



Full wwPDB X-ray Structure Validation Report ⓘ

May 21, 2020 – 11:26 am BST

PDB ID : 4BC7
Title : MAMMALIAN ALKYLDIHYDROXYACETONEPHOSPHATE SYN-
THASE: Arg419His mutant
Authors : Nenci, S.; Piano, V.; Rosati, S.; Aliverti, A.; Pandini, V.; Fraaije, M.W.; Heck,
A.J.R.; Edmondson, D.E.; Mattevi, A.
Deposited on : 2012-10-01
Resolution : 2.40 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 following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.11
buster-report : 1.1.7 (2018)
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.11

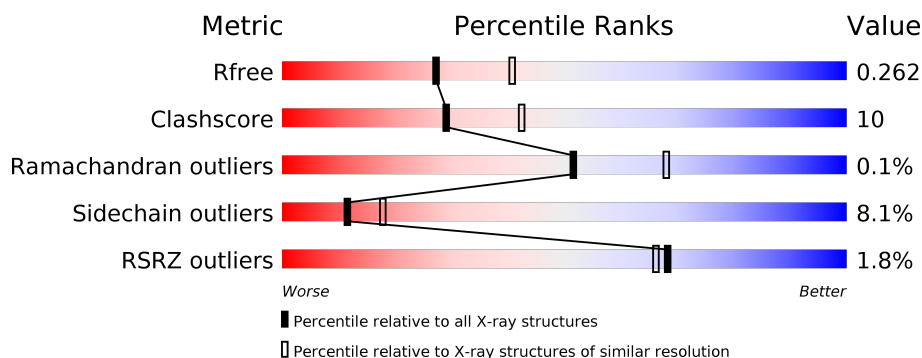
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.40 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}	130704	3907 (2.40-2.40)
Clashscore	141614	4398 (2.40-2.40)
Ramachandran outliers	138981	4318 (2.40-2.40)
Sidechain outliers	138945	4319 (2.40-2.40)
RSRZ outliers	127900	3811 (2.40-2.40)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria 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	658	<div> <div>2%</div> <div> <div></div> <div>65%</div> <div>17%</div> <div>•</div> <div>16%</div> </div> </div>
1	B	658	<div> <div>2%</div> <div> <div></div> <div>62%</div> <div>17%</div> <div>•</div> <div>17%</div> </div> </div>
1	C	658	<div> <div>%</div> <div> <div></div> <div>64%</div> <div>19%</div> <div>•</div> <div>15%</div> </div> </div>
1	D	658	<div> <div>2%</div> <div> <div></div> <div>62%</div> <div>18%</div> <div>•</div> <div>16%</div> </div> </div>

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 17858 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 ALKYLDIHYDROXYACETONEPHOSPHATE SYNTHASE, PEROXISOMAL.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	555	Total	C	N	O	S	0	1	0
			4396	2791	761	820	24			
1	B	543	Total	C	N	O	S	0	0	0
			4300	2732	746	798	24			
1	C	557	Total	C	N	O	S	0	0	0
			4404	2793	765	822	24			
1	D	550	Total	C	N	O	S	0	0	0
			4349	2757	756	812	24			

There are 4 discrepancies between the modelled and reference sequences:

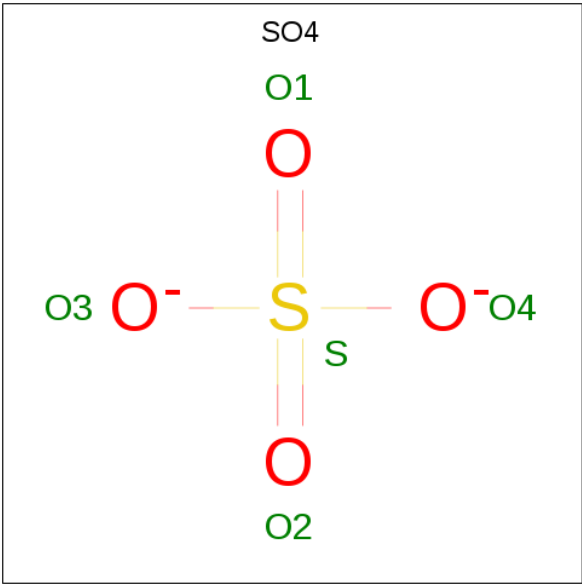
Chain	Residue	Modelled	Actual	Comment	Reference
A	419	HIS	ARG	engineered mutation	UNP P97275
B	419	HIS	ARG	engineered mutation	UNP P97275
C	419	HIS	ARG	engineered mutation	UNP P97275
D	419	HIS	ARG	engineered mutation	UNP P97275

- Molecule 2 is FLAVIN-ADENINE DINUCLEOTIDE (three-letter code: FAD) (formula: $C_{27}H_{33}N_9O_{15}P_2$).



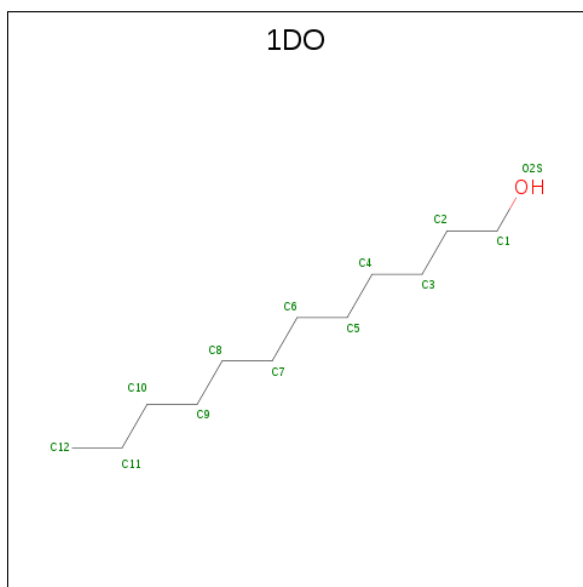
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	P	0	0
			53	27	9	15	2		
2	B	1	Total	C	N	O	P	0	0
			53	27	9	15	2		
2	C	1	Total	C	N	O	P	0	0
			53	27	9	15	2		
2	D	1	Total	C	N	O	P	0	0
			53	27	9	15	2		

- Molecule 3 is SULFATE ION (three-letter code: SO4) (formula: O₄S).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total O S 5 4 1	0	0
3	D	1	Total O S 5 4 1	0	0

- Molecule 4 is 1-DODECANOL (three-letter code: 1DO) (formula: C₁₂H₂₆O).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	B	1	Total C O 13 12 1	0	0
4	C	1	Total C O 13 12 1	0	0

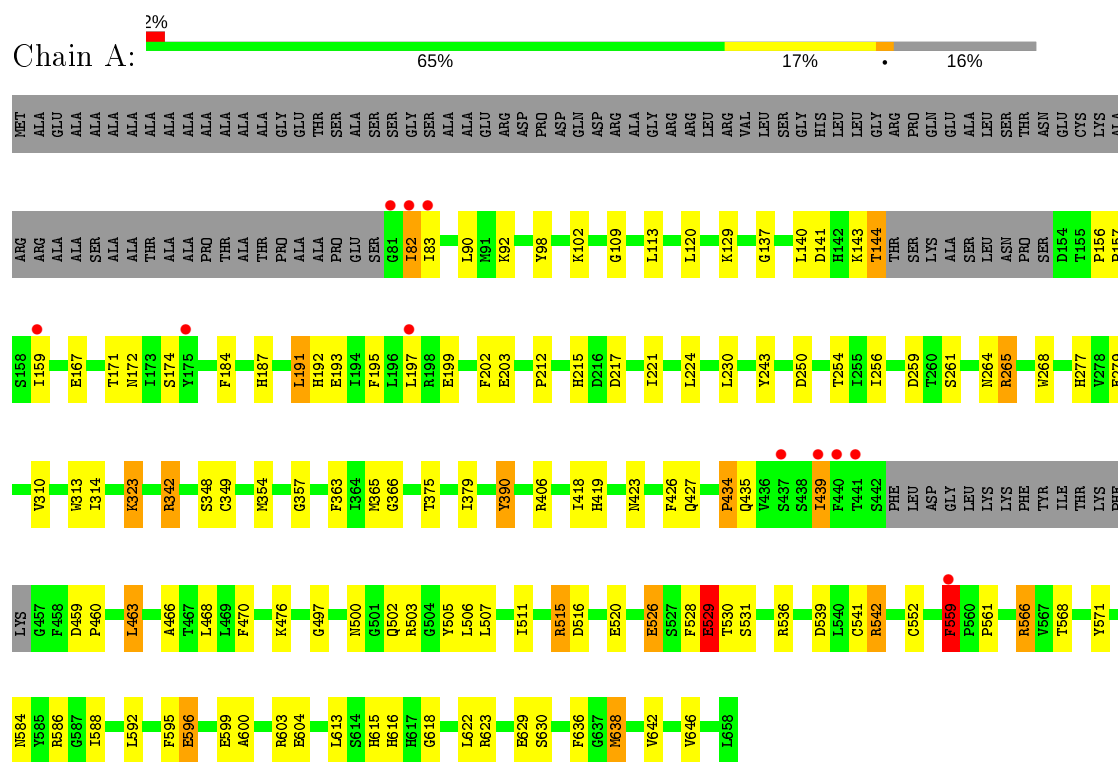
- Molecule 5 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	46	Total O 46 46	0	0
5	B	36	Total O 36 36	0	0
5	C	49	Total O 49 49	0	0
5	D	30	Total O 30 30	0	0

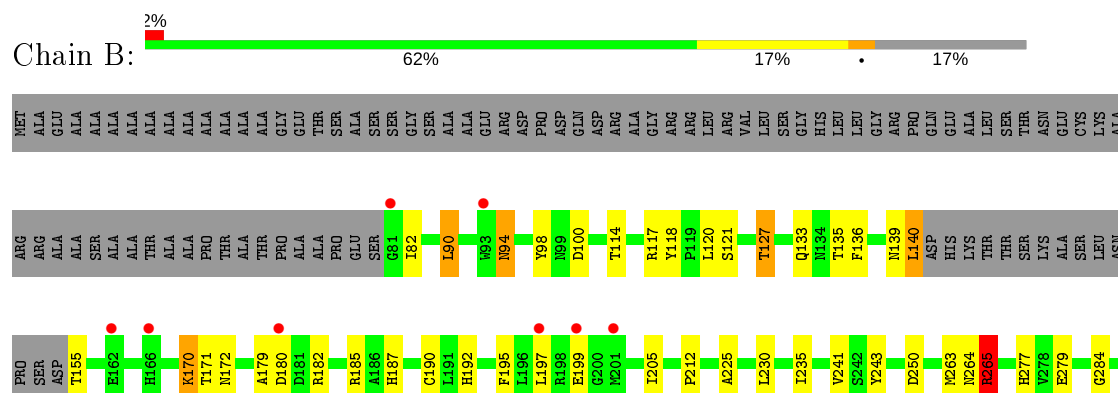
3 Residue-property plots

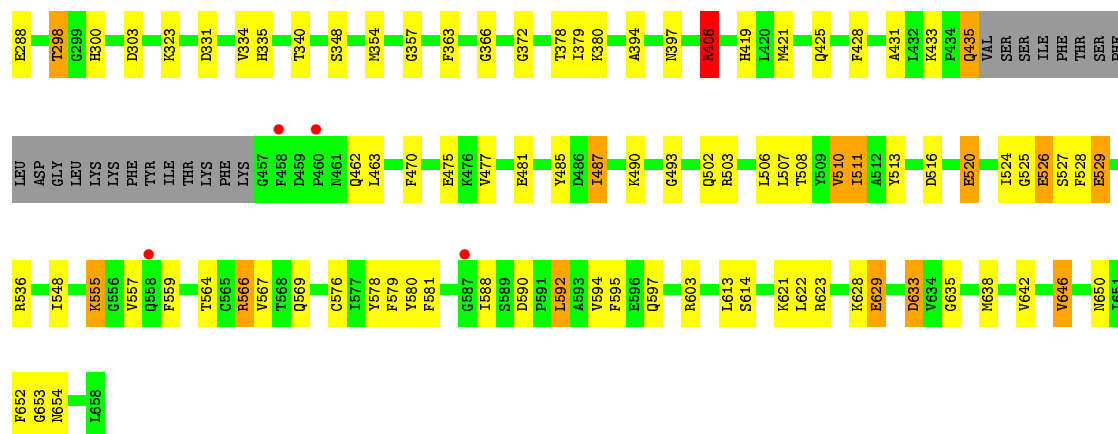
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are 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: ALKYLDIHYDROXYACETONEPHOSPHATE SYNTHASE, PEROXISOMAL

