	68	SER	N-CA-C	-5.15	105.36	110.97
1	B	55	TYR	N-CA-C	5.11	119.23	112.89
1	B	202	ASN	N-CA-C	5.09	118.63	112.93

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	2528	0	2540	110	0
1	B	2495	0	2510	138	0
1	C	2491	0	2513	110	0
1	D	2466	0	2488	121	0
2	A	48	0	32	0	0
2	B	48	0	32	0	0
2	C	48	0	32	0	0
2	D	48	0	32	0	0
3	A	67	0	0	1	0
3	B	78	0	0	3	0
3	C	72	0	0	0	0
3	D	84	0	0	1	0
All	All	10473	0	10179	437	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 21.

All (437) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:29:MSE:HE2	1:B:31:LEU:HB2	1.19	1.14
1:D:210:TYR:HB3	1:D:211:PRO:CD	1.81	1.10
1:C:29:MSE:HE2	1:C:31:LEU:HB2	1.20	1.09
1:D:29:MSE:HE2	1:D:31:LEU:HB2	1.17	1.09
1:A:29:MSE:HE2	1:A:31:LEU:HB2	1.13	1.09

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:215:HIS:CD2	1:B:216:HIS:H	1.71	1.08
1:D:210:TYR:HB3	1:D:211:PRO:HD2	1.05	1.02
1:A:65:TYR:CE2	1:B:75:VAL:HG21	1.96	1.00
1:D:75:VAL:O	1:D:78:GLN:O	1.80	1.00
1:D:29:MSE:HE1	1:D:51:VAL:HG11	1.43	0.98
1:B:85:GLN:HA	1:B:87:ILE:HD13	1.47	0.96
1:B:29:MSE:HE1	1:B:51:VAL:HG11	1.43	0.95
1:C:29:MSE:HE1	1:C:51:VAL:HG11	1.51	0.92
1:A:29:MSE:HE1	1:A:51:VAL:HG11	1.50	0.91
1:C:85:GLN:HE22	1:C:192:GLN:HE22	1.21	0.89
1:D:210:TYR:CB	1:D:211:PRO:HD2	1.99	0.88
1:A:86:ARG:O	1:A:86:ARG:HG3	1.73	0.87
1:A:86:ARG:HH22	1:A:194:ASP:HA	1.41	0.86
1:A:29:MSE:CE	1:A:31:LEU:HB2	2.05	0.85
1:D:76:LEU:O	1:D:80:LEU:HB2	1.82	0.80
1:D:261:ASN:HA	1:D:264:LYS:HE2	1.65	0.79
1:A:11:PRO:HG3	1:B:215:HIS:HB2	1.65	0.79
1:B:215:HIS:CG	1:B:216:HIS:H	1.98	0.79
1:C:72:ARG:HH11	1:C:72:ARG:CG	1.95	0.78
1:A:213:ASP:C	1:A:215:HIS:H	1.89	0.78
1:C:261:ASN:HA	1:C:264:LYS:HE2	1.66	0.78
1:D:211:PRO:HB2	1:D:216:HIS:HD2	1.47	0.78
1:B:75:VAL:HG22	3:B:529:HOH:O	1.83	0.77
1:A:261:ASN:HA	1:A:264:LYS:HE2	1.67	0.77
1:B:261:ASN:HA	1:B:264:LYS:HE2	1.67	0.77
1:C:29:MSE:CE	1:C:31:LEU:HB2	2.11	0.76
1:A:126:THR:HB	1:A:200:GLY:HA3	1.68	0.75
1:C:161:SER:HG	1:D:8:LEU:N	1.84	0.75
1:B:29:MSE:CE	1:B:31:LEU:HB2	2.10	0.75
1:C:126:THR:HB	1:C:200:GLY:HA3	1.68	0.75
1:D:11:PRO:O	1:D:316:LYS:HG2	1.87	0.75
1:C:8:LEU:O	1:C:8:LEU:HD22	1.87	0.74
1:B:213:ASP:O	1:B:214:PRO:O	2.06	0.73
1:A:266:THR:HG23	1:A:269:GLU:H	1.53	0.73
1:C:266:THR:HG23	1:C:269:GLU:H	1.52	0.73
1:B:266:THR:HG23	1:B:269:GLU:H	1.54	0.73
1:C:266:THR:HG22	1:C:269:GLU:CD	2.14	0.73
1:D:266:THR:HG23	1:D:269:GLU:H	1.54	0.73
1:C:85:GLN:HE22	1:C:192:GLN:NE2	1.86	0.72
1:C:64:PHE:CD2	1:D:79:PHE:HB2	2.24	0.72
1:A:11:PRO:CD	1:B:215:HIS:HB2	2.20	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:85:GLN:HA	1:B:87:ILE:CD1	2.19	0.72
1:A:266:THR:HG22	1:A:269:GLU:CD	2.14	0.72
1:B:266:THR:HG22	1:B:269:GLU:CD	2.15	0.71
1:A:25:ASP:CG	1:A:26:SER:H	1.97	0.71
1:C:85:GLN:HG3	1:C:86:ARG:N	2.05	0.71
1:D:29:MSE:CE	1:D:31:LEU:HB2	2.08	0.71
1:C:11:PRO:HG3	1:D:215:HIS:HA	1.72	0.71
1:B:126:THR:HB	1:B:200:GLY:HA3	1.73	0.71
1:D:286:LEU:HD22	1:D:291:LEU:HD22	1.73	0.71
1:D:25:ASP:CG	1:D:26:SER:H	1.98	0.70
1:B:286:LEU:HD22	1:B:291:LEU:HD22	1.73	0.70
1:C:286:LEU:HD22	1:C:291:LEU:HD22	1.72	0.70
1:A:139:ARG:HB3	1:D:264:LYS:HZ2	1.54	0.70
1:A:11:PRO:O	1:A:316:LYS:HG2	1.91	0.70
1:B:167:VAL:HG13	1:B:168:PRO:HD2	1.74	0.69
1:B:115:TRP:CE3	1:B:115:TRP:C	2.70	0.69
1:D:79:PHE:O	1:D:79:PHE:CD2	2.45	0.69
1:C:11:PRO:O	1:C:316:LYS:HG2	1.92	0.69
1:D:266:THR:HG22	1:D:269:GLU:CD	2.17	0.69
1:A:115:TRP:CE3	1:A:115:TRP:C	2.71	0.69
1:A:139:ARG:HB3	1:D:264:LYS:NZ	2.07	0.68
1:A:11:PRO:CG	1:B:215:HIS:HB2	2.22	0.68
1:B:126:THR:HG21	1:B:202:ASN:OD1	1.94	0.68
1:A:86:ARG:O	1:A:86:ARG:CG	2.41	0.68
1:A:11:PRO:HD3	1:B:215:HIS:HB2	1.75	0.68
1:C:115:TRP:CE3	1:C:115:TRP:C	2.72	0.67
1:D:126:THR:HG21	1:D:202:ASN:OD1	1.93	0.67
1:B:11:PRO:O	1:B:316:LYS:HG2	1.93	0.67
1:C:126:THR:HG21	1:C:202:ASN:OD1	1.94	0.67
1:C:306:ASN:ND2	1:C:308:ALA:HB3	2.09	0.67
1:D:126:THR:HB	1:D:200:GLY:HA3	1.74	0.67
1:A:126:THR:HG21	1:A:202:ASN:OD1	1.95	0.67
1:C:25:ASP:CG	1:C:26:SER:H	2.01	0.67
1:C:208:MSE:HA	1:D:209:ASP:OD1	1.93	0.66
1:B:164:LYS:HE2	3:B:658:HOH:O	1.96	0.66
1:D:115:TRP:CE3	1:D:115:TRP:C	2.73	0.66
1:C:9:MSE:HA	1:D:217:VAL:HG21	1.78	0.66
1:C:206:SER:O	1:C:208:MSE:HG2	1.94	0.66
1:A:286:LEU:HD22	1:A:291:LEU:HD22	1.76	0.66
1:B:213:ASP:N	1:B:214:PRO:HD2	2.10	0.66
1:C:64:PHE:HD2	1:D:79:PHE:HB2	1.60	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:24:ARG:NH1	1:A:27:VAL:O	2.28	0.65
1:C:24:ARG:O	1:C:27:VAL:HG13	1.97	0.65
1:A:9:MSE:HB2	1:B:217:VAL:HB	1.78	0.65
1:B:214:PRO:HG2	1:B:216:HIS:CE1	2.32	0.65
1:B:86:ARG:O	1:B:86:ARG:HG2	1.96	0.65
1:B:115:TRP:HB3	1:B:116:PRO:HD3	1.79	0.65
1:C:72:ARG:HH11	1:C:72:ARG:HG2	1.60	0.65
1:B:85:GLN:O	1:B:87:ILE:HD12	1.97	0.64
1:B:306:ASN:ND2	1:B:308:ALA:HB3	2.12	0.64
1:C:85:GLN:NE2	1:C:192:GLN:HE22	1.94	0.64
1:C:62:LEU:O	1:C:66:ILE:HG13	1.97	0.64
1:C:115:TRP:HB3	1:C:116:PRO:HD3	1.78	0.64
1:C:72:ARG:HG2	1:C:72:ARG:NH1	2.12	0.64
1:D:153:MSE:CG	1:D:156:LEU:HB3	2.28	0.63
