



Full wwPDB X-ray Structure Validation Report ⓘ

Jan 31, 2016 – 07:27 PM GMT

PDB ID : 1FP4
Title : CRYSTAL STRUCTURE OF THE ALPHA-H195Q MUTANT OF NITRO-GENASE
Authors : Sorlie, M.; Christiansen, J.; Lemon, B.J.; Peters, J.W.; Dean, D.R.; Hales, B.J.
Deposited on : 2000-08-30
Resolution : 2.50 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.
We welcome your comments at validation@mail.wwpdb.org
A user guide is available at
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467
Mogul : 1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix) : **NOT EXECUTED**
EDS : **NOT EXECUTED**
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

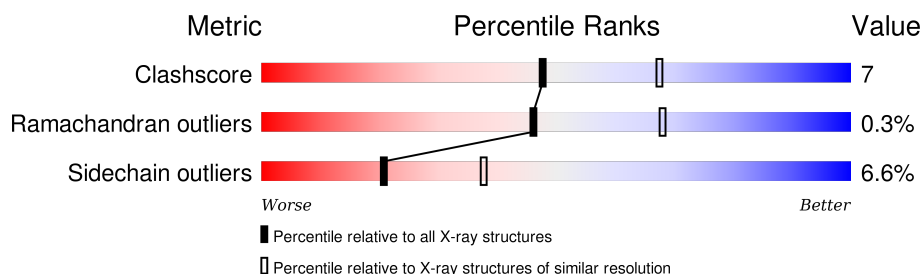
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 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))
Clashscore	102246	4242 (2.50-2.50)
Ramachandran outliers	100387	4156 (2.50-2.50)
Sidechain outliers	100360	4158 (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 on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	492	
1	C	492	
2	B	523	
2	D	523	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
5	CFM	A	496	-	-	X	-
5	CFM	C	497	-	-	X	-

2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 16295 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called NITROGENASE MOLYBDENUM-IRON PROTEIN ALPHA CHAIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	467	Total	C	N	O	S	0	0	0
			3708	2360	629	695	24			
1	C	468	Total	C	N	O	S	0	0	0
			3712	2363	630	695	24			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	195	GLN	HIS	ENGINEERED	UNP P07328
C	195	GLN	HIS	ENGINEERED	UNP P07328

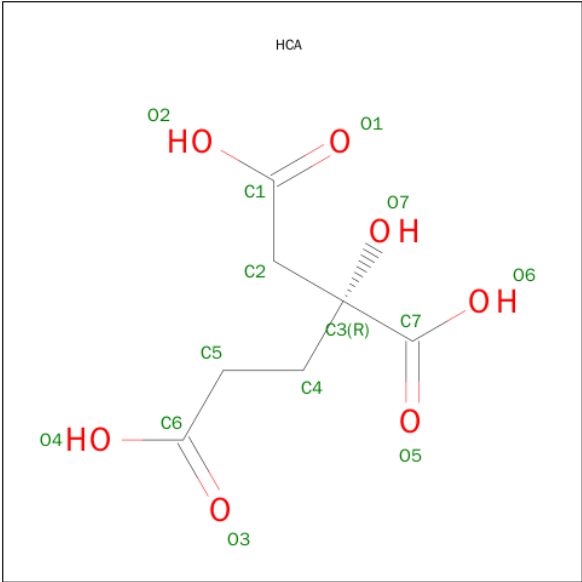
- Molecule 2 is a protein called NITROGENASE MOLYBDENUM-IRON PROTEIN BETA CHAIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	522	Total	C	N	O	S	0	0	0
			4174	2666	705	775	28			
2	D	522	Total	C	N	O	S	0	0	0
			4174	2666	705	775	28			

- Molecule 3 is CALCIUM ION (three-letter code: CA) (formula: Ca).