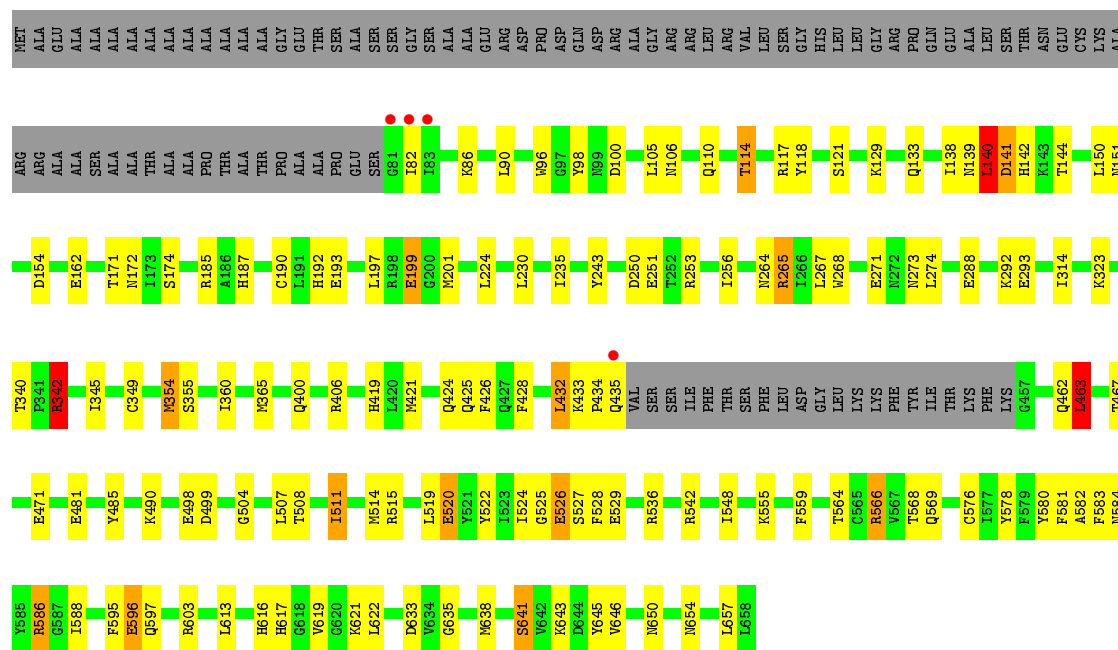


- Molecule 1: ALKYLDIHYDROXYACETONEPHOSPHATE SYNTHASE, PEROXISOMAL

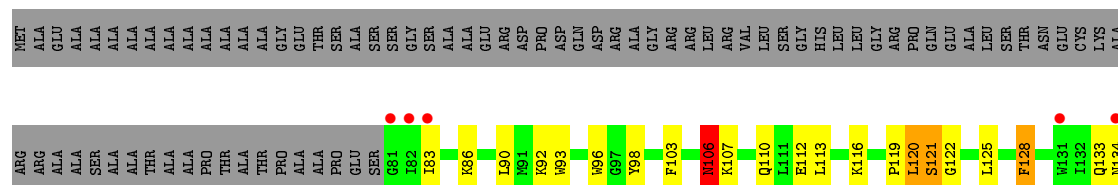


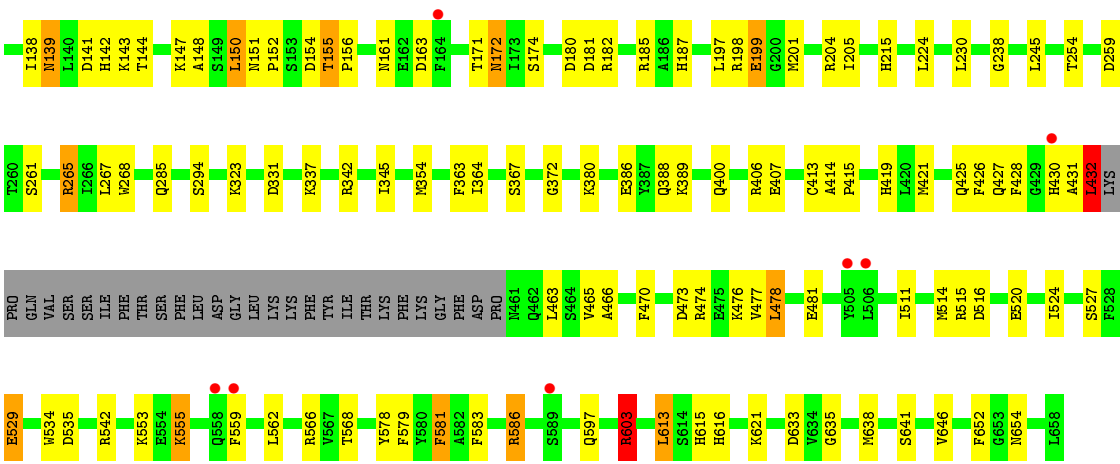


- Molecule 1: ALKYLDIHYDROXYACETONEPHOSPHATE SYNTHASE, PEROXISOMAL



- Molecule 1: ALKYLDIHYDROXYACETONEPHOSPHATE SYNTHASE, PEROXISOMAL





4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	61.41Å 99.19Å 107.46Å 90.58° 91.88° 95.03°	Depositor
Resolution (Å)	54.17 – 2.40 54.17 – 2.40	Depositor EDS
% Data completeness (in resolution range)	95.4 (54.17-2.40) 95.4 (54.17-2.40)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.95 (at 2.39Å)	Xtriage
Refinement program	REFMAC 5.5.0109	Depositor
R, R_{free}	0.211 , 0.270 0.210 , 0.262	Depositor DCC
R_{free} test set	1033 reflections (1.10%)	wwPDB-VP
Wilson B-factor (Å ²)	34.5	Xtriage
Anisotropy	0.229	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 36.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.46$, $\langle L^2 \rangle = 0.29$	Xtriage
Estimated twinning fraction	0.027 for -h,-k,l	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	17858	wwPDB-VP
Average B, all atoms (Å ²)	37.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.84% 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: 1DO, SO4, FAD

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	1.22	57/4500 (1.3%)	1.05	25/6084 (0.4%)
1	B	0.94	11/4398 (0.3%)	0.95	20/5945 (0.3%)
1	C	0.90	8/4505 (0.2%)	0.89	10/6092 (0.2%)
1	D	0.85	6/4447 (0.1%)	0.85	12/6013 (0.2%)
All	All	0.99	82/17850 (0.5%)	0.94	67/24134 (0.3%)

All (82) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	184	PHE	CE2-CZ	-11.11	1.16	1.37
1	A	595	PHE	CE1-CZ	-11.02	1.16	1.37
1	D	265	ARG	CG-CD	-9.74	1.27	1.51
1	A	528	PHE	CG-CD2	-9.57	1.24	1.38
1	A	195	PHE	CE1-CZ	-9.52	1.19	1.37
1	A	528	PHE	CE1-CZ	-9.51	1.19	1.37
1	A	390	TYR	CE2-CZ	-9.31	1.26	1.38
1	A	195	PHE	CG-CD2	-9.31	1.24	1.38
1	A	595	PHE	CG-CD2	-9.30	1.24	1.38
1	A	559	PHE	CG-CD2	-9.20	1.25	1.38
1	A	167	GLU	CD-OE1	-9.14	1.15	1.25
1	B	334	VAL	CB-CG2	-9.12	1.33	1.52
1	A	636	PHE	CE2-CZ	-9.09	1.20	1.37
1	A	390	TYR	CG-CD1	-9.04	1.27	1.39
1	A	542	ARG	CZ-NH1	-8.94	1.21	1.33
1	B	629	GLU	CB-CG	-8.82	1.35	1.52
1	A	195	PHE	CG-CD1	-8.77	1.25	1.38
1	A	199	GLU	CD-OE1	-8.50	1.16	1.25
1	A	470	PHE	CE2-CZ	-8.42	1.21	1.37
1	A	636	PHE	CG-CD1	-8.39	1.26	1.38
1	A	195	PHE	CE2-CZ	-8.32	1.21	1.37
1	B	623	ARG	CZ-NH1	-8.27	1.22	1.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	470	PHE	CE1-CZ	-8.21	1.21	1.37
1	A	390	TYR	CE1-CZ	-8.17	1.27	1.38
1	A	184	PHE	CG-CD1	-8.15	1.26	1.38
1	A	390	TYR	CG-CD2	-8.15	1.28	1.39
1	A	559	PHE	CE1-CZ	-8.00	1.22	1.37
1	A	536	ARG	CZ-NH1	-7.79	1.23	1.33
1	A	636	PHE	CE1-CZ	-7.73	1.22	1.37
1	A	470	PHE	CG-CD1	-7.65	1.27	1.38
1	A	363	PHE	CG-CD2	-7.54	1.27	1.38
1	A	203	GLU	CD-OE1	-7.50	1.17	1.25
1	A	526	GLU	CD-OE1	-7.49	1.17	1.25
1	A	184	PHE	CE1-CZ	-7.45	1.23	1.37
1	A	595	PHE	CE2-CZ	-7.41	1.23	1.37
1	B	559	PHE	CB-CG	-7.40	1.38	1.51
1	A	603	ARG	CZ-NH1	-7.39	1.23	1.33
1	B	334	VAL	CB-CG1	-7.32	1.37	1.52
1	A	167	GLU	CD-OE2	-7.32	1.17	1.25
1	A	470	PHE	CG-CD2	-7.12	1.28	1.38
1	A	529	GLU	CG-CD	-7.11	1.41	1.51
1	A	568	THR	CB-CG2	-6.94	1.29	1.52
1	D	199	GLU	CD-OE1	-6.82	1.18	1.25
1	A	515	ARG	CZ-NH2	-6.79	1.24	1.33
1	A	526	GLU	CD-OE2	-6.77	1.18	1.25
1	A	636	PHE	CG-CD2	-6.62	1.28	1.38
1	A	528	PHE	CG-CD1	-6.62	1.28	1.38
1	A	184	PHE	CG-CD2	-6.61	1.28	1.38
1	C	199	GLU	CD-OE1	-6.56	1.18	1.25
1	D	180	ASP	CB-CG	-6.49	1.38	1.51
1	A	342	ARG	CG-CD	-6.46	1.35	1.51
1	A	193	GLU	CD-OE2	-6.42	1.18	1.25
1	A	595	PHE	CG-CD1	-6.42	1.29	1.38
1	C	265	ARG	NE-CZ	-6.40	1.24	1.33
1	A	596	GLU	CD-OE1	-6.37	1.18	1.25
1	C	265	ARG	CG-CD	-6.30	1.36	1.51
1	B	559	PHE	CG-CD2	-6.14	1.29	1.38
1	A	193	GLU	CD-OE1	-6.08	1.19	1.25
1	B	529	GLU	CG-CD	-6.07	1.42	1.51
1	A	363	PHE	CE2-CZ	-6.03	1.25	1.37
1	A	541	CYS	CB-SG	-5.97	1.72	1.81
1	D	265	ARG	CD-NE	-5.95	1.36	1.46
1	B	363	PHE	CE2-CZ	-5.92	1.26	1.37
1	B	406	ARG	CG-CD	-5.91	1.37	1.51

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	471	GLU	CB-CG	-5.88	1.41	1.52
1	A	528	PHE	CE2-CZ	-5.86	1.26	1.37
1	A	515	ARG	CZ-NH1	-5.86	1.25	1.33
1	C	596	GLU	CD-OE1	-5.81	1.19	1.25
1	A	363	PHE	CE1-CZ	-5.72	1.26	1.37
1	A	566	ARG	CZ-NH1	-5.66	1.25	1.33
1	D	265	ARG	NE-CZ	-5.61	1.25	1.33
1	C	342	ARG	CG-CD	-5.40	1.38	1.51
1	D	413	CYS	CB-SG	-5.37	1.73	1.81
1	A	203	GLU	CD-OE2	-5.27	1.19	1.25
1	B	559	PHE	CD1-CE1	-5.27	1.28	1.39
1	C	162	GLU	CG-CD	-5.20	1.44	1.51
1	C	641	SER	CB-OG	-5.19	1.35	1.42
1	A	224	LEU	CG-CD1	-5.17	1.32	1.51
1	A	363	PHE	CG-CD1	-5.17	1.30	1.38
1	A	265	ARG	CZ-NH2	-5.06	1.26	1.33
1	A	224	LEU	CG-CD2	-5.05	1.33	1.51
1	B	567	VAL	CB-CG2	-5.02	1.42	1.52