1:A:86:ARG:NH2	1:A:194:ASP:HA	2.13	0.63
1:D:24:ARG:NH1	1:D:27:VAL:O	2.27	0.63
1:B:215:HIS:CG	1:B:216:HIS:N	2.66	0.63
1:A:115:TRP:HB3	1:A:116:PRO:HD3	1.80	0.62
1:C:201:LEU:HD22	1:C:290:ILE:HD11	1.80	0.62
1:B:75:VAL:HG23	1:B:76:LEU:N	2.14	0.62
1:B:25:ASP:CG	1:B:26:SER:H	2.07	0.62
1:D:115:TRP:HB3	1:D:116:PRO:HD3	1.80	0.62
1:C:207:GLY:O	1:D:209:ASP:OD1	2.18	0.62
1:A:167:VAL:HG13	1:A:168:PRO:HD2	1.81	0.61
1:A:306:ASN:ND2	1:A:308:ALA:HB3	2.15	0.61
1:D:306:ASN:ND2	1:D:308:ALA:HB3	2.15	0.61
1:A:201:LEU:HD22	1:A:290:ILE:HD11	1.83	0.61
1:D:167:VAL:HG13	1:D:168:PRO:HD2	1.81	0.61
1:D:313:ARG:HG2	1:D:313:ARG:HH11	1.66	0.61
1:C:9:MSE:HB2	1:D:217:VAL:HB	1.83	0.60
1:B:103:THR:O	1:B:107:VAL:HG12	2.01	0.60
1:A:65:TYR:HE2	1:B:75:VAL:HG21	1.62	0.60
1:C:25:ASP:CG	1:C:26:SER:N	2.60	0.60
1:A:69:ASN:C	1:A:69:ASN:HD22	2.09	0.59
1:A:25:ASP:CG	1:A:26:SER:N	2.61	0.59
1:C:29:MSE:HE2	1:C:31:LEU:CB	2.14	0.59
1:A:94:ALA:HB2	1:A:203:VAL:CG2	2.32	0.59
1:B:37:ALA:HA	1:B:40:LYS:HD2	1.84	0.59
1:B:115:TRP:CE3	1:B:115:TRP:O	2.56	0.59
1:C:64:PHE:HE2	1:D:79:PHE:HA	1.68	0.59
1:C:94:ALA:HB2	1:C:203:VAL:CG2	2.32	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:79:PHE:O	1:D:79:PHE:CG	2.56	0.58
1:C:313:ARG:HH11	1:C:313:ARG:HG2	1.68	0.58
1:D:24:ARG:O	1:D:27:VAL:HG13	2.03	0.58
1:C:167:VAL:HG13	1:C:168:PRO:HD2	1.85	0.58
1:A:232:PRO:HD2	1:A:235:LEU:HD12	1.84	0.58
1:B:33:GLU:HG3	1:B:48:LEU:HD13	1.86	0.58
1:C:276:THR:O	1:C:280:GLU:HG3	2.03	0.58
1:D:8:LEU:N	1:D:8:LEU:HD12	2.18	0.58
1:A:9:MSE:HA	1:B:217:VAL:HG21	1.86	0.58
1:A:24:ARG:O	1:A:27:VAL:HG13	2.03	0.58
1:B:94:ALA:HB2	1:B:203:VAL:CG2	2.34	0.57
1:B:201:LEU:HD22	1:B:290:ILE:HD11	1.85	0.57
1:C:37:ALA:HA	1:C:40:LYS:HD2	1.86	0.57
1:D:94:ALA:HB2	1:D:203:VAL:CG2	2.34	0.57
1:A:213:ASP:C	1:A:215:HIS:N	2.55	0.57
1:A:115:TRP:CB	1:A:116:PRO:HD3	2.35	0.57
1:A:272:LYS:O	1:A:276:THR:HG23	2.04	0.57
1:B:115:TRP:CB	1:B:116:PRO:HD3	2.35	0.57
1:D:241:ILE:HD11	1:D:275:MSE:HG3	1.86	0.57
1:A:153:MSE:CG	1:A:156:LEU:HB3	2.34	0.57
1:A:64:PHE:HE2	1:B:79:PHE:HA	1.68	0.56
1:B:24:ARG:O	1:B:27:VAL:HG13	2.04	0.56
1:C:115:TRP:CB	1:C:116:PRO:HD3	2.34	0.56
1:A:211:PRO:HB2	1:D:143:LYS:HD2	1.87	0.56
1:B:29:MSE:HE1	1:B:51:VAL:CG1	2.28	0.56
1:B:209:ASP:O	1:B:210:TYR:CB	2.53	0.56
1:D:25:ASP:CG	1:D:26:SER:N	2.59	0.56
1:A:70:LEU:HA	1:A:73:GLN:HE21	1.71	0.56
1:A:213:ASP:N	1:A:214:PRO:CD	2.67	0.56
1:B:115:TRP:C	1:B:115:TRP:CD2	2.84	0.56
1:C:103:THR:O	1:C:107:VAL:HG12	2.06	0.56
1:D:232:PRO:HD2	1:D:235:LEU:HD12	1.88	0.56
1:D:153:MSE:HG2	1:D:156:LEU:HB3	1.86	0.56
1:B:71:ARG:HH21	1:B:87:ILE:HG21	1.71	0.56
1:B:85:GLN:C	1:B:87:ILE:H	2.14	0.56
1:B:313:ARG:HG2	1:B:313:ARG:HH11	1.69	0.56
1:D:37:ALA:HA	1:D:40:LYS:HD2	1.87	0.56
1:D:272:LYS:O	1:D:276:THR:HG23	2.06	0.56
1:B:29:MSE:CE	1:B:51:VAL:HG11	2.28	0.56
1:A:313:ARG:HH11	1:A:313:ARG:HG2	1.70	0.56
1:D:201:LEU:HD22	1:D:290:ILE:HD11	1.88	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:115:TRP:CB	1:D:116:PRO:HD3	2.36	0.55
1:B:68:SER:O	1:B:69:ASN:C	2.50	0.55
1:A:73:GLN:O	1:A:77:GLU:HG3	2.07	0.55
1:B:25:ASP:CG	1:B:26:SER:N	2.64	0.55
1:B:85:GLN:C	1:B:87:ILE:HD12	2.32	0.55
1:B:215:HIS:C	1:B:216:HIS:O	2.44	0.55
1:A:103:THR:O	1:A:107:VAL:HG12	2.07	0.55
1:A:185:ASP:HB2	3:A:665:HOH:O	2.06	0.55
1:D:77:GLU:OE1	1:D:87:ILE:HD12	2.06	0.55
1:C:115:TRP:CE3	1:C:115:TRP:O	2.60	0.54
1:B:276:THR:O	1:B:280:GLU:HG3	2.06	0.54
1:A:90:ILE:HD11	1:A:164:LYS:HG3	1.89	0.54
1:B:153:MSE:CG	1:B:156:LEU:HB3	2.37	0.54
1:A:115:TRP:CE3	1:A:115:TRP:O	2.61	0.54
1:B:74:ALA:C	1:B:78:GLN:HE21	2.15	0.54
1:B:85:GLN:C	1:B:87:ILE:N	2.65	0.54
1:B:272:LYS:O	1:B:276:THR:HG23	2.08	0.54
1:C:232:PRO:HD2	1:C:235:LEU:HD12	1.89	0.54
1:D:207:GLY:C	1:D:210:TYR:HB2	2.33	0.54
1:A:11:PRO:HG3	1:B:215:HIS:CB	2.34	0.54
1:B:209:ASP:HB3	1:B:296:ARG:HH21	1.72	0.54
1:C:90:ILE:HD11	1:C:164:LYS:HG3	1.90	0.53
1:D:103:THR:O	1:D:107:VAL:HG12	2.08	0.53
1:D:115:TRP:CE3	1:D:115:TRP:O	2.62	0.53
1:B:85:GLN:O	1:B:86:ARG:HB3	2.09	0.53
1:A:153:MSE:HG3	1:A:156:LEU:HB3	1.90	0.53
1:C:272:LYS:O	1:C:276:THR:HG23	2.08	0.53
1:A:37:ALA:HA	1:A:40:LYS:HD2	1.91	0.53
1:C:115:TRP:C	1:C:115:TRP:CD2	2.87	0.53
1:A:33:GLU:HG3	1:A:48:LEU:HD13	1.91	0.53
1:C:153:MSE:HG3	1:C:156:LEU:HB3	1.90	0.53
1:D:69:ASN:O	1:D:71:ARG:N	2.42	0.53
1:B:68:SER:O	1:B:70:LEU:HD22	2.09	0.53
1:B:153:MSE:HG3	1:B:156:LEU:HB3	1.90	0.53
1:B:90:ILE:HD11	1:B:164:LYS:HG3	1.90	0.52
1:B:232:PRO:HD2	1:B:235:LEU:HD12	1.90	0.52
1:B:241:ILE:HD11	1:B:275:MSE:HG3	1.91	0.52
1:C:10:THR:HG22	1:D:215:HIS:NE2	2.23	0.52
1:C:24:ARG:NH1	1:C:27:VAL:O	2.34	0.52
1:D:115:TRP:C	1:D:115:TRP:CD2	2.87	0.52
1:C:97:VAL:O	1:C:98:ALA:HB3	2.09	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:97:VAL:O	1:A:98:ALA:HB3	2.10	0.52
1:A:115:TRP:CG	1:A:116:PRO:HD3	2.44	0.52
1:A:276:THR:O	1:A:280:GLU:HG3	2.10	0.52
1:C:208:MSE:CA	1:D:209:ASP:OD1	2.58	0.52