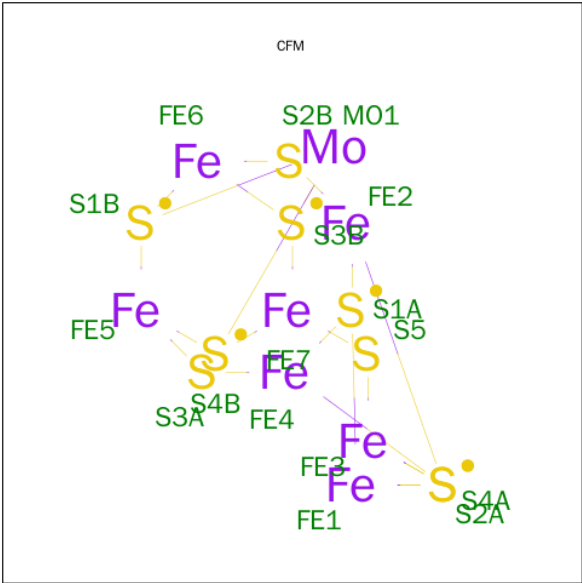
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	B	1	Total	Ca	0	0
			1	1		
3	D	1	Total	Ca	0	0
			1	1		

- Molecule 4 is 3-HYDROXY-3-CARBOXY-ADIPIIC ACID (three-letter code: HCA) (formula: C₇H₁₀O₇).



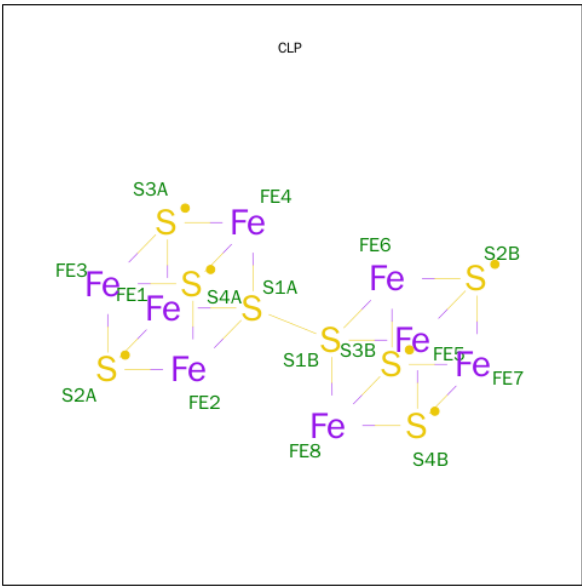
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			14	7	7		
4	C	1	Total	C	O	0	0
			14	7	7		

- Molecule 5 is FE-MO-S CLUSTER (three-letter code: CFM) (formula: Fe₇MoS₉).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	A	1	Total	Fe	Mo	S	0	0
			17	7	1	9		
5	C	1	Total	Fe	Mo	S	0	0
			17	7	1	9		

- Molecule 6 is FE-S CLUSTER (three-letter code: CLP) (formula: Fe₈S₈).



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

- Molecule 7 is water.

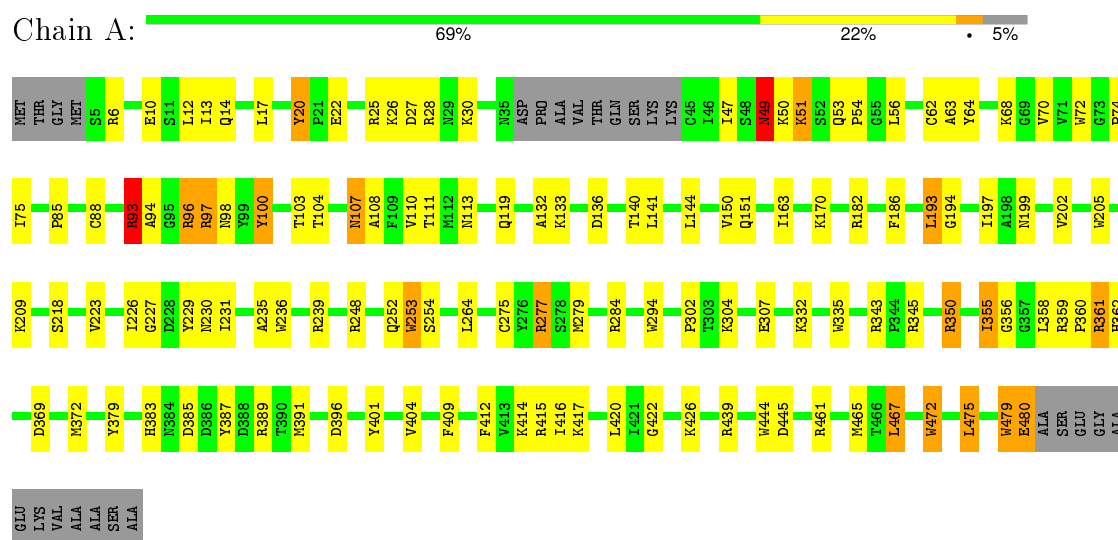
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	102	Total	O	0	0
			102	102		
7	B	114	Total	O	0	0
			114	114		
7	C	74	Total	O	0	0
			74	74		
7	D	143	Total	O	0	0
			143	143		