All (67) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	536	ARG	NE-CZ-NH2	15.53	128.06	120.30
1	B	623	ARG	NE-CZ-NH2	13.76	127.18	120.30
1	A	542	ARG	NE-CZ-NH2	13.56	127.08	120.30
1	A	515	ARG	NE-CZ-NH1	13.36	126.98	120.30
1	C	603	ARG	NE-CZ-NH1	12.80	126.70	120.30
1	B	559	PHE	CB-CG-CD2	12.04	129.23	120.80
1	A	603	ARG	NE-CZ-NH2	11.69	126.14	120.30
1	A	566	ARG	NE-CZ-NH2	10.69	125.65	120.30
1	B	603	ARG	NE-CZ-NH1	9.88	125.24	120.30
1	A	536	ARG	NE-CZ-NH1	-9.62	115.49	120.30
1	B	633	ASP	CB-CG-OD1	9.50	126.85	118.30
1	A	526	GLU	OE1-CD-OE2	-9.20	112.26	123.30
1	C	342	ARG	NE-CZ-NH2	-8.83	115.88	120.30
1	A	203	GLU	OE1-CD-OE2	-8.53	113.07	123.30
1	B	265	ARG	CG-CD-NE	-8.33	94.31	111.80
1	B	265	ARG	NE-CZ-NH2	-8.21	116.19	120.30
1	C	603	ARG	NE-CZ-NH2	-8.13	116.24	120.30
1	A	193	GLU	OE1-CD-OE2	-7.98	113.73	123.30
1	A	167	GLU	OE1-CD-OE2	-7.95	113.76	123.30
1	C	354	MET	CA-CB-CG	7.52	126.08	113.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	334	VAL	CG1-CB-CG2	-7.05	99.62	110.90
1	D	180	ASP	CB-CG-OD1	-7.05	111.95	118.30
1	D	515	ARG	NE-CZ-NH1	6.97	123.79	120.30
1	C	250	ASP	CB-CG-OD1	6.89	124.50	118.30
1	A	542	ARG	NE-CZ-NH1	-6.82	116.89	120.30
1	A	515	ARG	CG-CD-NE	-6.77	97.59	111.80
1	A	265	ARG	CB-CG-CD	-6.68	94.23	111.60
1	D	180	ASP	CB-CG-OD2	6.58	124.22	118.30
1	C	86	LYS	CD-CE-NZ	6.54	126.74	111.70
1	D	603	ARG	CD-NE-CZ	6.51	132.72	123.60
1	C	515	ARG	NE-CZ-NH1	6.42	123.51	120.30
1	A	191	LEU	CD1-CG-CD2	-6.40	91.30	110.50
1	B	406	ARG	NE-CZ-NH2	-6.40	117.10	120.30
1	B	180	ASP	CB-CG-OD2	6.38	124.04	118.30
1	A	638	MET	CG-SD-CE	6.36	110.37	100.20
1	D	633	ASP	CB-CG-OD2	6.31	123.98	118.30
1	A	595	PHE	CB-CG-CD1	6.05	125.03	120.80
1	B	406	ARG	NE-CZ-NH1	5.98	123.29	120.30
1	B	421	MET	CG-SD-CE	5.96	109.73	100.20
1	D	603	ARG	NE-CZ-NH1	5.88	123.24	120.30
1	D	566	ARG	CB-CG-CD	-5.87	96.35	111.60
1	D	204	ARG	NE-CZ-NH1	5.84	123.22	120.30
1	B	559	PHE	CB-CG-CD1	-5.80	116.74	120.80
1	A	250	ASP	CB-CG-OD2	5.79	123.51	118.30
1	D	342	ARG	NE-CZ-NH1	-5.75	117.42	120.30
1	B	623	ARG	NE-CZ-NH1	-5.75	117.43	120.30
1	D	90	LEU	CA-CB-CG	5.72	128.47	115.30
1	D	265	ARG	CD-NE-CZ	-5.72	115.59	123.60
1	B	170	LYS	CD-CE-NZ	5.70	124.81	111.70
1	A	596	GLU	OE1-CD-OE2	-5.66	116.51	123.30
1	A	559	PHE	CB-CG-CD1	5.58	124.71	120.80
1	B	90	LEU	CB-CG-CD1	-5.54	101.59	111.00
1	A	224	LEU	CD1-CG-CD2	-5.52	93.94	110.50
1	A	566	ARG	NE-CZ-NH1	-5.47	117.56	120.30
1	A	603	ARG	NH1-CZ-NH2	-5.46	113.40	119.40
1	B	90	LEU	CA-CB-CG	5.45	127.83	115.30
1	B	379	ILE	CG1-CB-CG2	-5.36	99.61	111.40
1	B	265	ARG	CD-NE-CZ	-5.35	116.11	123.60
1	C	140	LEU	CA-CB-CG	5.28	127.43	115.30
1	B	536	ARG	NE-CZ-NH2	5.25	122.93	120.30
1	A	265	ARG	NE-CZ-NH1	-5.19	117.71	120.30
1	C	463	LEU	CA-CB-CG	5.15	127.15	115.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	432	LEU	CA-CB-CG	5.14	127.12	115.30
1	C	603	ARG	CD-NE-CZ	5.11	130.75	123.60
1	B	250	ASP	CB-CG-OD2	5.10	122.89	118.30
1	A	342	ARG	CA-CB-CG	-5.07	102.24	113.40
1	A	390	TYR	CD1-CE1-CZ	5.02	124.32	119.80

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	4396	0	4325	77	0
1	B	4300	0	4236	100	2
1	C	4404	0	4336	88	2
1	D	4349	0	4285	91	0
2	A	53	0	31	1	0
2	B	53	0	31	0	0
2	C	53	0	31	2	0
2	D	53	0	31	2	0
3	A	5	0	0	0	0
3	D	5	0	0	0	0
4	B	13	0	26	2	0
4	C	13	0	26	2	0
5	A	46	0	0	1	0
5	B	36	0	0	1	0
5	C	49	0	0	2	0
5	D	30	0	0	0	0
All	All	17858	0	17358	337	2

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 10.