1:D:153:MSE:HG3	1:D:156:LEU:HB3	1.91	0.52
1:A:8:LEU:HD22	1:B:158:LYS:HD2	1.91	0.52
1:B:24:ARG:NH1	1:B:27:VAL:O	2.33	0.52
1:A:29:MSE:CE	1:A:51:VAL:HG11	2.31	0.51
1:A:115:TRP:C	1:A:115:TRP:CD2	2.87	0.51
1:B:97:VAL:O	1:B:98:ALA:HB3	2.10	0.51
1:C:115:TRP:CG	1:C:116:PRO:HD3	2.45	0.51
1:C:153:MSE:CG	1:C:156:LEU:HB3	2.40	0.51
1:D:211:PRO:HB2	1:D:216:HIS:CD2	2.38	0.51
1:D:252:PHE:O	1:D:260:HIS:HD2	1.93	0.51
1:B:77:GLU:O	1:B:81:GLY:N	2.44	0.51
1:D:65:TYR:CD2	1:D:70:LEU:HD23	2.46	0.51
1:B:252:PHE:O	1:B:260:HIS:HD2	1.94	0.51
1:B:206:SER:C	1:B:208:MSE:H	2.17	0.51
1:D:207:GLY:HA2	1:D:210:TYR:HB2	1.92	0.51
1:B:115:TRP:CG	1:B:116:PRO:HD3	2.45	0.50
1:C:29:MSE:HG3	1:C:31:LEU:H	1.75	0.50
1:D:29:MSE:CE	1:D:51:VAL:HG11	2.29	0.50
1:A:76:LEU:O	1:A:80:LEU:HG	2.12	0.50
1:A:139:ARG:O	1:D:260:HIS:HE1	1.95	0.50
1:C:33:GLU:HG3	1:C:48:LEU:HD13	1.92	0.50
1:D:112:LEU:O	1:D:119:ARG:HD2	2.11	0.50
1:D:207:GLY:O	1:D:210:TYR:HD1	1.94	0.50
1:C:64:PHE:HE2	1:D:79:PHE:CA	2.25	0.49
1:D:97:VAL:O	1:D:98:ALA:HB3	2.11	0.49
1:A:283:TRP:CZ2	1:A:287:LYS:HD2	2.47	0.49
1:D:276:THR:O	1:D:280:GLU:HG3	2.12	0.49
1:A:73:GLN:HG2	1:A:85:GLN:CD	2.37	0.49
1:A:85:GLN:O	1:A:86:ARG:HB3	2.12	0.49
1:A:252:PHE:O	1:A:260:HIS:HD2	1.95	0.49
1:A:29:MSE:HG3	1:A:31:LEU:H	1.78	0.49
1:A:58:LEU:O	1:A:62:LEU:HB2	2.13	0.49
1:B:58:LEU:O	1:B:62:LEU:HB2	2.12	0.49
1:C:252:PHE:O	1:C:260:HIS:HD2	1.96	0.49
1:A:8:LEU:CD2	1:B:158:LYS:HD2	2.42	0.48
1:C:11:PRO:CG	1:D:215:HIS:HA	2.41	0.48
1:A:213:ASP:O	1:A:215:HIS:N	2.47	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:313:ARG:HG2	1:D:313:ARG:NH1	2.28	0.48
1:A:29:MSE:HE2	1:A:31:LEU:CB	2.09	0.48
1:C:29:MSE:HE1	1:C:51:VAL:CG1	2.34	0.48
1:D:90:ILE:HD11	1:D:164:LYS:HG3	1.96	0.48
1:B:233:GLU:OE1	1:B:287:LYS:HE3	2.14	0.47
1:B:74:ALA:O	1:B:78:GLN:HG2	2.13	0.47
1:B:112:LEU:O	1:B:119:ARG:HD2	2.13	0.47
1:B:176:SER:HB3	1:B:179:ILE:HG12	1.96	0.47
1:D:33:GLU:HG3	1:D:48:LEU:HD13	1.95	0.47
1:C:129:PHE:CZ	1:C:173:PRO:HD2	2.49	0.47
1:A:112:LEU:O	1:A:119:ARG:HD2	2.14	0.47
1:B:313:ARG:HG2	1:B:313:ARG:NH1	2.30	0.47
1:A:75:VAL:HG22	1:A:76:LEU:N	2.29	0.47
1:A:129:PHE:CZ	1:A:173:PRO:HD2	2.49	0.47
1:D:64:PHE:O	1:D:68:SER:HB2	2.14	0.47
1:D:115:TRP:CG	1:D:116:PRO:HD3	2.49	0.47
1:B:137:LYS:NZ	3:B:760:HOH:O	2.47	0.47
1:B:316:LYS:HG2	1:B:316:LYS:H	1.54	0.47
1:D:266:THR:HG22	1:D:269:GLU:HB2	1.96	0.47
1:C:233:GLU:OE1	1:C:287:LYS:HE3	2.15	0.47
1:A:209:ASP:OD1	1:A:296:ARG:NH2	2.47	0.47
1:D:68:SER:O	1:D:70:LEU:N	2.48	0.47
1:B:126:THR:CG2	1:B:151:TYR:CE2	2.98	0.47
1:D:233:GLU:OE1	1:D:287:LYS:HE3	2.15	0.47
1:A:85:GLN:O	1:A:86:ARG:CB	2.63	0.46
1:B:153:MSE:O	1:B:153:MSE:HG2	2.15	0.46
1:C:64:PHE:CE2	1:D:79:PHE:HB2	2.49	0.46
1:D:291:LEU:HD11	1:D:294:ARG:NH1	2.30	0.46
1:B:68:SER:O	1:B:70:LEU:N	2.48	0.46
1:B:215:HIS:CD2	1:B:216:HIS:N	2.57	0.46
1:C:112:LEU:O	1:C:119:ARG:HD2	2.15	0.46
1:D:207:GLY:CA	1:D:210:TYR:HB2	2.45	0.46
1:A:153:MSE:HG2	1:A:156:LEU:HB3	1.98	0.46
1:B:264:LYS:HZ2	1:C:139:ARG:HB3	1.80	0.46
1:A:316:LYS:HG2	1:A:316:LYS:H	1.54	0.46
1:C:71:ARG:HE	1:C:71:ARG:HB2	1.41	0.46
1:C:313:ARG:HG2	1:C:313:ARG:NH1	2.29	0.46
1:B:75:VAL:HG23	1:B:76:LEU:H	1.81	0.46
1:C:215:HIS:N	1:C:215:HIS:CD2	2.84	0.46
1:A:128:GLY:HA2	1:A:175:TYR:HB2	1.98	0.45
1:A:212:HIS:N	1:A:214:PRO:HD3	2.31	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:96:SER:O	1:B:99:VAL:HG12	2.15	0.45
1:B:266:THR:HG22	1:B:269:GLU:HB2	1.99	0.45
1:C:208:MSE:HB3	1:D:209:ASP:OD1	2.16	0.45
1:C:58:LEU:O	1:C:62:LEU:HB2	2.16	0.45
1:D:65:TYR:HD2	1:D:70:LEU:HD23	1.80	0.45
1:D:129:PHE:CZ	1:D:173:PRO:HD2	2.51	0.45
1:D:208:MSE:O	1:D:209:ASP:HB3	2.14	0.45
1:A:153:MSE:CE	1:A:202:ASN:ND2	2.80	0.45
1:A:75:VAL:CG2	1:A:76:LEU:N	2.80	0.45
1:A:233:GLU:OE1	1:A:287:LYS:HE3	2.17	0.45
1:B:116:PRO:HG2	1:B:119:ARG:NH2	2.32	0.45
1:C:241:ILE:HD11	1:C:275:MSE:HG3	1.98	0.45
1:D:29:MSE:HG3	1:D:31:LEU:H	1.82	0.45
1:B:123:LEU:C	1:B:123:LEU:HD12	2.42	0.44
1:A:313:ARG:HG2	1:A:313:ARG:NH1	2.32	0.44
1:B:213:ASP:O	1:B:214:PRO:C	2.61	0.44
1:D:28:PRO:HD2	1:D:115:TRP:CZ3	2.52	0.44
1:B:36:ILE:HD12	1:B:48:LEU:HD12	1.99	0.44
1:B:129:PHE:CZ	1:B:173:PRO:HD2	2.52	0.44
1:D:58:LEU:O	1:D:62:LEU:HB2	2.16	0.44
1:A:176:SER:HB3	1:A:179:ILE:HG12	2.00	0.44
1:B:209:ASP:O	1:B:210:TYR:HB3	2.18	0.44
1:C:163:LEU:HD12	1:C:163:LEU:HA	1.86	0.44
1:C:296:ARG:HD3	1:D:208:MSE:HA	2.00	0.44
1:D:29:MSE:HE1	1:D:51:VAL:CG1	2.31	0.44
1:D:86:ARG:HA	1:D:86:ARG:HD2	1.72	0.44
1:A:36:ILE:HD12	1:A:48:LEU:HD12	2.00	0.44
1:C:8:LEU:HD13	1:C:9:MSE:HB3	1.99	0.44
1:C:266:THR:HG22	1:C:269:GLU:HB2	1.99	0.44
1:A:206:SER:HA	1:A:218:PHE:CD1	2.52	0.44
1:C:291:LEU:HD11	1:C:294:ARG:NH1	2.32	0.44
1:D:128:GLY:HA2	1:D:175:TYR:HB2	2.00	0.44
1:B:215:HIS:HD2	1:B:216:HIS:H	1.47	0.44
1:C:12:TYR:CE2	1:C:315:ARG:HB2	2.53	0.44
1:C:153:MSE:O	1:C:153:MSE:HG2	2.17	0.44
1:B:306:ASN:HD21	1:B:308:ALA:HB3	1.83	0.44
1:A:17:ARG:HH22	1:A:50:GLU:HA	1.82	0.43