3 Residue-property plots

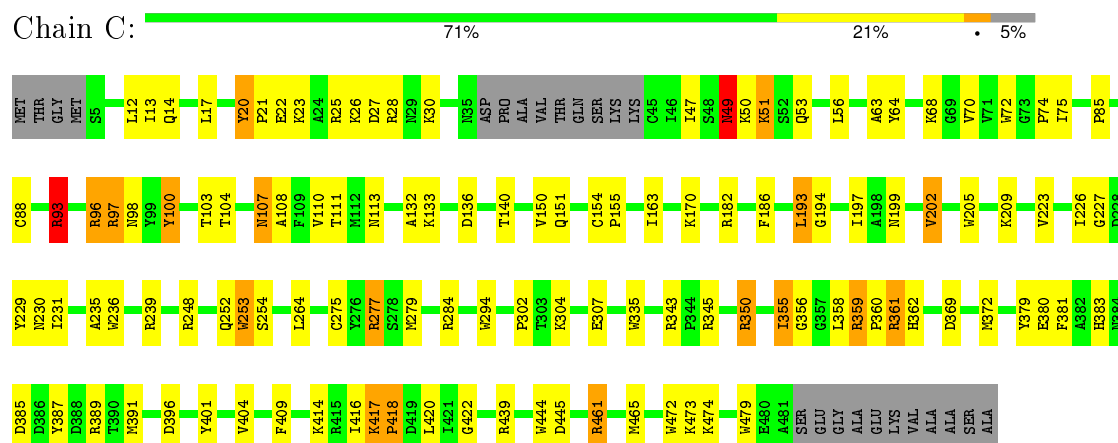
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according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

Note EDS was not executed.

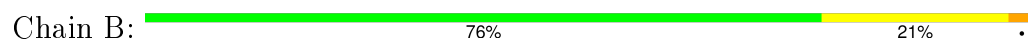
• Molecule 1: NITROGENASE MOLYBDENUM-IRON PROTEIN ALPHA CHAIN