All (337) 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:507:LEU:O	1:B:511:ILE:CD1	1.65	1.44
1:B:511:ILE:N	1:B:511:ILE:HD13	1.47	1.24
1:B:511:ILE:CD1	1:B:511:ILE:H	1.57	1.13
1:B:621:LYS:NZ	1:B:654:ASN:O	1.80	1.13
1:B:507:LEU:O	1:B:511:ILE:HD12	1.49	1.11
1:B:507:LEU:O	1:B:511:ILE:HD11	1.33	1.07
1:C:586:ARG:HG3	1:C:586:ARG:HH11	1.03	1.07
1:C:139:ASN:HB3	1:C:141:ASP:OD1	1.53	1.05
1:B:265:ARG:NH1	1:B:265:ARG:HA	1.71	1.05
1:B:507:LEU:C	1:B:511:ILE:HD11	1.79	1.01
1:B:265:ARG:HA	1:B:265:ARG:HH11	1.24	0.99
1:B:265:ARG:CA	1:B:265:ARG:HH11	1.77	0.98
1:A:615:HIS:HD2	1:A:616:HIS:HD2	1.10	0.98
1:C:100:ASP:O	1:C:114:THR:HG22	1.63	0.98
1:B:511:ILE:H	1:B:511:ILE:HD13	0.81	0.97
1:B:139:ASN:O	1:B:140:LEU:HB2	1.65	0.97
1:D:586:ARG:HG3	1:D:586:ARG:HH11	1.29	0.96
1:B:511:ILE:CD1	1:B:511:ILE:N	2.26	0.90
1:C:586:ARG:HG3	1:C:586:ARG:NH1	1.82	0.89
1:C:419:HIS:HD2	1:C:566:ARG:HH21	1.20	0.89
1:A:82:ILE:HG13	1:A:264:ASN:ND2	1.87	0.89
1:A:615:HIS:HD2	1:A:616:HIS:CD2	1.93	0.86
1:A:265:ARG:HG2	1:A:265:ARG:HH11	1.40	0.85
1:B:406:ARG:HH11	1:B:406:ARG:HG3	1.39	0.85
1:A:615:HIS:CD2	1:A:616:HIS:HD2	1.95	0.84
1:B:192:HIS:ND1	1:B:592:LEU:HD11	1.93	0.83
1:B:100:ASP:O	1:B:114:THR:HG22	1.80	0.82
1:D:586:ARG:NH1	1:D:586:ARG:HG3	1.90	0.81
1:C:139:ASN:CB	1:C:141:ASP:OD1	2.28	0.80
1:D:133:GLN:HG3	1:D:138:ILE:O	1.81	0.80
1:D:389:LYS:HE3	1:D:481:GLU:OE2	1.82	0.80
1:D:106:ASN:HD21	1:D:110:GLN:H	1.29	0.78
1:D:86:LYS:NZ	1:D:181:ASP:OD2	2.16	0.76
1:D:106:ASN:ND2	1:D:110:GLN:H	1.83	0.75
1:A:439:ILE:HG13	1:D:535:ASP:HB2	1.67	0.75
1:A:265:ARG:NH1	1:A:265:ARG:HG2	2.02	0.75
1:C:621:LYS:NZ	1:C:654:ASN:O	2.20	0.74
1:C:100:ASP:O	1:C:114:THR:CG2	2.35	0.74
1:D:473:ASP:O	1:D:477:VAL:HG23	1.88	0.73
1:D:529:GLU:OE2	1:D:615:HIS:N	2.18	0.73
1:A:507:LEU:O	1:A:511:ILE:HG12	1.87	0.72
1:D:154:ASP:O	1:D:201:MET:HG2	1.89	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:139:ASN:ND2	1:D:139:ASN:H	1.88	0.71
1:D:603:ARG:HH11	1:D:603:ARG:HG2	1.56	0.71
1:D:555:LYS:NZ	1:D:597:GLN:HE21	1.89	0.71
1:C:139:ASN:O	1:C:140:LEU:HB2	1.91	0.70
1:A:571:TYR:OH	1:A:615:HIS:HE1	1.72	0.70
1:B:192:HIS:CB	1:B:243:TYR:OH	2.39	0.70
1:C:342:ARG:NE	1:C:645:TYR:O	2.21	0.70
1:D:430:HIS:C	1:D:432:LEU:H	1.95	0.70
1:D:92:LYS:HE3	1:D:98:TYR:O	1.93	0.69
1:C:144:THR:HG21	1:C:519:LEU:O	1.93	0.69
1:C:526:GLU:HG3	1:C:527:SER:N	2.08	0.68
1:A:463:LEU:HD12	1:A:463:LEU:O	1.92	0.68
1:B:527:SER:OG	4:B:888:IDO:H1C2	1.93	0.68
1:C:106:ASN:HD21	1:C:110:GLN:HE21	1.41	0.68
1:B:192:HIS:HB3	1:B:243:TYR:OH	1.94	0.68
1:D:93:TRP:NE1	1:D:148:ALA:O	2.26	0.66
1:C:434:PRO:O	1:C:435:GLN:HB2	1.95	0.66
1:C:586:ARG:HH11	1:C:586:ARG:CG	1.94	0.66
1:A:265:ARG:CG	1:A:265:ARG:HH11	2.01	0.65
1:B:481:GLU:HG3	1:B:485:TYR:CE2	2.31	0.65
1:C:144:THR:HG22	1:C:520:GLU:HA	1.76	0.65
1:C:419:HIS:CD2	1:C:566:ARG:HH21	2.08	0.65
1:D:139:ASN:HD22	1:D:139:ASN:H	1.43	0.65
1:A:82:ILE:HG13	1:A:264:ASN:HD21	1.61	0.64
1:B:592:LEU:O	1:B:595:PHE:HB3	1.96	0.64
1:B:225:ALA:HA	1:B:230:LEU:HD12	1.79	0.64
1:B:265:ARG:NH1	1:B:265:ARG:HG3	2.03	0.64
1:C:314:ILE:HG23	1:C:365:MET:HG2	1.79	0.64
1:C:421:MET:CE	1:C:426:PHE:HA	2.28	0.64
1:D:586:ARG:CG	1:D:586:ARG:HH11	2.06	0.64
1:D:139:ASN:N	1:D:139:ASN:ND2	2.45	0.64
1:B:635:GLY:HA2	1:B:638:MET:HE3	1.80	0.63
1:A:187:HIS:CE1	1:A:197:LEU:HD11	2.34	0.63
1:B:133:GLN:OE1	1:B:139:ASN:O	2.17	0.62
1:B:507:LEU:O	1:B:511:ILE:CG1	2.45	0.62
1:A:215:HIS:HD2	1:A:375:THR:OG1	1.83	0.62
1:C:192:HIS:HB3	1:C:243:TYR:OH	1.99	0.62
1:D:144:THR:HG22	1:D:520:GLU:HA	1.81	0.62
1:B:650:ASN:HD21	1:B:653:GLY:HA2	1.65	0.61
1:B:481:GLU:HG3	1:B:485:TYR:HE2	1.65	0.61
1:D:142:HIS:CE1	1:D:586:ARG:HH22	2.18	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:340:THR:HB	1:B:646:VAL:HG13	1.82	0.61
1:D:474:ARG:O	1:D:478:LEU:HG	2.01	0.60
1:C:98:TYR:CD2	1:C:117:ARG:HD3	2.36	0.60
1:B:265:ARG:NH1	1:B:265:ARG:CG	2.53	0.60
1:C:419:HIS:HD2	1:C:566:ARG:NH2	1.96	0.60
1:C:421:MET:HE3	1:C:426:PHE:HA	1.84	0.60
1:A:439:ILE:HG13	1:D:535:ASP:CB	2.31	0.60
1:B:243:TYR:HD2	1:B:622:LEU:HB2	1.67	0.59
1:D:555:LYS:HZ1	1:D:597:GLN:HE21	1.48	0.59
1:B:182:ARG:HB3	1:B:205:ILE:HD12	1.85	0.59
1:D:635:GLY:HA2	1:D:638:MET:HE3	1.83	0.59
1:A:419:HIS:O	1:A:466:ALA:HA	2.03	0.59
1:D:428:PHE:HZ	1:D:514:MET:SD	2.25	0.58
1:D:142:HIS:CG	1:D:586:ARG:HH12	2.21	0.58
1:D:86:LYS:NZ	1:D:181:ASP:CG	2.57	0.58
1:A:642:VAL:HG13	1:B:638:MET:HG2	1.84	0.58
1:B:190:CYS:SG	1:B:241:VAL:O	2.61	0.58
1:C:243:TYR:HE2	1:C:622:LEU:HD13	1.70	0.57
1:C:555:LYS:NZ	1:C:597:GLN:HE21	2.03	0.57
1:D:182:ARG:HB3	1:D:205:ILE:HD12	1.86	0.57
1:B:185:ARG:HG2	1:B:235:ILE:HD13	1.87	0.57
1:D:524:ILE:HD11	1:D:583:PHE:CZ	2.39	0.57
1:C:142:HIS:CD2	1:C:586:ARG:NH2	2.73	0.57
1:C:467:THR:HG21	1:C:504:GLY:HA3	1.87	0.56
1:C:526:GLU:HB3	1:C:595:PHE:HZ	1.69	0.56
1:A:171:THR:O	1:A:172:ASN:HB2	2.04	0.56
1:A:615:HIS:CD2	1:A:616:HIS:CD2	2.81	0.56
1:B:526:GLU:HG3	1:B:527:SER:H	1.70	0.56
1:A:265:ARG:CG	1:A:265:ARG:NH1	2.58	0.56
1:B:298:THR:CG2	1:B:300:HIS:H	2.18	0.56
1:B:265:ARG:NH1	1:B:265:ARG:CA	2.47	0.56
1:A:129:LYS:HG3	1:A:140:LEU:HD23	1.88	0.56
1:B:481:GLU:CG	1:B:485:TYR:HE2	2.19	0.56
1:C:342:ARG:HD3	1:C:645:TYR:CZ	2.41	0.56
1:B:419:HIS:HD2	1:B:566:ARG:HH21	1.54	0.55
1:C:133:GLN:HG2	1:C:138:ILE:O	2.06	0.55
1:C:524:ILE:O	1:C:582:ALA:HA	2.06	0.55
1:B:470:PHE:HB3	1:B:477:VAL:HG13	1.88	0.55
1:C:192:HIS:CB	1:C:243:TYR:OH	2.55	0.55
1:D:430:HIS:O	1:D:432:LEU:N	2.38	0.55
1:A:426:PHE:CD2	1:A:463:LEU:HD11	2.42	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:497:GLY:HA2	5:A:2038:HOH:O	2.06	0.54
1:B:288:GLU:OE1	1:B:298:THR:HB	2.07	0.54
1:C:481:GLU:HG2	1:C:485:TYR:CE2	2.43	0.54
1:D:120:LEU:HD13	1:D:120:LEU:N	2.22	0.54
1:A:92:LYS:HE3	1:A:98:TYR:O	2.07	0.54
1:B:243:TYR:HE2	1:B:622:LEU:HD13	1.72	0.54
1:C:185:ARG:HG2	1:C:235:ILE:HD13	1.89	0.54
1:C:511:ILE:HD13	4:C:888:1DO:H5C2	1.89	0.54
1:C:432:LEU:HD21	1:C:514:MET:HE2	1.90	0.54
1:D:150:LEU:O	1:D:152:PRO:HD3	2.07	0.54
1:A:613:LEU:HD11	1:A:623:ARG:HB3	1.90	0.54
1:C:139:ASN:O	1:C:140:LEU:CB	2.56	0.53
1:C:638:MET:CE	1:D:345:ILE:HD13	2.37	0.53
1:D:185:ARG:NE	1:D:259:ASP:OD2	2.31	0.53
1:A:531:SER:HB3	1:A:615:HIS:HB2	1.89	0.53
1:C:528:PHE:HZ	1:C:548:ILE:HD11	1.72	0.53
1:B:303:ASP:OD2	1:B:508:THR:HB	2.09	0.53
1:D:407:GLU:HA	1:D:407:GLU:OE1	2.08	0.53
1:C:635:GLY:HA2	1:C:638:MET:HE3	1.90	0.53
1:D:112:GLU:OE2	1:D:122:GLY:HA2	2.08	0.53
1:B:555:LYS:NZ	1:B:597:GLN:HE21	2.07	0.52
1:D:86:LYS:NZ	1:D:181:ASP:OD1	2.42	0.52
1:B:335:HIS:HD2	5:B:2023:HOH:O	1.92	0.52
1:A:243:TYR:CE2	1:A:622:LEU:HD13	2.44	0.51
1:B:525:GLY:HA3	4:B:888:1DO:H8C2	1.92	0.51
1:A:459:ASP:OD1	1:A:460:PRO:HD2	2.09	0.51
1:B:331:ASP:O	1:B:380:LYS:HE3	2.11	0.51
1:C:526:GLU:HG3	1:C:527:SER:H	1.73	0.51
1:A:129:LYS:HG3	1:A:140:LEU:CD2	2.40	0.51
1:C:230:LEU:HD13	1:C:256:ILE:HD11	1.93	0.51
1:B:506:LEU:O	1:B:510:VAL:HG22	2.10	0.51
1:A:426:PHE:CE2	1:A:463:LEU:HD11	2.46	0.50
1:B:98:TYR:CD2	1:B:117:ARG:HD3	2.46	0.50
1:B:155:THR:HG21	1:B:179:ALA:HB1	1.93	0.50
1:B:528:PHE:HZ	1:B:548:ILE:HD11	1.76	0.50
1:A:82:ILE:CG1	1:A:264:ASN:ND2	2.70	0.50
1:A:109:GLY:HA3	1:C:268:TRP:CE3	2.46	0.50
1:A:137:GLY:HA3	1:A:559:PHE:CE2	2.46	0.50
1:A:434:PRO:HD2	1:A:435:GLN:OE1	2.12	0.49
1:A:515:ARG:HG2	1:A:515:ARG:O	2.04	0.49
1:B:435:GLN:OE1	1:B:435:GLN:HA	2.11	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:481:GLU:HG2	1:C:485:TYR:HE2	1.77	0.49
1:B:569:GLN:HB2	1:B:576:CYS:HB3	1.94	0.49
1:D:147:LYS:HG3	1:D:198:ARG:O	2.12	0.49
1:A:129:LYS:HD2	1:A:140:LEU:HD23	1.95	0.49
1:B:470:PHE:CB	1:B:477:VAL:HG13	2.42	0.49
1:A:348:SER:HB3	1:B:629:GLU:O	2.12	0.49
1:C:526:GLU:CB	1:C:595:PHE:HZ	2.26	0.49
1:D:421:MET:HG2	1:D:465:VAL:O	2.13	0.49
1:D:529:GLU:O	1:D:603:ARG:NH2	2.46	0.49
1:C:525:GLY:HA2	1:C:581:PHE:O	2.12	0.49
1:D:171:THR:O	1:D:172:ASN:HB2	2.12	0.49
1:D:555:LYS:NZ	1:D:597:GLN:NE2	2.60	0.49
1:B:192:HIS:ND1	1:B:592:LEU:CD1	2.72	0.48
1:C:345:ILE:HD13	1:D:638:MET:CE	2.43	0.48
1:B:187:HIS:NE2	1:B:197:LEU:HD11	2.28	0.48
1:A:357:GLY:HA2	1:B:366:GLY:O	2.13	0.48
1:B:406:ARG:NH1	1:B:406:ARG:HG3	2.11	0.48
1:D:119:PRO:HB2	1:D:120:LEU:HD13	1.94	0.48
1:B:406:ARG:O	1:B:406:ARG:HG3	2.11	0.48
1:A:539:ASP:OD1	1:A:542:ARG:NH2	2.47	0.48
1:A:82:ILE:CG1	1:A:264:ASN:HD21	2.25	0.48
1:A:638:MET:HG2	1:B:642:VAL:HG13	1.96	0.48
1:C:243:TYR:CE2	1:C:622:LEU:HD13	2.49	0.48
1:A:439:ILE:CG1	1:D:535:ASP:HB2	2.40	0.48
1:D:419:HIS:O	1:D:466:ALA:HA	2.13	0.48
1:B:277:HIS:HD2	1:B:378:THR:OG1	1.97	0.48
1:D:230:LEU:HD22	1:D:254:THR:HB	1.96	0.47
1:D:516:ASP:O	1:D:520:GLU:HG2	2.14	0.47
1:B:394:ALA:O	1:B:493:GLY:HA2	2.14	0.47
1:C:569:GLN:HB2	1:C:576:CYS:HB3	1.97	0.47
1:C:586:ARG:CG	1:C:586:ARG:NH1	2.63	0.47
1:C:345:ILE:CD1	1:D:638:MET:HE2	2.44	0.47
1:B:372:GLY:HA2	1:B:652:PHE:CZ	2.50	0.47
1:A:314:ILE:HG23	1:A:365:MET:HG2	1.95	0.47
1:B:564:THR:HG23	1:B:580:TYR:HB2	1.97	0.47
1:B:82:ILE:HG12	1:B:264:ASN:ND2	2.30	0.47
1:C:400:GLN:NE2	1:C:400:GLN:HA	2.28	0.47
1:A:629:GLU:O	1:B:348:SER:HB3	2.15	0.47
1:D:527:SER:HA	1:D:579:PHE:O	2.15	0.47
1:C:463:LEU:HD23	1:C:463:LEU:O	2.15	0.46
1:D:238:GLY:HA2	1:D:245:LEU:HD11	1.96	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:192:HIS:HB3	1:A:243:TYR:OH	2.15	0.46
1:C:267:LEU:O	1:C:268:TRP:HB3	2.15	0.46
1:C:511:ILE:HG23	4:C:888:IDO:H4C1	1.97	0.46
1:A:366:GLY:O	1:B:357:GLY:HA2	2.15	0.46
1:C:355:SER:HB2	1:D:616:HIS:HA	1.98	0.46
1:D:155:THR:HA	1:D:156:PRO:HD2	1.76	0.46
1:A:230:LEU:HD22	1:A:254:THR:HB	1.96	0.46
1:B:298:THR:HG22	1:B:300:HIS:H	1.79	0.46
1:C:511:ILE:HD12	1:C:580:TYR:CE1	2.51	0.46
1:C:424:GLN:HB2	1:C:564:THR:HG22	1.98	0.46
1:A:516:ASP:O	1:A:520:GLU:HG3	2.16	0.46
1:C:144:THR:HG22	1:C:520:GLU:CA	2.43	0.46
1:C:251:GLU:OE2	1:C:253:ARG:HB2	2.16	0.45
1:C:522:TYR:CG	1:C:586:ARG:HG2	2.51	0.45
1:D:103:PHE:HA	1:D:112:GLU:O	2.16	0.45
1:D:430:HIS:C	1:D:432:LEU:N	2.66	0.45
1:C:524:ILE:HD11	1:C:583:PHE:CZ	2.51	0.45
1:B:127:THR:HG22	1:B:431:ALA:HB1	1.98	0.45
1:B:590:ASP:O	1:B:594:VAL:HG23	2.16	0.45
1:A:230:LEU:HD13	1:A:256:ILE:HD11	1.97	0.45
1:A:212:PRO:HD2	1:A:259:ASP:O	2.16	0.45
1:B:298:THR:HG23	1:B:300:HIS:H	1.82	0.45
1:A:143:LYS:O	1:A:144:THR:HB	2.16	0.45
1:C:144:THR:CG2	1:C:520:GLU:HA	2.43	0.45
1:B:516:ASP:O	1:B:520:GLU:HG2	2.17	0.45
1:C:340:THR:HB	1:C:646:VAL:HG13	1.99	0.45
1:D:331:ASP:O	1:D:380:LYS:HE3	2.16	0.45
1:B:520:GLU:H	1:B:520:GLU:HG2	1.57	0.44
1:B:557:VAL:HA	1:B:588:ILE:HD11	1.99	0.44
1:A:323:LYS:HD2	1:A:323:LYS:C	2.38	0.44
1:A:439:ILE:HD13	1:A:439:ILE:HA	1.81	0.44
1:A:423:ASN:HD21	1:A:427:GLN:NE2	2.15	0.44
1:A:618:GLY:O	1:A:623:ARG:NH1	2.46	0.44
1:D:400:GLN:HA	1:D:400:GLN:NE2	2.33	0.44
1:C:273:ASN:OD1	1:D:534:TRP:HB2	2.17	0.44
1:B:171:THR:O	1:B:172:ASN:HB2	2.16	0.44
1:A:463:LEU:CD1	1:A:463:LEU:C	2.86	0.44
1:D:83:ILE:HB	1:D:261:SER:HB2	1.98	0.44
1:A:265:ARG:HD2	1:A:279:GLU:OE1	2.17	0.44
1:A:500:ASN:ND2	1:A:503:ARG:HH12	2.15	0.44
1:A:506:LEU:HA	1:A:506:LEU:HD23	1.84	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:243:TYR:O	1:B:621:LYS:HE2	2.17	0.44
1:C:507:LEU:O	1:C:511:ILE:HB	2.17	0.44
1:B:212:PRO:HG2	1:B:263:MET:HE2	2.00	0.44
1:C:421:MET:HE3	1:C:426:PHE:CA	2.47	0.44
1:C:638:MET:HE1	1:D:345:ILE:HD13	1.98	0.44
1:D:529:GLU:HG3	1:D:616:HIS:CE1	2.53	0.44
1:B:284:GLY:O	1:B:288:GLU:HG2	2.18	0.43
1:D:142:HIS:CD2	1:D:586:ARG:HH12	2.35	0.43
1:C:643:LYS:NZ	1:C:650:ASN:HD22	2.16	0.43
1:D:265:ARG:HH11	1:D:265:ARG:HD2	1.38	0.43
1:C:638:MET:HE2	1:D:345:ILE:CD1	2.48	0.43
1:B:118:TYR:O	1:B:121:SER:HB2	2.19	0.43
1:C:555:LYS:HZ1	1:C:597:GLN:HE21	1.65	0.43
1:A:143:LYS:HB3	1:A:144:THR:H	1.53	0.43
1:A:268:TRP:CZ2	1:A:277:HIS:HB2	2.54	0.43
1:A:463:LEU:HD12	1:A:463:LEU:C	2.38	0.43
1:B:526:GLU:HB3	1:B:595:PHE:HZ	1.83	0.43
1:C:96:TRP:CZ3	2:C:999:FAD:HM83	2.53	0.43
1:D:511:ILE:HA	1:D:514:MET:HE3	2.01	0.43
1:C:498:GLU:HG2	5:C:2038:HOH:O	2.18	0.43
1:A:529:GLU:HG2	1:A:530:THR:N	2.32	0.43
1:C:154:ASP:O	1:C:201:MET:HG2	2.18	0.43
1:C:82:ILE:HG12	1:C:264:ASN:ND2	2.34	0.43
1:D:616:HIS:HD2	2:D:999:FAD:C2	2.32	0.43
1:A:600:ALA:O	1:A:604:GLU:HG2	2.18	0.43
1:D:171:THR:O	1:D:172:ASN:CB	2.67	0.43
1:D:562:LEU:O	1:D:581:PHE:HA	2.19	0.43
1:D:113:LEU:HB3	1:D:121:SER:HA	2.01	0.42
1:B:397:ASN:HA	1:B:462:GLN:O	2.19	0.42
1:B:510:VAL:O	1:B:513:TYR:N	2.45	0.42
1:D:426:PHE:CD1	1:D:465:VAL:HG21	2.53	0.42
1:B:243:TYR:CD2	1:B:622:LEU:HB2	2.50	0.42
1:C:529:GLU:OE2	1:C:617:HIS:HB2	2.19	0.42
1:B:265:ARG:CG	1:B:265:ARG:HH11	2.20	0.42
1:C:118:TYR:O	1:C:121:SER:HB2	2.19	0.42
1:D:586:ARG:HD2	1:D:586:ARG:C	2.39	0.42
1:A:507:LEU:O	1:A:511:ILE:CG1	2.63	0.42
1:B:187:HIS:CD2	1:B:197:LEU:HD11	2.55	0.42
1:B:526:GLU:HG3	1:B:527:SER:N	2.34	0.42
1:B:527:SER:HA	1:B:579:PHE:O	2.20	0.42
1:A:268:TRP:CE2	1:A:277:HIS:HB2	2.55	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:425:GLN:OE1	1:B:566:ARG:HB3	2.20	0.42
1:C:171:THR:O	1:C:172:ASN:HB2	2.20	0.42
1:D:161:ASN:OD1	1:D:163:ASP:N	2.51	0.42
1:D:187:HIS:CE1	1:D:197:LEU:HD11	2.55	0.42
1:A:390:TYR:HE2	1:A:505:TYR:HB2	1.85	0.42
1:A:418:ILE:HG13	1:A:468:LEU:HD23	2.02	0.42
1:C:619:VAL:HB	1:C:657:LEU:HD23	2.02	0.42
1:D:364:ILE:O	1:D:367:SER:OG	2.29	0.42
1:D:215:HIS:CE1	1:D:337:LYS:HD3	2.54	0.42
2:A:999:FAD:H9	2:A:999:FAD:H1'2	1.87	0.41
1:B:94:ASN:C	1:B:94:ASN:HD22	2.22	0.41
1:A:217:ASP:O	1:A:221:ILE:HG13	2.20	0.41
1:A:310:VAL:HA	1:A:313:TRP:CE3	2.55	0.41
1:C:616:HIS:HD2	2:C:999:FAD:C2	2.33	0.41
1:D:621:LYS:NZ	1:D:654:ASN:O	2.52	0.41
1:D:96:TRP:CZ3	2:D:999:FAD:HM83	2.55	0.41
1:A:83:ILE:HB	1:A:261:SER:HB2	2.01	0.41
1:B:127:THR:HG22	1:B:431:ALA:CB	2.51	0.41
1:B:265:ARG:HB2	1:B:279:GLU:OE1	2.20	0.41
1:D:187:HIS:NE2	1:D:197:LEU:HD11	2.36	0.41
1:D:267:LEU:O	1:D:268:TRP:HB3	2.21	0.41
1:B:127:THR:CG2	1:B:431:ALA:HA	2.50	0.41
1:C:117:ARG:HB3	1:C:118:TYR:CD2	2.56	0.41
1:C:638:MET:HE2	1:D:345:ILE:HD13	2.01	0.41
1:D:421:MET:HB2	1:D:425:GLN:HB2	2.02	0.41
1:D:613:LEU:HD23	1:D:613:LEU:HA	1.89	0.41
1:D:470:PHE:HB3	1:D:477:VAL:HG13	2.03	0.41
1:A:552:CYS:SG	1:A:561:PRO:HG3	2.61	0.41
1:C:190:CYS:HB2	1:C:193:GLU:OE1	2.21	0.41
1:A:156:PRO:HA	1:A:157:PRO:HD3	1.94	0.40
1:B:135:THR:HG22	1:B:136:PHE:CD1	2.57	0.40
1:B:481:GLU:CG	1:B:485:TYR:CE2	2.99	0.40
1:B:487:ILE:HA	1:B:490:LYS:HE2	2.03	0.40
1:C:293:GLU:HG3	5:C:2020:HOH:O	2.21	0.40
1:D:372:GLY:HA2	1:D:652:PHE:CZ	2.57	0.40
1:A:439:ILE:CD1	1:D:535:ASP:HB2	2.50	0.40
1:D:414:ALA:HA	1:D:415:PRO:HD3	1.85	0.40
1:A:102:LYS:C	1:A:113:LEU:HD12	2.41	0.40
1:C:274:LEU:HD23	1:C:274:LEU:HA	1.80	0.40
1:D:363:PHE:N	1:D:363:PHE:CD1	2.89	0.40
1:A:197:LEU:HG	1:A:202:PHE:CZ	2.56	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:277:HIS:CD2	1:B:378:THR:OG1	2.74	0.40
1:B:481:GLU:O	1:B:485:TYR:CD2	2.74	0.40
1:A:379:ILE:HG21	1:A:379:ILE:HD13	1.78	0.40
1:B:192:HIS:HB2	1:B:243:TYR:OH	2.19	0.40
1:C:187:HIS:CE1	1:C:197:LEU:HD11	2.57	0.40
1:C:288:GLU:O	1:C:292:LYS:HB2	2.21	0.40
1:D:128:PHE:HD1	1:D:128:PHE:O	2.05	0.40
1:C:345:ILE:HD13	1:D:638:MET:HE2	2.03	0.40