1:C:316:LYS:HG2	1:C:316:LYS:H	1.56	0.43
1:A:42:ILE:HD13	1:A:247:PHE:HE2	1.83	0.43
1:A:69:ASN:C	1:A:69:ASN:ND2	2.75	0.43
1:B:86:ARG:CZ	1:B:192:GLN:HE22	2.30	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:163:LEU:HD13	1:B:170:VAL:HG11	2.00	0.43
1:B:286:LEU:CD2	1:B:291:LEU:HD22	2.46	0.43
1:A:266:THR:HG22	1:A:269:GLU:HB2	2.01	0.43
1:C:267:LYS:O	1:C:271:ILE:HG13	2.19	0.43
1:D:123:LEU:HD12	1:D:123:LEU:C	2.43	0.43
1:B:85:GLN:HE21	1:B:85:GLN:N	2.17	0.43
1:B:283:TRP:CZ2	1:B:287:LYS:HD2	2.53	0.43
1:B:291:LEU:HD11	1:B:294:ARG:NH1	2.33	0.43
1:C:36:ILE:HD12	1:C:48:LEU:HD12	2.00	0.43
1:C:306:ASN:HD21	1:C:308:ALA:HB3	1.81	0.43
1:C:96:SER:O	1:C:99:VAL:HG12	2.18	0.43
1:D:92:SER:C	1:D:93:ILE:HG12	2.42	0.43
1:D:176:SER:HB3	1:D:179:ILE:HG12	1.99	0.43
1:D:207:GLY:HA2	1:D:210:TYR:CB	2.49	0.43
1:C:79:PHE:HB2	1:D:64:PHE:CD2	2.54	0.43
1:C:176:SER:HB3	1:C:179:ILE:HG12	2.01	0.43
1:B:47:SER:OG	1:B:49:GLU:HG2	2.19	0.43
1:C:283:TRP:CZ2	1:C:287:LYS:HD2	2.53	0.43
1:D:291:LEU:HD13	1:D:291:LEU:HA	1.81	0.43
1:B:28:PRO:HD2	1:B:115:TRP:CZ3	2.54	0.42
1:B:56:LEU:HD23	1:B:56:LEU:HA	1.86	0.42
1:D:241:ILE:O	1:D:244:PHE:HB3	2.18	0.42
1:B:121:VAL:HA	1:B:195:ILE:O	2.19	0.42
1:A:267:LYS:O	1:A:271:ILE:HG13	2.20	0.42
1:C:115:TRP:CB	1:C:116:PRO:CD	2.97	0.42
1:B:163:LEU:HD12	1:B:163:LEU:HA	1.88	0.42
1:B:210:TYR:HA	1:B:213:ASP:OD1	2.19	0.42
1:C:123:LEU:HD12	1:C:123:LEU:C	2.45	0.42
1:C:207:GLY:O	1:D:209:ASP:CG	2.62	0.42
1:D:73:GLN:O	1:D:73:GLN:CG	2.68	0.42
1:D:283:TRP:CZ2	1:D:287:LYS:HD2	2.54	0.42
1:C:108:LEU:HD12	1:C:108:LEU:HA	1.94	0.42
1:C:128:GLY:HA2	1:C:175:TYR:HB2	2.01	0.42
1:B:29:MSE:HG3	1:B:31:LEU:H	1.83	0.42
1:C:42:ILE:HD13	1:C:247:PHE:HE2	1.84	0.42
1:C:121:VAL:HA	1:C:195:ILE:O	2.19	0.42
1:C:126:THR:CG2	1:C:151:TYR:CE2	3.03	0.42
1:D:186:GLY:O	1:D:187:ASP:C	2.62	0.42
1:B:71:ARG:HG3	1:B:71:ARG:HH11	1.84	0.42
1:B:75:VAL:CG2	1:B:76:LEU:N	2.82	0.42
1:B:92:SER:C	1:B:93:ILE:HG12	2.44	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:28:PRO:HD2	1:C:115:TRP:CZ3	2.54	0.42
1:C:29:MSE:CE	1:C:51:VAL:HG11	2.35	0.42
1:A:126:THR:CG2	1:A:151:TYR:CE2	3.03	0.42
1:B:264:LYS:NZ	1:C:139:ARG:HB3	2.35	0.42
1:C:72:ARG:HA	1:D:70:LEU:HD21	2.01	0.42
1:D:126:THR:CG2	1:D:151:TYR:CE2	3.03	0.42
1:A:11:PRO:CD	1:B:215:HIS:CB	2.96	0.42
1:A:304:SER:OG	1:A:310:GLU:HG2	2.20	0.42
1:D:237:GLN:NE2	1:D:275:MSE:HG2	2.35	0.42
1:B:70:LEU:HD13	1:B:70:LEU:HA	1.69	0.42
1:B:83:ASN:HB3	1:B:84:GLY:H	1.25	0.42
1:D:12:TYR:CE2	1:D:315:ARG:HB2	2.55	0.42
1:D:304:SER:OG	1:D:310:GLU:HG2	2.20	0.42
1:A:54:ILE:O	1:A:57:PRO:HD2	2.20	0.41
1:A:71:ARG:HH21	1:B:70:LEU:HD13	1.84	0.41
1:B:153:MSE:HG2	1:B:156:LEU:HB3	2.02	0.41
1:D:316:LYS:HG2	1:D:316:LYS:H	1.55	0.41
1:B:115:TRP:CB	1:B:116:PRO:CD	2.98	0.41
1:C:127:ASP:OD1	1:C:128:GLY:N	2.53	0.41
1:A:115:TRP:CB	1:A:116:PRO:CD	2.98	0.41
1:B:17:ARG:HH22	1:B:50:GLU:HA	1.85	0.41
1:B:33:GLU:CG	1:B:48:LEU:HD13	2.50	0.41
1:D:36:ILE:HD12	1:D:48:LEU:HD12	2.01	0.41
1:D:133:ASN:O	1:D:137:LYS:HD3	2.21	0.41
1:D:210:TYR:CB	1:D:211:PRO:CD	2.69	0.41
1:A:64:PHE:CE2	1:B:79:PHE:HA	2.52	0.41
1:A:186:GLY:O	1:A:187:ASP:C	2.63	0.41
1:B:127:ASP:OD1	1:B:128:GLY:N	2.53	0.41
1:B:215:HIS:O	1:B:216:HIS:O	2.37	0.41
1:C:72:ARG:HH11	1:C:72:ARG:HG3	1.76	0.41
1:D:47:SER:OG	1:D:49:GLU:HG2	2.20	0.41
1:D:69:ASN:O	1:D:69:ASN:CG	2.63	0.41
1:A:291:LEU:HD11	1:A:294:ARG:NH1	2.36	0.41
1:B:128:GLY:HA2	1:B:175:TYR:HB2	2.03	0.41
1:D:223:VAL:HG21	3:D:736:HOH:O	2.20	0.41
1:B:85:GLN:CA	1:B:87:ILE:CD1	2.93	0.41
1:C:55:TYR:HE2	1:C:104:THR:HG23	1.84	0.41
1:C:129:PHE:CD2	1:C:155:ARG:HG2	2.55	0.41
1:D:204:LEU:HD12	1:D:204:LEU:HA	1.90	0.41
1:A:56:LEU:HD23	1:A:56:LEU:HA	1.85	0.41
1:A:163:LEU:HD13	1:A:170:VAL:HG11	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:40:LYS:HE3	1:B:46:LEU:H	1.86	0.41
1:B:97:VAL:HG12	1:B:201:LEU:HD21	2.02	0.41
1:B:115:TRP:CG	1:B:116:PRO:CD	3.04	0.41
1:B:126:THR:HG23	1:B:151:TYR:CE2	2.55	0.41
1:B:133:ASN:O	1:B:137:LYS:HD3	2.21	0.41
1:C:116:PRO:HG2	1:C:119:ARG:NH2	2.35	0.41
1:C:65:TYR:CD2	1:D:75:VAL:HG21	2.56	0.41
1:D:133:ASN:HD22	1:D:133:ASN:HA	1.74	0.41
1:A:71:ARG:HH21	1:B:70:LEU:CD1	2.34	0.40
1:A:123:LEU:HD12	1:A:123:LEU:C	2.46	0.40
1:C:72:ARG:HD2	1:C:76:LEU:HD22	2.02	0.40
1:C:163:LEU:HD13	1:C:170:VAL:HG11	2.03	0.40
1:A:12:TYR:CE2	1:A:315:ARG:HB2	2.56	0.40
1:A:163:LEU:HD12	1:A:163:LEU:HA	1.86	0.40
1:C:17:ARG:HH22	1:C:50:GLU:HA	1.85	0.40
1:D:70:LEU:HD12	1:D:70:LEU:HA	1.86	0.40
1:B:291:LEU:HD13	1:B:291:LEU:HA	1.83	0.40
1:A:47:SER:OG	1:A:49:GLU:HG2	2.22	0.40
1:A:92:SER:C	1:A:93:ILE:HG12	2.47	0.40
1:C:306:ASN:HD22	1:C:308:ALA:HB3	1.86	0.40
1:D:17:ARG:HH22	1:D:50:GLU:HA	1.85	0.40
1:D:126:THR:HG23	1:D:151:TYR:CE2	2.56	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	309/316 (98%)	284 (92%)	18 (6%)	7 (2%)	5 8
1	B	303/316 (96%)	279 (92%)	17 (6%)	7 (2%)	5 8
1	C	303/316 (96%)	278 (92%)	20 (7%)	5 (2%)	7 13