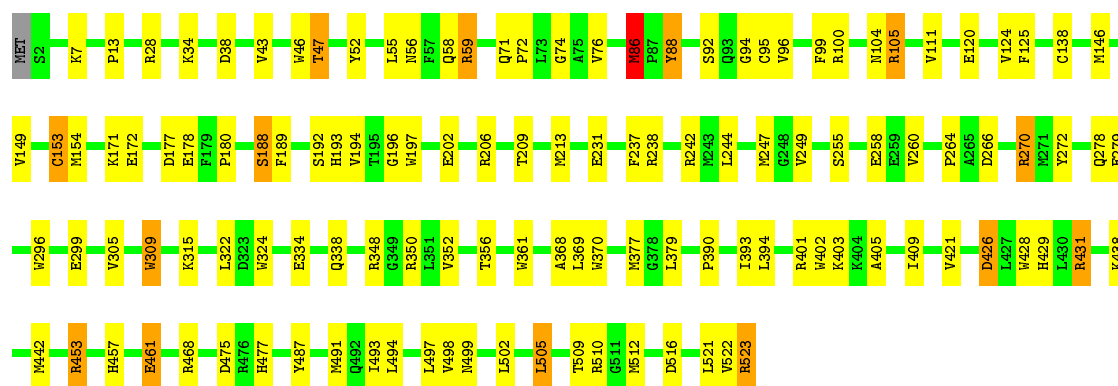


• Molecule 1: NITROGENASE MOLYBDENUM-IRON PROTEIN ALPHA CHAIN



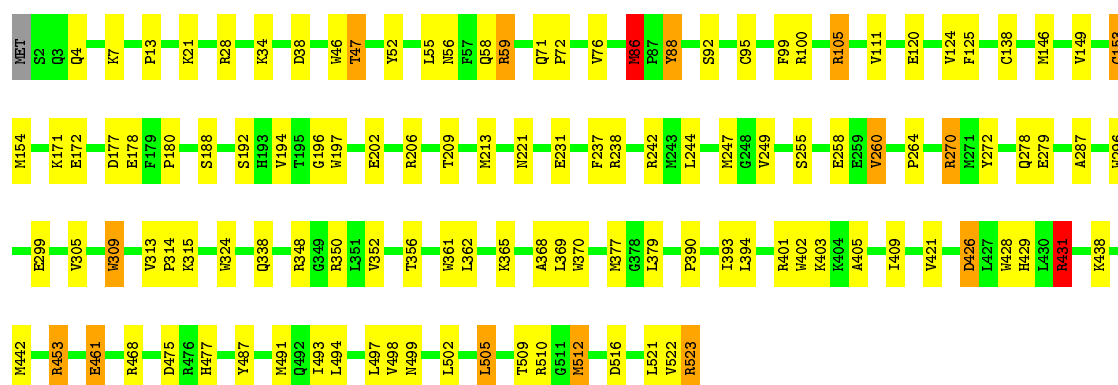
• Molecule 2: NITROGENASE MOLYBDENUM-IRON PROTEIN BETA CHAIN





• Molecule 2: NITROGENASE MOLYBDENUM-IRON PROTEIN BETA CHAIN

Chain D: 77% 20%



4 Data and refinement statistics

Xtriage (Phenix) and EDS were not executed - this section will therefore be incomplete.

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	107.20 Å 130.20 Å 80.40 Å 90.00° 111.20° 90.00°	Depositor
Resolution (Å)	20.00 – 2.50	Depositor
% Data completeness (in resolution range)	(Not available) (20.00-2.50)	Depositor
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	X-PLOR	Depositor
R, R_{free}	0.184 , 0.240	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	16295	wwPDB-VP
Average B, all atoms (Å ²)	28.0	wwPDB-VP

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: CA, HCA, CLP, CFM

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	0.74	0/3793	1.41	49/5114 (1.0%)
1	C	0.85	1/3797 (0.0%)	1.44	56/5120 (1.1%)
2	B	0.72	0/4280	1.31	55/5786 (1.0%)
2	D	0.72	0/4280	1.30	56/5786 (1.0%)
All	All	0.76	1/16150 (0.0%)	1.36	216/21806 (1.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	418	PRO	N-CD	-26.97	1.10	1.47