All (2) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:139:ASN:ND2	1:C:536:ARG:NH2[1_546]	2.04	0.16
1:B:265:ARG:CD	1:C:151:ASN:OD1[1_556]	2.13	0.07

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	550/658 (84%)	539 (98%)	11 (2%)	0	100	100
1	B	537/658 (82%)	521 (97%)	16 (3%)	0	100	100
1	C	553/658 (84%)	536 (97%)	16 (3%)	1 (0%)	47	62
1	D	546/658 (83%)	524 (96%)	20 (4%)	2 (0%)	34	48
All	All	2186/2632 (83%)	2120 (97%)	63 (3%)	3 (0%)	51	68

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	431	ALA

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Mol	Chain	Res	Type
1	C	140	LEU
1	D	106	ASN

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	477/545 (88%)	447 (94%)	30 (6%)	18	28
1	B	464/545 (85%)	427 (92%)	37 (8%)	12	18
1	C	477/545 (88%)	435 (91%)	42 (9%)	10	15
1	D	471/545 (86%)	428 (91%)	43 (9%)	9	14
All	All	1889/2180 (87%)	1737 (92%)	152 (8%)	11	18

All (152) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	82	ILE
1	A	90	LEU
1	A	120	LEU
1	A	141	ASP
1	A	144	THR
1	A	159	ILE
1	A	174	SER
1	A	191	LEU
1	A	323	LYS
1	A	342	ARG
1	A	349	CYS
1	A	354	MET
1	A	406	ARG
1	A	434	PRO
1	A	439	ILE
1	A	463	LEU
1	A	476	LYS
1	A	502	GLN
1	A	526	GLU

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Mol	Chain	Res	Type
1	A	529	GLU
1	A	559	PHE
1	A	566	ARG
1	A	584	ASN
1	A	586	ARG
1	A	588	ILE
1	A	592	LEU
1	A	596	GLU
1	A	599	GLU
1	A	630	SER
1	A	646	VAL
1	B	90	LEU
1	B	94	ASN
1	B	120	LEU
1	B	127	THR
1	B	140	LEU
1	B	170	LYS
1	B	195	PHE
1	B	199	GLU
1	B	265	ARG
1	B	298	THR
1	B	323	LYS
1	B	354	MET
1	B	406	ARG
1	B	428	PHE
1	B	433	LYS
1	B	435	GLN
1	B	463	LEU
1	B	475	GLU
1	B	487	ILE
1	B	502	GLN
1	B	503	ARG
1	B	510	VAL
1	B	511	ILE
1	B	520	GLU
1	B	524	ILE
1	B	526	GLU
1	B	529	GLU
1	B	555	LYS
1	B	566	ARG
1	B	578	TYR
1	B	581	PHE

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Mol	Chain	Res	Type
1	B	592	LEU
1	B	613	LEU
1	B	614	SER
1	B	628	LYS
1	B	633	ASP
1	B	646	VAL
1	C	90	LEU
1	C	105	LEU
1	C	114	THR
1	C	129	LYS
1	C	140	LEU
1	C	141	ASP
1	C	150	LEU
1	C	174	SER
1	C	199	GLU
1	C	224	LEU
1	C	265	ARG
1	C	271	GLU
1	C	323	LYS
1	C	342	ARG
1	C	349	CYS
1	C	354	MET
1	C	360	ILE
1	C	406	ARG
1	C	425	GLN
1	C	428	PHE
1	C	432	LEU
1	C	433	LYS
1	C	462	GLN
1	C	463	LEU
1	C	490	LYS
1	C	499	ASP
1	C	508	THR
1	C	511	ILE
1	C	520	GLU
1	C	526	GLU
1	C	542	ARG
1	C	559	PHE
1	C	566	ARG
1	C	568	THR
1	C	578	TYR
1	C	584	ASN

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Mol	Chain	Res	Type
1	C	586	ARG
1	C	588	ILE
1	C	596	GLU
1	C	613	LEU
1	C	633	ASP
1	C	641	SER
1	D	106	ASN
1	D	107	LYS
1	D	116	LYS
1	D	120	LEU
1	D	121	SER
1	D	125	LEU
1	D	128	PHE
1	D	134	ASN
1	D	139	ASN
1	D	141	ASP
1	D	143	LYS
1	D	150	LEU
1	D	151	ASN
1	D	155	THR
1	D	172	ASN
1	D	174	SER
1	D	199	GLU
1	D	224	LEU
1	D	285	GLN
1	D	294	SER
1	D	323	LYS
1	D	354	MET
1	D	386	GLU
1	D	388	GLN
1	D	406	ARG
1	D	427	GLN
1	D	432	LEU
1	D	463	LEU
1	D	476	LYS
1	D	478	LEU
1	D	529	GLU
1	D	542	ARG
1	D	553	LYS
1	D	555	LYS
1	D	559	PHE
1	D	568	THR