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
1	D	297/316 (94%)	273 (92%)	15 (5%)	9 (3%)	3 5
All	All	1212/1264 (96%)	1114 (92%)	70 (6%)	28 (2%)	5 8

All (28) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	85	GLN
1	A	86	ARG
1	A	168	PRO
1	B	69	ASN
1	B	168	PRO
1	B	214	PRO
1	C	168	PRO
1	D	69	ASN
1	D	115	TRP
1	D	168	PRO
1	D	209	ASP
1	D	210	TYR
1	A	115	TRP
1	B	115	TRP
1	B	216	HIS
1	C	115	TRP
1	A	120	ARG
1	B	120	ARG
1	C	87	ILE
1	D	120	ARG
1	A	121	VAL
1	A	210	TYR
1	B	121	VAL
1	C	121	VAL
1	D	121	VAL
1	C	120	ARG
1	D	70	LEU
1	D	79	PHE

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	280/278 (101%)	226 (81%)	54 (19%)	1	2
1	B	276/278 (99%)	222 (80%)	54 (20%)	1	2
1	C	276/278 (99%)	218 (79%)	58 (21%)	1	2
1	D	273/278 (98%)	215 (79%)	58 (21%)	1	2
All	All	1105/1112 (99%)	881 (80%)	224 (20%)	1	2

All (224) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	6	GLN
1	A	7	THR
1	A	8	LEU
1	A	10	THR
1	A	17	ARG
1	A	24	ARG
1	A	27	VAL
1	A	29	MSE
1	A	38	ARG
1	A	48	LEU
1	A	49	GLU
1	A	62	LEU
1	A	68	SER
1	A	69	ASN
1	A	70	LEU
1	A	75	VAL
1	A	78	GLN
1	A	83	ASN
1	A	85	GLN
1	A	86	ARG
1	A	90	ILE
1	A	93	ILE
1	A	97	VAL
1	A	101	LYS
1	A	107	VAL
1	A	108	LEU
1	A	114	ARG
1	A	115	TRP
1	A	120	ARG
1	A	126	THR
1	A	137	LYS

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Mol	Chain	Res	Type
1	A	145	LYS
1	A	182	VAL
1	A	191	VAL
1	A	199	GLU
1	A	204	LEU
1	A	238	THR
1	A	248	ARG
1	A	264	LYS
1	A	267	LYS
1	A	269	GLU
1	A	272	LYS
1	A	276	THR
1	A	284	LEU
1	A	286	LEU
1	A	287	LYS
1	A	289	ASN
1	A	291	LEU
1	A	296	ARG
1	A	298	SER
1	A	304	SER
1	A	306	ASN
1	A	313	ARG
1	A	316	LYS
1	B	9	MSE
1	B	10	THR
1	B	17	ARG
1	B	24	ARG
1	B	27	VAL
1	B	29	MSE
1	B	38	ARG
1	B	48	LEU
1	B	49	GLU
1	B	62	LEU
1	B	70	LEU
1	B	72	ARG
1	B	76	LEU
1	B	80	LEU
1	B	82	THR
1	B	83	ASN
1	B	86	ARG
1	B	90	ILE
1	B	93	ILE

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Mol	Chain	Res	Type
1	B	97	VAL
1	B	101	LYS
1	B	107	VAL
1	B	114	ARG
1	B	115	TRP
1	B	120	ARG
1	B	123	LEU
1	B	126	THR
1	B	137	LYS
1	B	144	LYS
1	B	145	LYS
1	B	182	VAL
1	B	191	VAL
1	B	199	GLU
1	B	204	LEU
1	B	205	GLN
1	B	206	SER
1	B	215	HIS
1	B	248	ARG
1	B	264	LYS
1	B	267	LYS
1	B	269	GLU
1	B	272	LYS
1	B	276	THR
1	B	284	LEU
1	B	286	LEU
1	B	287	LYS
1	B	289	ASN
1	B	291	LEU
1	B	296	ARG
1	B	298	SER
1	B	304	SER
1	B	306	ASN
1	B	313	ARG
1	B	316	LYS
1	C	6	GLN
1	C	7	THR
1	C	8	LEU
1	C	10	THR
1	C	17	ARG
1	C	24	ARG
1	C	27	VAL

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Mol	Chain	Res	Type
1	C	29	MSE
1	C	38	ARG
1	C	48	LEU
1	C	49	GLU
1	C	62	LEU
1	C	66	ILE
1	C	71	ARG
1	C	72	ARG
1	C	75	VAL
1	C	76	LEU
1	C	78	GLN
1	C	80	LEU
1	C	85	GLN
1	C	86	ARG
1	C	90	ILE
1	C	93	ILE
1	C	97	VAL
1	C	101	LYS
1	C	107	VAL
1	C	108	LEU
1	C	114	ARG
1	C	115	TRP
1	C	120	ARG
1	C	123	LEU
1	C	126	THR
1	C	137	LYS
1	C	144	LYS
1	C	145	LYS
1	C	182	VAL
1	C	191	VAL
1	C	199	GLU
1	C	204	LEU
1	C	205	GLN
1	C	215	HIS
1	C	248	ARG
1	C	264	LYS
1	C	267	LYS
1	C	269	GLU
1	C	272	LYS
1	C	276	THR
1	C	284	LEU
1	C	286	LEU

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Mol	Chain	Res	Type
1	C	287	LYS
1	C	289	ASN
1	C	291	LEU
1	C	296	ARG
1	C	298	SER
1	C	304	SER
1	C	306	ASN
1	C	313	ARG
1	C	316	LYS
1	D	8	LEU
1	D	9	MSE
1	D	17	ARG
1	D	24	ARG
1	D	27	VAL
1	D	29	MSE
1	D	38	ARG
1	D	48	LEU
1	D	49	GLU
1	D	62	LEU
1	D	68	SER
1	D	70	LEU
1	D	71	ARG
1	D	72	ARG
1	D	73	GLN
1	D	76	LEU
1	D	77	GLU
1	D	78	GLN
1	D	80	LEU
1	D	82	THR
1	D	86	ARG
1	D	87	ILE
1	D	90	ILE
1	D	93	ILE
1	D	97	VAL
1	D	101	LYS
1	D	107	VAL
1	D	108	LEU
1	D	114	ARG
1	D	115	TRP
1	D	120	ARG
1	D	123	LEU
1	D	126	THR

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Mol	Chain	Res	Type
1	D	137	LYS
1	D	145	LYS
1	D	182	VAL
1	D	191	VAL
1	D	199	GLU
1	D	204	LEU
1	D	209	ASP
1	D	210	TYR
1	D	248	ARG
1	D	264	LYS
1	D	267	LYS
1	D	269	GLU
1	D	272	LYS
1	D	276	THR
1	D	284	LEU
1	D	286	LEU
1	D	287	LYS
1	D	289	ASN
1	D	291	LEU
1	D	296	ARG
1	D	298	SER
1	D	304	SER
1	D	306	ASN
1	D	313	ARG
1	D	316	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (35) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	14	GLN
1	A	69	ASN
1	A	73	GLN
1	A	78	GLN
1	A	85	GLN
1	A	133	ASN
1	A	260	HIS
1	A	289	ASN
1	A	306	ASN
1	B	14	GLN
1	B	78	GLN
1	B	85	GLN
1	B	118	HIS

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Mol	Chain	Res	Type
1	B	133	ASN
1	B	192	GLN
1	B	215	HIS
1	B	216	HIS
1	B	260	HIS
1	B	306	ASN
1	C	14	GLN
1	C	73	GLN
1	C	133	ASN
1	C	192	GLN
1	C	215	HIS
1	C	260	HIS
1	C	306	ASN
1	D	14	GLN
1	D	73	GLN
1	D	118	HIS
1	D	133	ASN
1	D	216	HIS
1	D	260	HIS
1	D	261	ASN
1	D	289	ASN
1	D	306	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](#)

4 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	COA	C	402	-	47,50,50	2.73	8 (17%)	69,75,75	2.67	16 (23%)
2	COA	A	401	-	47,50,50	2.71	6 (12%)	69,75,75	1.95	15 (21%)
2	COA	B	404	-	47,50,50	2.81	7 (14%)	69,75,75	1.94	13 (18%)
2	COA	D	403	-	47,50,50	2.74	6 (12%)	69,75,75	1.95	13 (18%)

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
2	COA	C	402	-	-	10/48/64/64	0/3/3/3
2	COA	A	401	-	-	10/48/64/64	0/3/3/3
2	COA	B	404	-	-	8/48/64/64	0/3/3/3
2	COA	D	403	-	-	6/48/64/64	0/3/3/3