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Mol	Chain	Res	Type
1	D	578	TYR
1	D	581	PHE
1	D	586	ARG
1	D	603	ARG
1	D	613	LEU
1	D	641	SER
1	D	646	VAL

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (46) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	172	ASN
1	A	177	GLN
1	A	187	HIS
1	A	215	HIS
1	A	262	GLN
1	A	290	GLN
1	A	328	ASN
1	A	423	ASN
1	A	479	GLN
1	A	500	ASN
1	A	502	GLN
1	A	615	HIS
1	A	616	HIS
1	B	94	ASN
1	B	110	GLN
1	B	133	GLN
1	B	277	HIS
1	B	335	HIS
1	B	419	HIS
1	B	423	ASN
1	B	427	GLN
1	B	558	GLN
1	B	597	GLN
1	B	650	ASN
1	B	656	ASN
1	C	110	GLN
1	C	142	HIS
1	C	361	HIS
1	C	388	GLN
1	C	400	GLN
1	C	419	HIS

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Mol	Chain	Res	Type
1	C	597	GLN
1	C	650	ASN
1	C	656	ASN
1	D	106	ASN
1	D	110	GLN
1	D	139	ASN
1	D	142	HIS
1	D	151	ASN
1	D	177	GLN
1	D	277	HIS
1	D	400	GLN
1	D	424	GLN
1	D	597	GLN
1	D	650	ASN
1	D	656	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry ⓘ

8 ligands are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	1DO	B	888	-	12,12,12	0.76	0	11,11,11	0.40	0
3	SO4	D	1659	-	4,4,4	0.40	0	6,6,6	0.71	0
4	1DO	C	888	-	12,12,12	0.74	0	11,11,11	0.51	0
2	FAD	B	999	-	51,58,58	1.85	10 (19%)	60,89,89	2.12	14 (23%)
3	SO4	A	1659	-	4,4,4	0.22	0	6,6,6	0.39	0
2	FAD	D	999	-	51,58,58	1.55	7 (13%)	60,89,89	1.82	16 (26%)
2	FAD	C	999	-	51,58,58	1.42	6 (11%)	60,89,89	1.96	9 (15%)
2	FAD	A	999	-	51,58,58	1.57	6 (11%)	60,89,89	1.90	14 (23%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	1DO	B	888	-	-	6/10/10/10	-
4	1DO	C	888	-	-	7/10/10/10	-
2	FAD	B	999	-	-	3/30/50/50	0/6/6/6
2	FAD	D	999	-	-	4/30/50/50	0/6/6/6
2	FAD	C	999	-	-	4/30/50/50	0/6/6/6
2	FAD	A	999	-	-	3/30/50/50	0/6/6/6

All (29) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	999	FAD	C4X-N5	6.36	1.42	1.33
2	B	999	FAD	C10-N1	5.87	1.40	1.33
2	D	999	FAD	C1'-N10	5.00	1.53	1.48
2	B	999	FAD	C1'-N10	4.98	1.53	1.48
2	B	999	FAD	C2A-N3A	4.84	1.39	1.32
2	B	999	FAD	C4X-N5	4.79	1.40	1.33
2	D	999	FAD	C4X-N5	4.37	1.39	1.33
2	C	999	FAD	C10-N1	3.94	1.38	1.33
2	C	999	FAD	C1'-N10	3.88	1.52	1.48
2	A	999	FAD	C2A-N3A	3.54	1.37	1.32
2	B	999	FAD	C4X-C10	3.45	1.42	1.38
2	A	999	FAD	C4-N3	3.38	1.38	1.33
2	C	999	FAD	C4-N3	3.29	1.38	1.33
2	D	999	FAD	C4-N3	3.22	1.38	1.33
2	D	999	FAD	C2A-N3A	3.22	1.37	1.32

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	999	FAD	C10-N1	3.21	1.37	1.33
2	B	999	FAD	C2A-N1A	3.02	1.39	1.33
2	B	999	FAD	C4-N3	2.92	1.38	1.33
2	C	999	FAD	C2A-N3A	2.89	1.36	1.32
2	C	999	FAD	C4X-N5	2.72	1.37	1.33
2	D	999	FAD	C10-N1	2.70	1.36	1.33
2	C	999	FAD	C5X-N5	2.63	1.39	1.35
2	A	999	FAD	C5X-N5	2.56	1.39	1.35
2	D	999	FAD	C2A-N1A	2.55	1.38	1.33
2	B	999	FAD	O4'-C4'	-2.53	1.38	1.43
2	B	999	FAD	C5X-N5	2.28	1.39	1.35
2	A	999	FAD	C2A-N1A	2.18	1.38	1.33
2	D	999	FAD	C5X-N5	2.17	1.38	1.35
2	B	999	FAD	O4B-C4B	-2.01	1.40	1.45

All (53) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	999	FAD	C4-N3-C2	8.16	122.03	115.14
2	A	999	FAD	N3A-C2A-N1A	-7.36	117.17	128.68
2	C	999	FAD	C4-N3-C2	7.32	121.32	115.14
2	B	999	FAD	C1'-N10-C9A	6.84	123.67	118.29
2	C	999	FAD	N3A-C2A-N1A	-6.00	119.31	128.68
2	D	999	FAD	N3A-C2A-N1A	-5.67	119.82	128.68
2	A	999	FAD	C4-N3-C2	5.08	119.43	115.14
2	C	999	FAD	C1'-N10-C9A	4.93	122.17	118.29
2	B	999	FAD	N3A-C2A-N1A	-4.34	121.89	128.68
2	C	999	FAD	C4X-N5-C5X	4.31	121.07	116.77
2	D	999	FAD	C4-N3-C2	4.20	118.69	115.14
2	A	999	FAD	C5X-C9A-N10	3.94	120.57	117.72
2	D	999	FAD	C4X-N5-C5X	3.83	120.59	116.77
2	B	999	FAD	C4-C4X-N5	3.81	122.95	118.60
2	C	999	FAD	C4X-C4-N3	-3.80	118.23	123.43
2	A	999	FAD	C1B-N9A-C4A	-3.64	120.24	126.64
2	D	999	FAD	C10-C4X-N5	-3.57	118.79	121.26
2	B	999	FAD	C10-C4X-N5	-3.52	118.83	121.26
2	D	999	FAD	C5'-C4'-C3'	3.42	118.81	112.20
2	C	999	FAD	O4'-C4'-C5'	-3.40	102.27	109.92
2	A	999	FAD	C4-C4X-C10	-3.39	117.70	119.95
2	D	999	FAD	C1'-N10-C9A	3.35	120.93	118.29
2	B	999	FAD	O4'-C4'-C5'	-3.32	102.45	109.92
2	A	999	FAD	C4-C4X-N5	3.10	122.14	118.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	999	FAD	C4-C4X-N5	2.97	122.00	118.60
2	B	999	FAD	C5X-C9A-N10	2.87	119.80	117.72
2	D	999	FAD	O3'-C3'-C2'	-2.83	101.98	108.81
2	B	999	FAD	C4X-N5-C5X	2.79	119.56	116.77
2	D	999	FAD	C5X-C9A-N10	2.78	119.73	117.72
2	C	999	FAD	O3'-C3'-C2'	-2.77	102.12	108.81
2	D	999	FAD	O5'-C5'-C4'	-2.69	102.19	109.36
2	B	999	FAD	O5'-C5'-C4'	-2.63	102.33	109.36
2	B	999	FAD	C4-C4X-C10	-2.61	118.22	119.95
2	A	999	FAD	O2'-C2'-C1'	2.61	115.88	109.59
2	A	999	FAD	C1'-N10-C10	2.61	120.74	118.41
2	C	999	FAD	C10-C4X-N5	-2.57	119.48	121.26
2	B	999	FAD	C5'-C4'-C3'	2.56	117.15	112.20
2	D	999	FAD	C9A-N10-C10	-2.39	118.78	121.91
2	A	999	FAD	O3B-C3B-C4B	-2.39	104.15	111.05
2	B	999	FAD	C4X-C4-N3	-2.38	120.17	123.43
2	D	999	FAD	O4'-C4'-C3'	2.35	114.80	109.10
2	A	999	FAD	C5A-C6A-N6A	-2.33	116.80	120.35
2	B	999	FAD	O3B-C3B-C4B	-2.32	104.33	111.05
2	A	999	FAD	C1'-N10-C9A	2.28	120.09	118.29
2	C	999	FAD	O3B-C3B-C4B	-2.22	104.64	111.05
2	A	999	FAD	P-O3P-PA	-2.21	125.25	132.83
2	D	999	FAD	O3'-C3'-C4'	2.14	113.97	108.81
2	A	999	FAD	C9A-N10-C10	-2.09	119.17	121.91
2	D	999	FAD	C1'-N10-C10	2.07	120.26	118.41
2	B	999	FAD	C9A-N10-C10	-2.06	119.22	121.91
2	D	999	FAD	P-O3P-PA	-2.05	125.81	132.83
2	A	999	FAD	C4X-N5-C5X	2.02	118.80	116.77
2	D	999	FAD	C3B-C2B-C1B	2.02	104.02	100.98

There are no chirality outliers.

All (27) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	B	999	FAD	N10-C1'-C2'-O2'
2	B	999	FAD	N10-C1'-C2'-C3'
2	D	999	FAD	N10-C1'-C2'-O2'
2	C	999	FAD	N10-C1'-C2'-O2'
2	C	999	FAD	N10-C1'-C2'-C3'
2	A	999	FAD	N10-C1'-C2'-O2'
4	C	888	1DO	C4-C5-C6-C7
4	B	888	1DO	C2-C3-C4-C5

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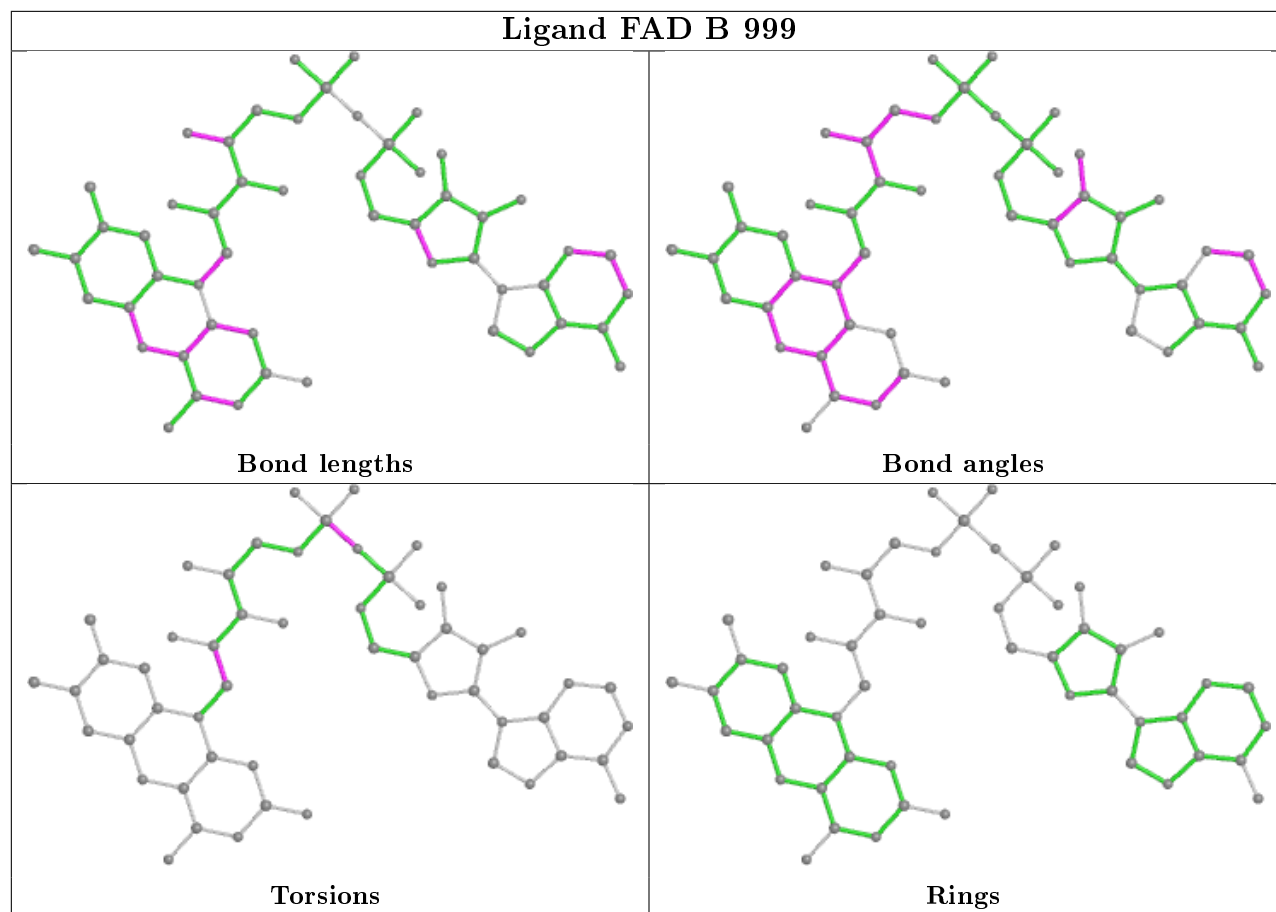
Mol	Chain	Res	Type	Atoms
4	B	888	1DO	C3-C4-C5-C6
4	C	888	1DO	C3-C4-C5-C6
4	B	888	1DO	C6-C7-C8-C9
4	C	888	1DO	C2-C3-C4-C5
4	B	888	1DO	C1-C2-C3-C4
4	B	888	1DO	O2S-C1-C2-C3
4	C	888	1DO	O2S-C1-C2-C3
4	B	888	1DO	C7-C8-C9-C10
4	C	888	1DO	C6-C7-C8-C9
2	D	999	FAD	PA-O3P-P-O2P
4	C	888	1DO	C9-C10-C11-C12
2	D	999	FAD	N10-C1'-C2'-C3'
2	A	999	FAD	N10-C1'-C2'-C3'
2	A	999	FAD	PA-O3P-P-O2P
4	C	888	1DO	C1-C2-C3-C4
2	B	999	FAD	PA-O3P-P-O2P
2	C	999	FAD	PA-O3P-P-O2P
2	D	999	FAD	C3'-C4'-C5'-O5'
2	C	999	FAD	C3'-C4'-C5'-O5'

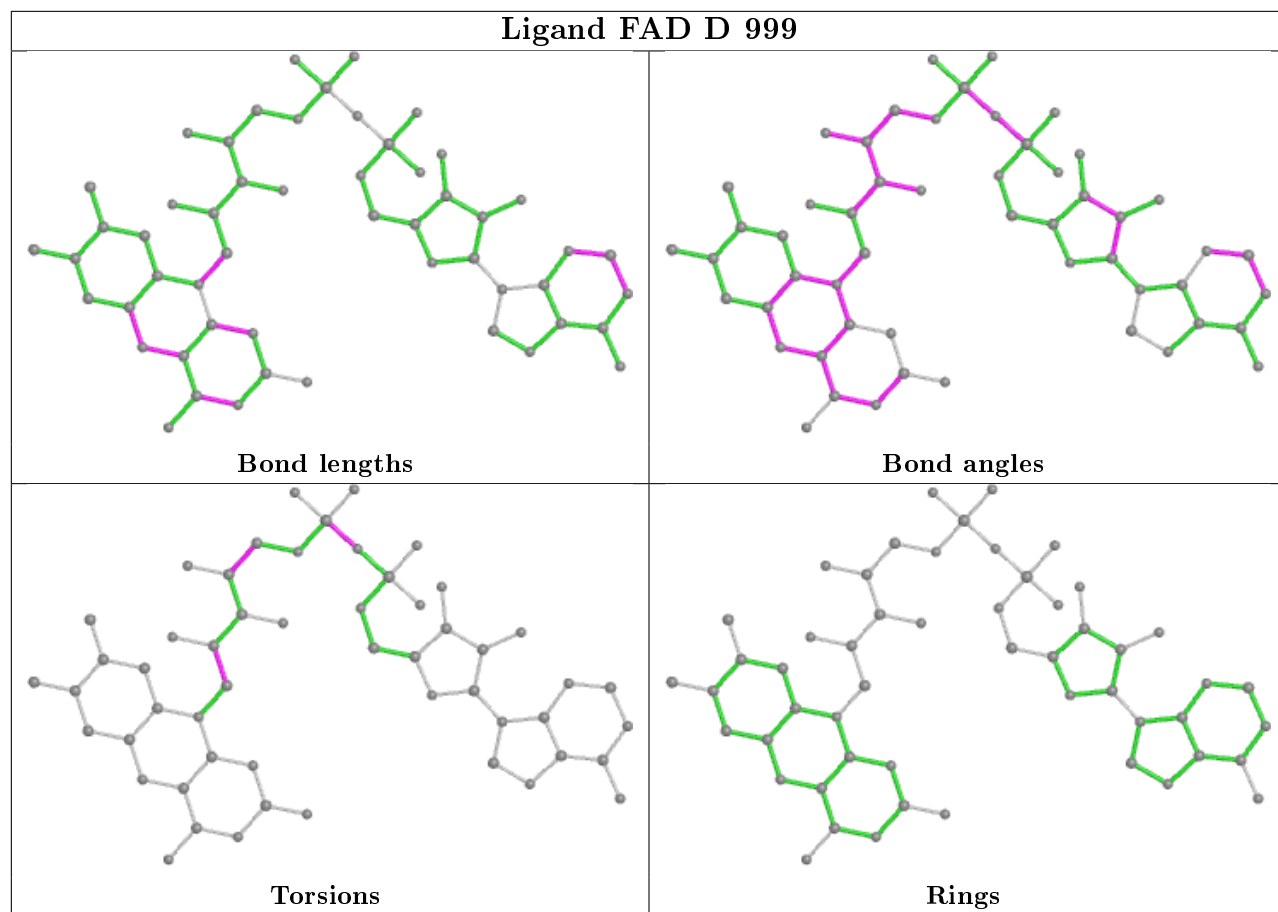
There are no ring outliers.

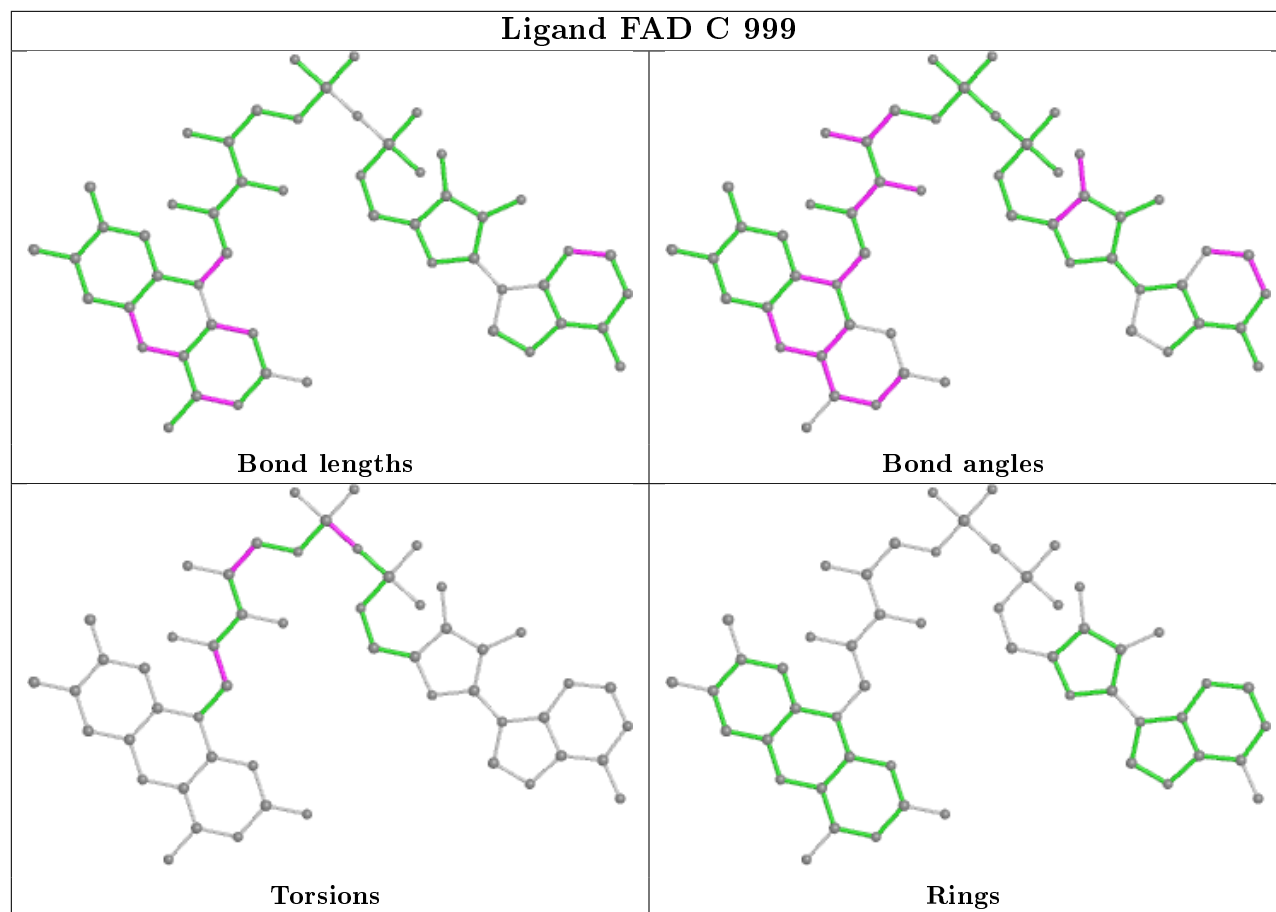
5 monomers are involved in 9 short contacts:

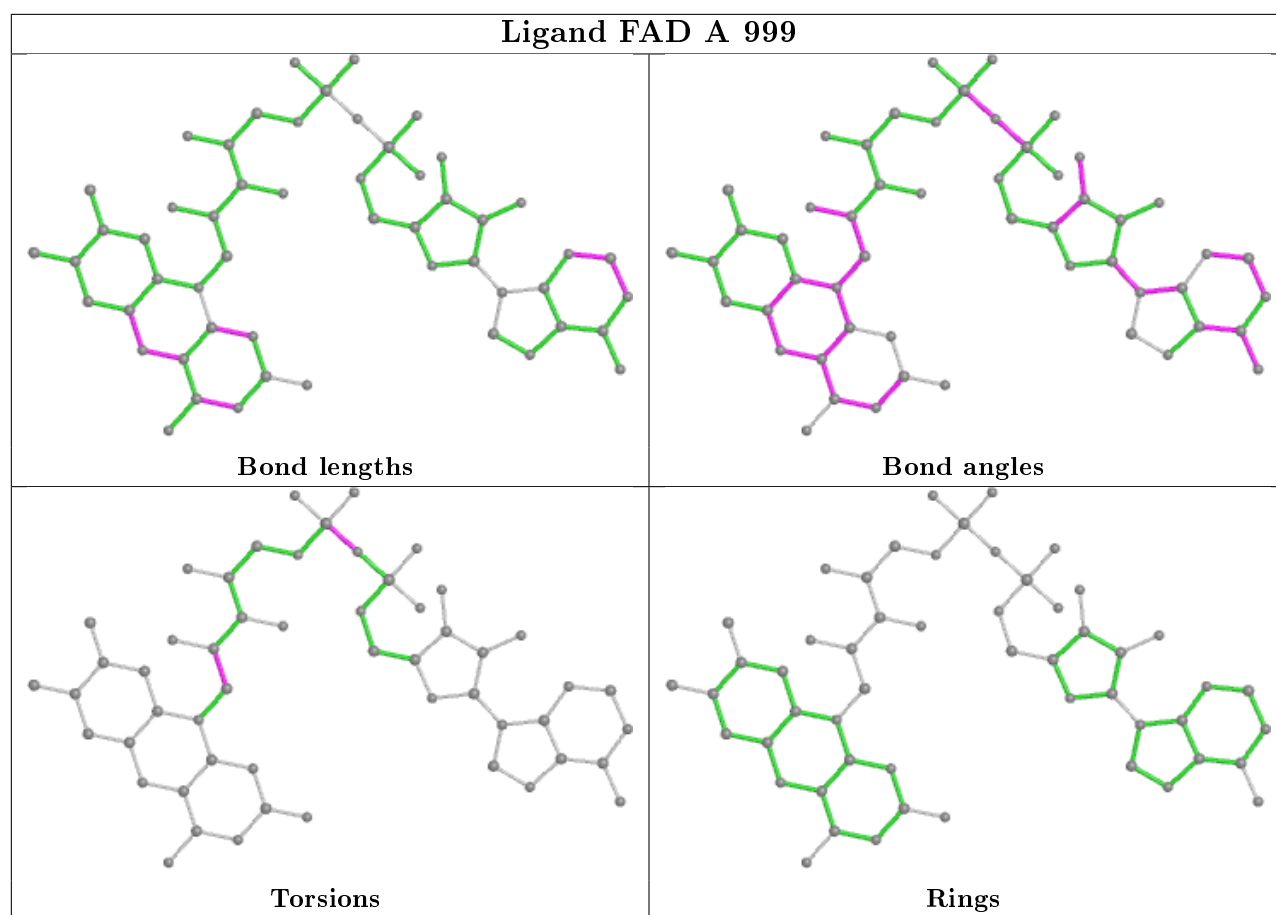
Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	B	888	1DO	2	0
4	C	888	1DO	2	0
2	D	999	FAD	2	0
2	C	999	FAD	2	0
2	A	999	FAD	1	0