All (27) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	404	COA	O9P-C9P	-12.19	1.00	1.23
2	A	401	COA	O9P-C9P	-12.05	1.00	1.23
2	C	402	COA	O9P-C9P	-12.04	1.00	1.23
2	D	403	COA	O9P-C9P	-11.87	1.00	1.23
2	A	401	COA	C9P-N8P	11.63	1.60	1.33
2	D	403	COA	C9P-N8P	11.56	1.60	1.33
2	B	404	COA	C9P-N8P	11.33	1.60	1.33
2	C	402	COA	C9P-N8P	11.16	1.59	1.33
2	B	404	COA	P1A-O3A	-5.04	1.54	1.59
2	D	403	COA	P1A-O3A	-4.40	1.54	1.59
2	B	404	COA	P2A-O3A	-3.57	1.55	1.59
2	C	402	COA	P1A-O3A	-3.29	1.55	1.59
2	B	404	COA	C7P-N8P	3.14	1.53	1.46
2	D	403	COA	C7P-N8P	3.02	1.53	1.46
2	C	402	COA	C7P-N8P	2.99	1.52	1.46
2	C	402	COA	OAP-CAP	2.98	1.47	1.42

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	401	COA	P1A-O3A	-2.96	1.56	1.59
2	A	401	COA	C7P-N8P	2.85	1.52	1.46
2	D	403	COA	C4A-N3A	2.56	1.39	1.34
2	C	402	COA	P2A-O3A	-2.49	1.56	1.59
2	A	401	COA	C4A-N3A	2.44	1.39	1.34
2	C	402	COA	C4A-N3A	2.41	1.38	1.34
2	B	404	COA	C7P-C6P	2.32	1.59	1.51
2	C	402	COA	P3B-O9A	-2.24	1.46	1.54
2	D	403	COA	P3B-O9A	-2.20	1.46	1.54
2	B	404	COA	P3B-O9A	-2.18	1.46	1.54
2	A	401	COA	P3B-O9A	-2.17	1.46	1.54

All (57) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	402	COA	OAP-CAP-CBP	-13.44	79.03	110.18
2	C	402	COA	O9P-C9P-CAP	7.48	141.79	120.89
2	D	403	COA	O9P-C9P-CAP	7.47	141.75	120.89
2	B	404	COA	O9P-C9P-CAP	7.46	141.72	120.89
2	A	401	COA	O9P-C9P-CAP	7.36	141.43	120.89
2	A	401	COA	CAP-C9P-N8P	-7.35	102.54	116.48
2	C	402	COA	OAP-CAP-C9P	7.30	139.84	109.38
2	D	403	COA	CAP-C9P-N8P	-7.28	102.67	116.48
2	B	404	COA	CAP-C9P-N8P	-7.14	102.94	116.48
2	C	402	COA	CAP-C9P-N8P	-6.99	103.22	116.48
2	C	402	COA	C6P-C5P-N4P	-4.31	108.48	116.34
2	B	404	COA	C6P-C5P-N4P	-4.27	108.57	116.34
2	A	401	COA	C6P-C5P-N4P	-4.13	108.82	116.34
2	D	403	COA	C6P-C5P-N4P	-4.00	109.05	116.34
2	B	404	COA	C2B-C1B-N9A	3.87	122.92	113.30
2	C	402	COA	C2B-C1B-N9A	3.79	122.72	113.30
2	C	402	COA	O9P-C9P-N8P	-3.78	114.99	122.98
2	D	403	COA	C2B-C1B-N9A	3.68	122.44	113.30
2	B	404	COA	O9P-C9P-N8P	-3.61	115.33	122.98
2	A	401	COA	C2P-C3P-N4P	-3.54	104.27	112.31
2	D	403	COA	C2P-C3P-N4P	-3.51	104.34	112.31
2	D	403	COA	O9P-C9P-N8P	-3.50	115.57	122.98
2	A	401	COA	C2B-C1B-N9A	3.45	121.88	113.30
2	C	402	COA	C2P-C3P-N4P	-3.44	104.51	112.31
2	B	404	COA	C2P-C3P-N4P	-3.36	104.68	112.31
2	A	401	COA	O9P-C9P-N8P	-3.29	116.02	122.98
2	C	402	COA	CEP-CBP-CDP	-2.85	103.52	109.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	401	COA	CEP-CBP-CDP	-2.77	103.67	109.20
2	B	404	COA	CEP-CBP-CDP	-2.66	103.89	109.20
2	D	403	COA	C3P-N4P-C5P	2.62	127.71	122.82
2	C	402	COA	CEP-CBP-CAP	2.56	113.13	108.77
2	C	402	COA	C3P-N4P-C5P	2.51	127.50	122.82
2	A	401	COA	O3A-P2A-O4A	-2.50	103.18	110.70
2	A	401	COA	CEP-CBP-CAP	2.48	113.00	108.77
2	D	403	COA	CEP-CBP-CAP	2.47	112.98	108.77
2	D	403	COA	CEP-CBP-CDP	-2.45	104.31	109.20
2	D	403	COA	CDP-CBP-CCP	-2.43	104.22	108.22
2	C	402	COA	O3A-P2A-O4A	-2.40	103.50	110.70
2	C	402	COA	O5P-C5P-N4P	2.38	127.70	123.03
2	A	401	COA	C3P-N4P-C5P	2.36	127.22	122.82
2	D	403	COA	O5P-C5P-N4P	2.35	127.64	123.03
2	A	401	COA	CDP-CBP-CCP	-2.32	104.40	108.22
2	B	404	COA	CEP-CBP-CAP	2.30	112.68	108.77
2	B	404	COA	O5P-C5P-N4P	2.30	127.53	123.03
2	B	404	COA	CDP-CBP-CCP	-2.28	104.47	108.22
2	B	404	COA	O3A-P2A-O4A	-2.27	103.89	110.70
2	B	404	COA	C3P-N4P-C5P	2.25	127.02	122.82
2	A	401	COA	O9A-P3B-O7A	2.25	119.60	110.83
2	D	403	COA	O3A-P2A-O4A	-2.22	104.01	110.70
2	D	403	COA	O9A-P3B-O7A	2.22	119.49	110.83
2	C	402	COA	O9A-P3B-O7A	2.22	119.48	110.83
2	A	401	COA	O5P-C5P-N4P	2.16	127.27	123.03
2	A	401	COA	O4B-C4B-C3B	2.15	109.46	104.92
2	B	404	COA	O9A-P3B-O7A	2.06	118.88	110.83
2	C	402	COA	CDP-CBP-CCP	-2.06	104.83	108.22
2	C	402	COA	O4B-C4B-C3B	2.06	109.25	104.92
2	A	401	COA	OAP-CAP-CBP	-2.00	105.54	110.18

There are no chirality outliers.

All (34) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	401	COA	C5P-C6P-C7P-N8P
2	B	404	COA	C5P-C6P-C7P-N8P
2	C	402	COA	C5P-C6P-C7P-N8P
2	D	403	COA	C5P-C6P-C7P-N8P
2	A	401	COA	P2A-O3A-P1A-O1A
2	B	404	COA	P2A-O3A-P1A-O1A
2	C	402	COA	P2A-O3A-P1A-O1A

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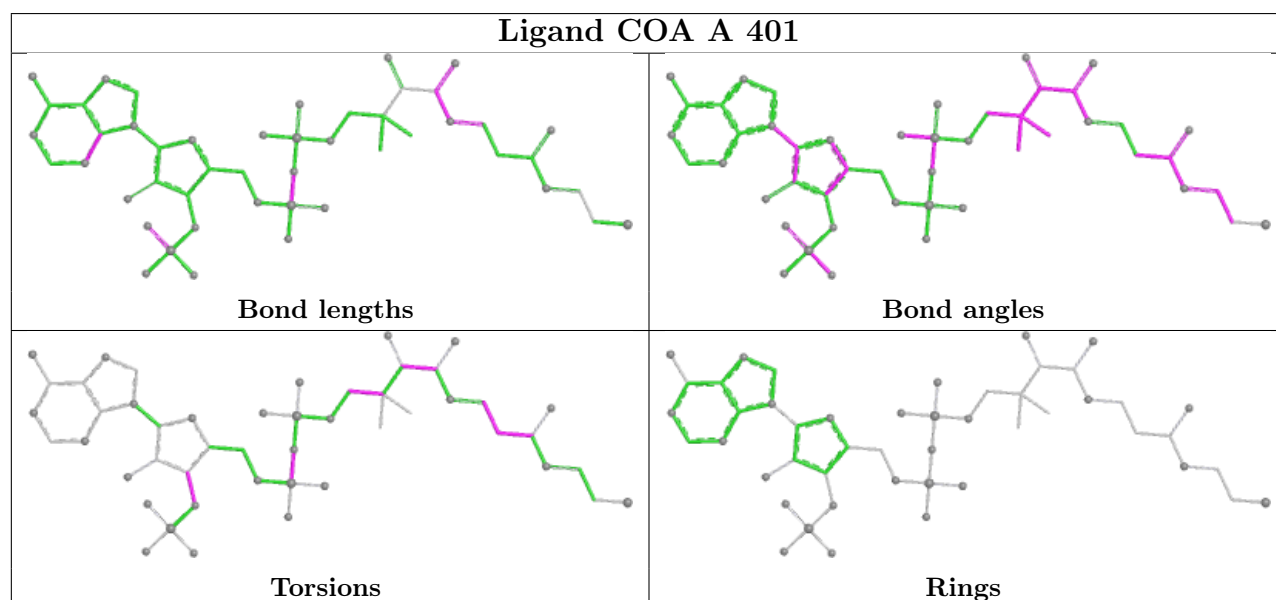
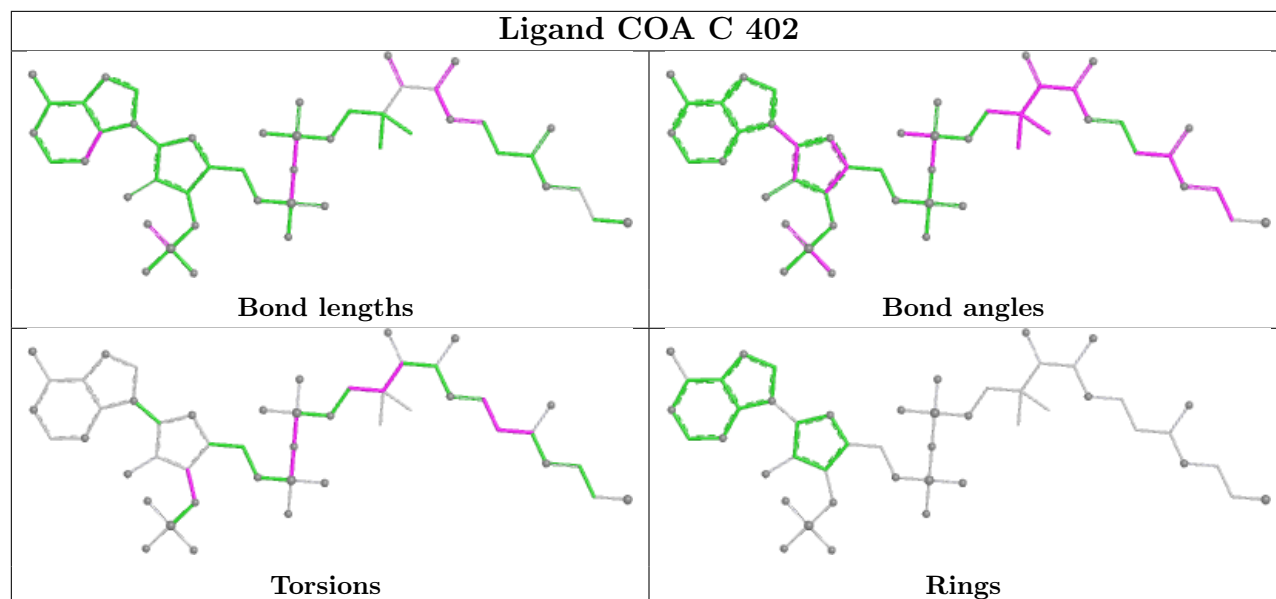
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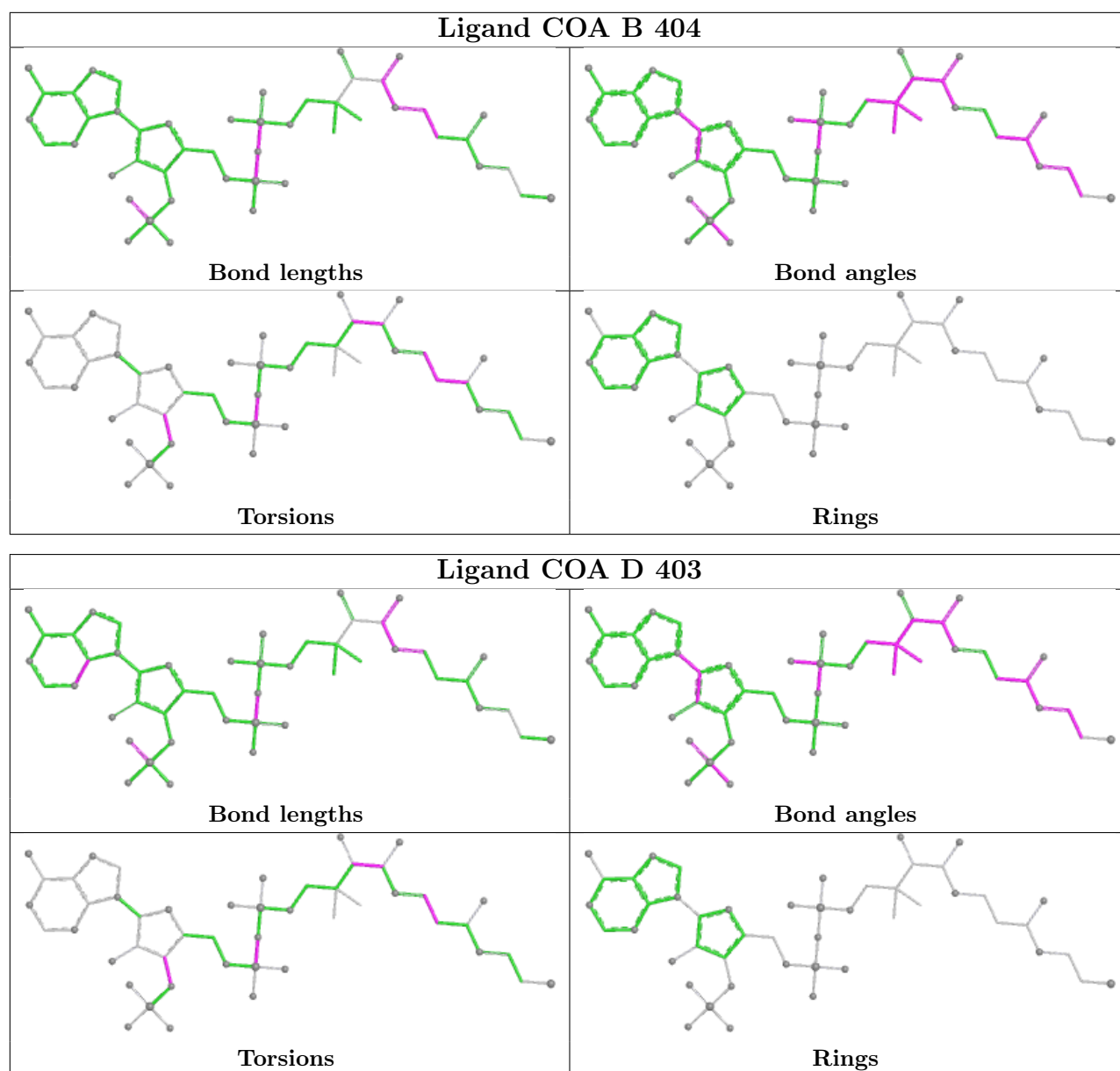
Mol	Chain	Res	Type	Atoms
2	D	403	COA	P2A-O3A-P1A-O1A
2	B	404	COA	O9P-C9P-CAP-OAP
2	D	403	COA	O9P-C9P-CAP-OAP
2	A	401	COA	C2B-C3B-O3B-P3B
2	D	403	COA	C2B-C3B-O3B-P3B
2	C	402	COA	C2B-C3B-O3B-P3B
2	B	404	COA	C2B-C3B-O3B-P3B
2	A	401	COA	O9P-C9P-CAP-OAP
2	A	401	COA	C4B-C3B-O3B-P3B
2	C	402	COA	C4B-C3B-O3B-P3B
2	D	403	COA	C4B-C3B-O3B-P3B
2	C	402	COA	P1A-O3A-P2A-O6A
2	B	404	COA	C4B-C3B-O3B-P3B
2	A	401	COA	O5P-C5P-C6P-C7P
2	B	404	COA	O5P-C5P-C6P-C7P
2	C	402	COA	O5P-C5P-C6P-C7P
2	C	402	COA	OAP-CAP-CBP-CEP
2	A	401	COA	CEP-CBP-CCP-O6A
2	C	402	COA	CEP-CBP-CCP-O6A
2	A	401	COA	N8P-C9P-CAP-OAP
2	B	404	COA	N8P-C9P-CAP-OAP
2	D	403	COA	N8P-C9P-CAP-OAP
2	A	401	COA	N4P-C5P-C6P-C7P
2	C	402	COA	N4P-C5P-C6P-C7P
2	A	401	COA	P2A-O3A-P1A-O2A
2	B	404	COA	P2A-O3A-P1A-O2A
2	C	402	COA	P2A-O3A-P1A-O2A

There are no ring outliers.

No monomer is involved in short contacts.