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









5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data

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	555/658 (84%)	-0.27	11 (1%) 65 63	13, 33, 63, 83	0
1	B	543/658 (82%)	-0.24	12 (2%) 62 60	14, 35, 65, 85	0
1	C	557/658 (84%)	-0.31	4 (0%) 87 86	14, 33, 59, 72	0
1	D	550/658 (83%)	-0.18	12 (2%) 62 60	15, 39, 71, 84	0
All	All	2205/2632 (83%)	-0.25	39 (1%) 68 66	13, 35, 66, 85	0

All (39) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	82	ILE	5.0
1	A	440	PHE	4.3
1	B	458	PHE	3.9
1	A	82	ILE	3.9
1	B	197	LEU	3.7
1	D	559	PHE	3.6
1	B	162	GLU	3.5
1	A	437	SER	3.5
1	A	81	GLY	3.5
1	D	82	ILE	3.4
1	B	558	GLN	3.1
1	D	83	ILE	3.0
1	D	558	GLN	3.0
1	D	430	HIS	2.8
1	A	83	ILE	2.7
1	D	505	TYR	2.7
1	B	180	ASP	2.7
1	B	460	PRO	2.7
1	D	81	GLY	2.7
1	C	81	GLY	2.7
1	C	83	ILE	2.6

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Mol	Chain	Res	Type	RSRZ
1	B	81	GLY	2.6
1	A	441	THR	2.5
1	D	589	SER	2.5
1	A	439	ILE	2.5
1	B	93	TRP	2.4
1	B	587	GLY	2.3
1	A	159	ILE	2.3
1	D	134	ASN	2.3
1	B	166	HIS	2.2
1	B	199	GLU	2.2
1	C	435	GLN	2.1
1	D	131	TRP	2.1
1	A	559	PHE	2.1
1	B	201	MET	2.1
1	A	175	TYR	2.1
1	A	197	LEU	2.1
1	D	506	LEU	2.0
1	D	164	PHE	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 carbohydrates 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(\AA^2)	Q<0.9
4	1DO	C	888	13/13	0.87	0.17	31,34,41,42	0
4	1DO	B	888	13/13	0.90	0.15	29,33,36,37	0
3	SO4	D	1659	5/5	0.95	0.13	48,49,51,53	0
3	SO4	A	1659	5/5	0.95	0.14	53,53,54,57	0
2	FAD	B	999	53/53	0.98	0.10	12,17,21,23	0

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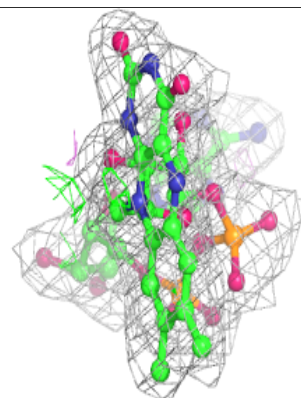
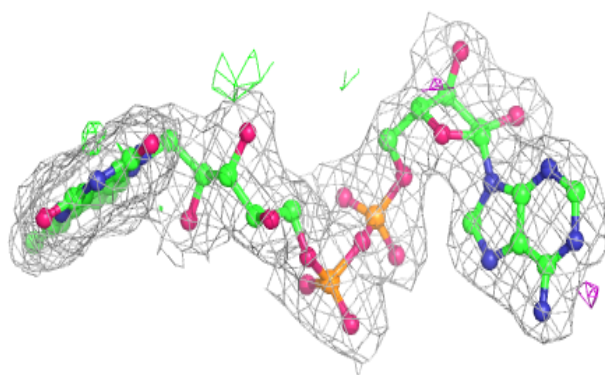
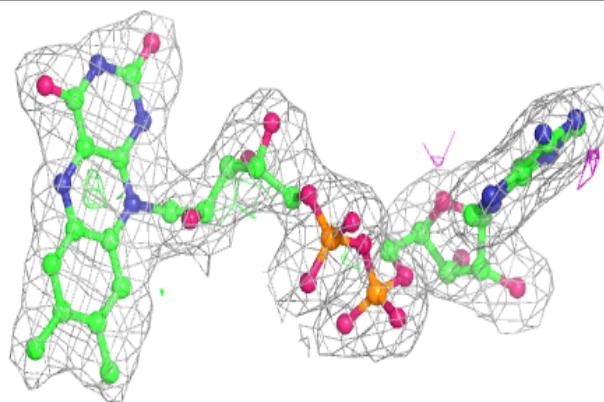
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
2	FAD	D	999	53/53	0.98	0.11	15,22,26,27	0
2	FAD	C	999	53/53	0.98	0.11	6,11,16,18	0
2	FAD	A	999	53/53	0.98	0.11	15,19,24,28	0

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.

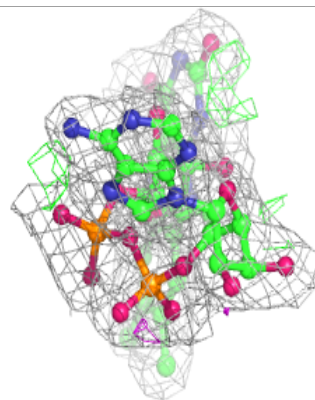
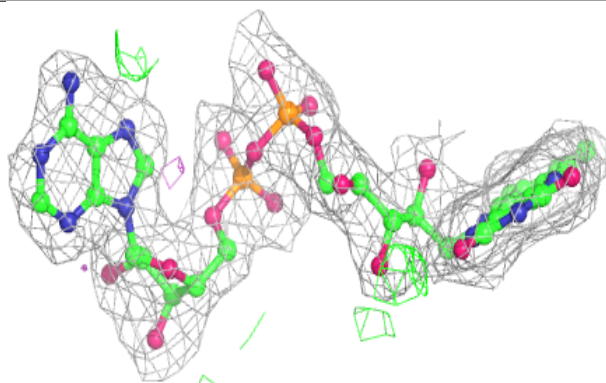
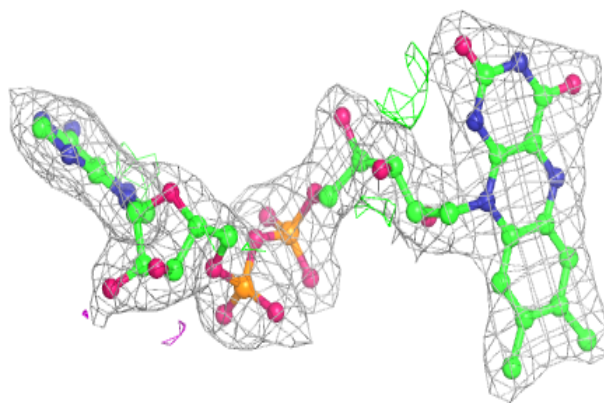
Electron density around FAD B 999:

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

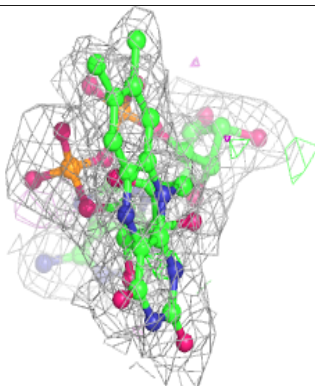
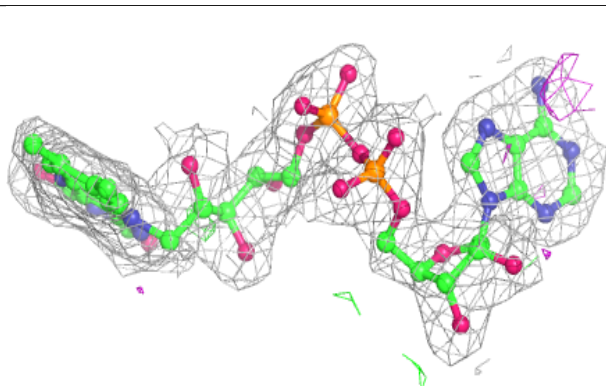
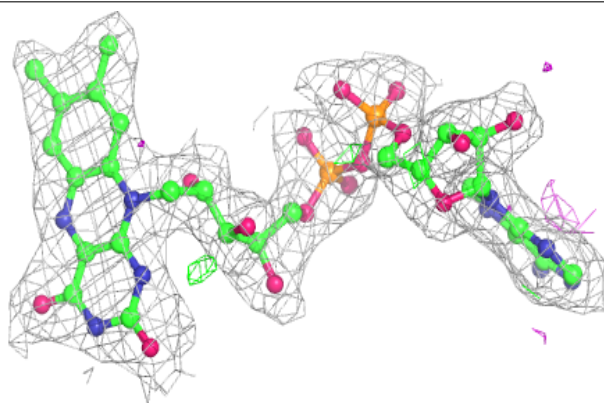


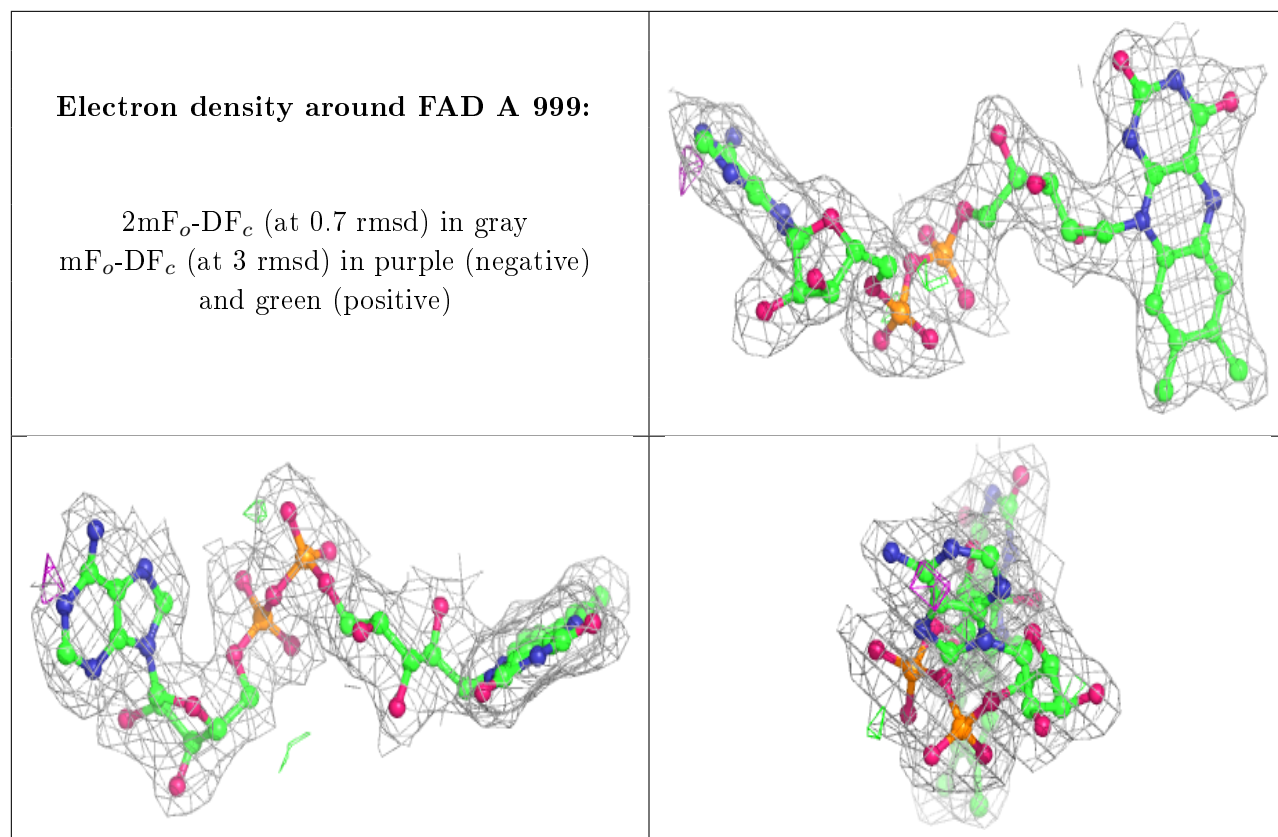
Electron density around FAD D 999:

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

**Electron density around FAD C 999:**

$2mF_o-DF_c$ (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.