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	305/316 (96%)	0.15	8 (2%) 57 52	14, 31, 54, 78	0
1	B	301/316 (95%)	0.10	11 (3%) 45 40	10, 28, 53, 94	0
1	C	301/316 (95%)	0.09	7 (2%) 61 57	15, 30, 51, 75	0
1	D	297/316 (93%)	0.10	10 (3%) 48 43	15, 29, 48, 82	0
All	All	1204/1264 (95%)	0.11	36 (2%) 52 48	10, 29, 52, 94	0

All (36) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	210	TYR	4.6
1	B	81	GLY	4.5
1	D	115	TRP	4.4
1	B	115	TRP	4.1
1	D	211	PRO	4.0
1	D	210	TYR	3.8
1	A	213	ASP	3.7
1	B	84	GLY	3.6
1	D	209	ASP	3.6
1	B	70	LEU	3.5
1	B	86	ARG	3.5
1	D	207	GLY	3.5
1	C	214	PRO	3.4
1	B	210	TYR	3.3
1	A	115	TRP	3.3
1	B	215	HIS	3.3
1	C	115	TRP	3.3
1	A	212	HIS	3.2
1	A	85	GLN	2.8
1	D	8	LEU	2.6
1	B	82	THR	2.6

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Mol	Chain	Res	Type	RSRZ
1	C	86	ARG	2.6
1	A	211	PRO	2.6
1	C	120	ARG	2.5
1	D	82	THR	2.5
1	A	185	ASP	2.4
1	A	120	ARG	2.3
1	B	306	ASN	2.3
1	C	215	HIS	2.3
1	B	69	ASN	2.2
1	D	86	ARG	2.3
1	D	120	ARG	2.3
1	C	209	ASP	2.1
1	B	209	ASP	2.0
1	C	207	GLY	2.0
1	D	81	GLY	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](#)

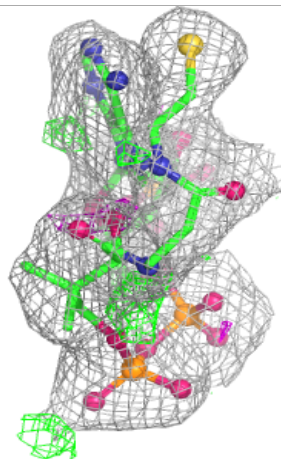
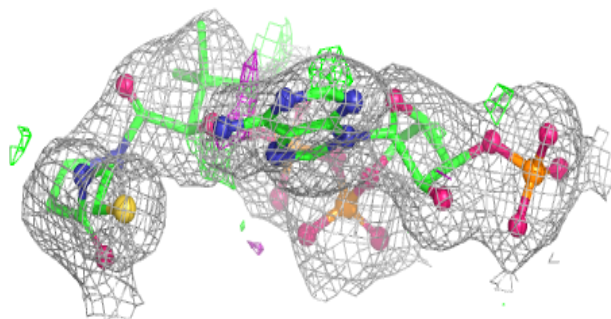
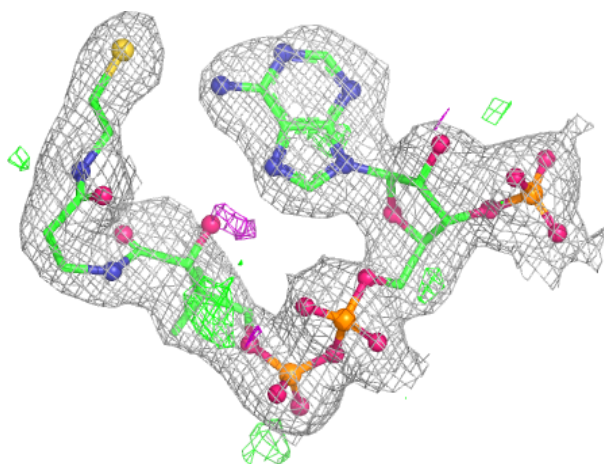
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	COA	A	401	48/48	0.93	0.09	25,35,39,44	0
2	COA	D	403	48/48	0.93	0.10	23,34,41,48	0
2	COA	C	402	48/48	0.94	0.10	18,32,40,46	0
2	COA	B	404	48/48	0.95	0.09	22,29,38,42	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.

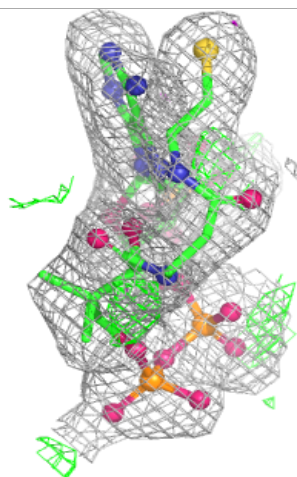
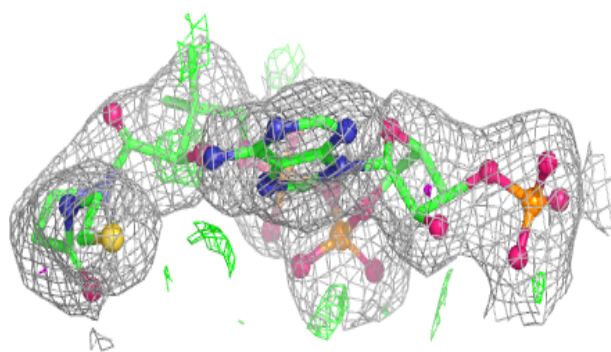
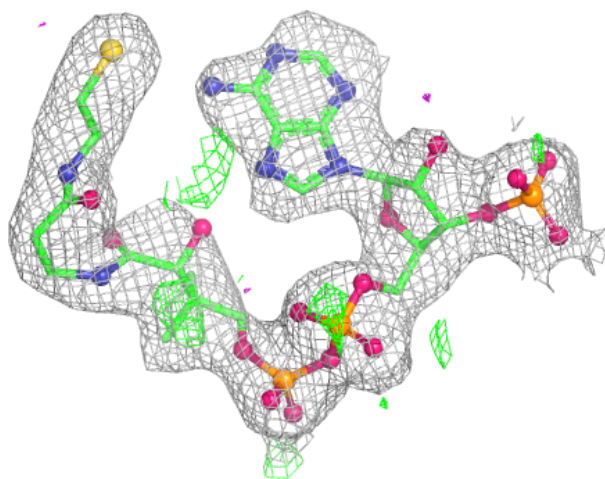
Electron density around COA A 401:

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



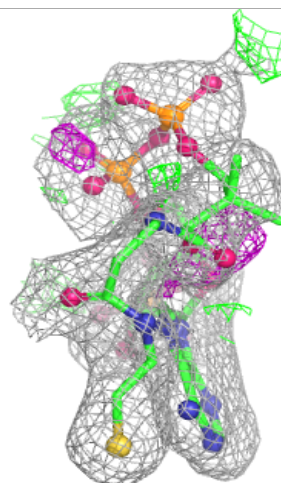
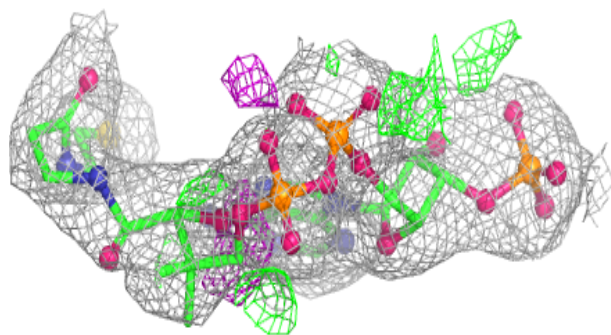
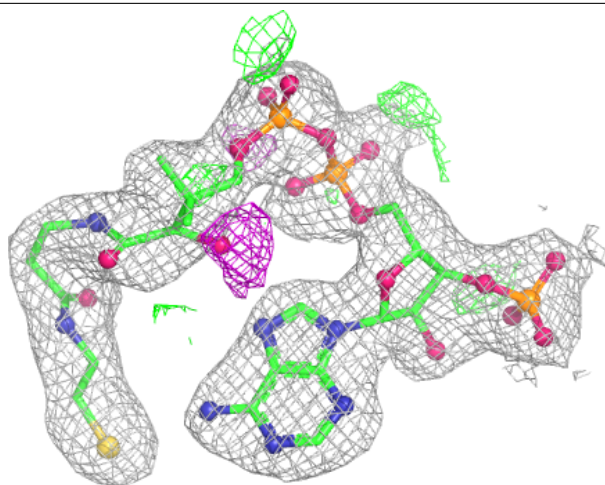
Electron density around COA D 403:

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



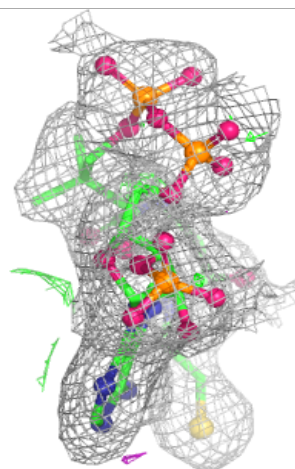
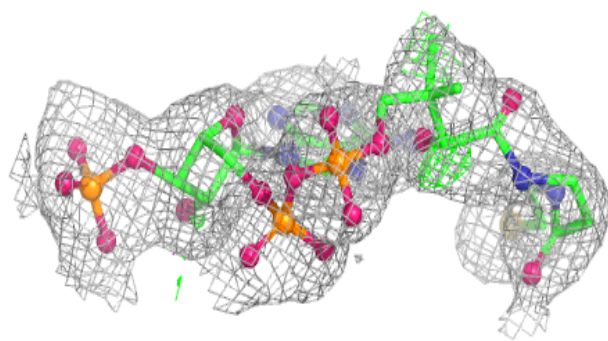
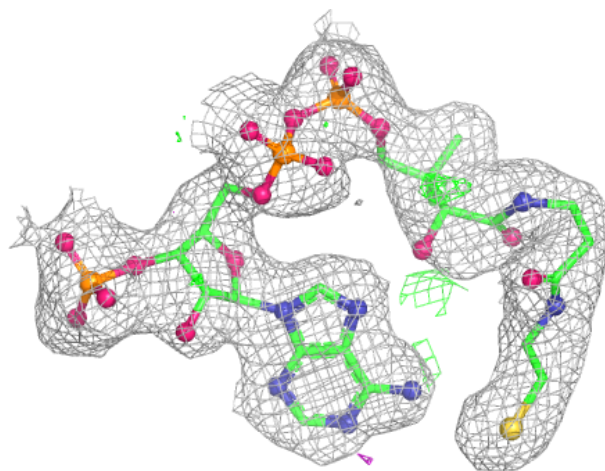
Electron density around COA C 402:

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



Electron density around COA B 404:

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



6.5 Other polymers [i](#)

There are no such residues in this entry.