All (216) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	49	ASN	CB-CA-C	-14.28	81.84	110.40
1	C	49	ASN	CB-CA-C	-13.93	82.54	110.40
1	C	418	PRO	CA-N-CD	13.66	130.82	111.70
1	C	418	PRO	N-CA-CB	-10.43	90.78	103.30
1	C	50	LYS	N-CA-CB	-10.30	92.05	110.60
1	A	50	LYS	N-CA-CB	-10.11	92.40	110.60
2	D	59	ARG	NE-CZ-NH2	9.66	125.13	120.30
2	D	270	ARG	NE-CZ-NH2	9.42	125.01	120.30
2	B	270	ARG	NE-CZ-NH2	9.40	125.00	120.30
2	D	59	ARG	NE-CZ-NH1	-9.37	115.62	120.30
2	B	59	ARG	NE-CZ-NH2	9.27	124.94	120.30
2	D	105	ARG	NE-CZ-NH2	9.22	124.91	120.30
1	C	253	TRP	CA-C-N	-8.84	97.76	117.20
2	D	523	ARG	NE-CZ-NH1	-8.79	115.90	120.30
1	A	253	TRP	CA-C-N	-8.75	97.96	117.20
2	B	59	ARG	NE-CZ-NH1	-8.68	115.96	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	361	TRP	CD1-CG-CD2	8.66	113.23	106.30
1	C	294	TRP	CD1-CG-CD2	8.62	113.19	106.30
1	C	472	TRP	CD1-CG-CD2	8.57	113.16	106.30
2	B	361	TRP	CD1-CG-CD2	8.56	113.15	106.30
2	B	270	ARG	NE-CZ-NH1	-8.52	116.04	120.30
1	C	444	TRP	CD1-CG-CD2	8.52	113.12	106.30
1	A	417	LYS	N-CA-CB	8.50	125.90	110.60
1	A	93	ARG	NE-CZ-NH1	-8.45	116.08	120.30
2	B	296	TRP	CD1-CG-CD2	8.42	113.04	106.30
1	A	72	TRP	CD1-CG-CD2	8.36	112.99	106.30
1	A	444	TRP	CD1-CG-CD2	8.34	112.97	106.30
2	D	370	TRP	CD1-CG-CD2	8.29	112.93	106.30
2	B	46	TRP	CD1-CG-CD2	8.28	112.93	106.30
1	A	472	TRP	CD1-CG-CD2	8.24	112.89	106.30
1	C	205	TRP	CD1-CG-CD2	8.21	112.87	106.30
2	B	523	ARG	NE-CZ-NH1	-8.18	116.21	120.30
2	D	296	TRP	CD1-CG-CD2	8.17	112.83	106.30
1	C	51	LYS	N-CA-C	8.16	133.02	111.00
1	A	294	TRP	CD1-CG-CD2	8.15	112.82	106.30
2	D	46	TRP	CD1-CG-CD2	8.13	112.80	106.30
1	C	72	TRP	CD1-CG-CD2	8.12	112.79	106.30
2	B	402	TRP	CD1-CG-CD2	8.10	112.78	106.30
1	A	444	TRP	CE2-CD2-CG	-8.08	100.83	107.30
1	C	444	TRP	CE2-CD2-CG	-8.06	100.85	107.30
2	B	370	TRP	CD1-CG-CD2	8.06	112.75	106.30
2	D	361	TRP	CE2-CD2-CG	-8.01	100.89	107.30
2	D	428	TRP	CE2-CD2-CG	-8.00	100.90	107.30
1	C	472	TRP	CE2-CD2-CG	-7.96	100.93	107.30
1	A	205	TRP	CD1-CG-CD2	7.94	112.66	106.30
2	B	361	TRP	CE2-CD2-CG	-7.94	100.95	107.30
2	B	242	ARG	NE-CZ-NH1	-7.93	116.33	120.30
2	B	523	ARG	NE-CZ-NH2	7.89	124.25	120.30
2	D	428	TRP	CD1-CG-CD2	7.83	112.57	106.30
1	C	97	ARG	NE-CZ-NH1	-7.81	116.39	120.30
1	C	93	ARG	NE-CZ-NH1	-7.80	116.40	120.30
2	B	428	TRP	CD1-CG-CD2	7.80	112.54	106.30
2	B	105	ARG	NE-CZ-NH2	7.76	124.18	120.30
1	A	236	TRP	CD1-CG-CD2	7.75	112.50	106.30
2	D	270	ARG	NE-CZ-NH1	-7.74	116.43	120.30
1	A	472	TRP	CE2-CD2-CG	-7.73	101.12	107.30
1	C	236	TRP	CD1-CG-CD2	7.71	112.47	106.30
1	C	93	ARG	NE-CZ-NH2	7.71	124.16	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	46	TRP	CE2-CD2-CG	-7.71	101.13	107.30
2	D	242	ARG	NE-CZ-NH2	7.69	124.15	120.30
2	B	238	ARG	NE-CZ-NH2	7.68	124.14	120.30
1	C	253	TRP	O-C-N	7.67	134.97	122.70
2	D	402	TRP	CD1-CG-CD2	7.67	112.44	106.30
2	B	428	TRP	CE2-CD2-CG	-7.61	101.22	107.30
2	D	296	TRP	CE2-CD2-CG	-7.61	101.22	107.30
1	C	343	ARG	NE-CZ-NH1	-7.59	116.50	120.30
1	A	97	ARG	NE-CZ-NH1	-7.59	116.50	120.30
1	C	294	TRP	CE2-CD2-CG	-7.59	101.23	107.30
2	B	370	TRP	CE2-CD2-CG	-7.58	101.23	107.30
2	B	296	TRP	CE2-CD2-CG	-7.54	101.26	107.30
2	B	309	TRP	CD1-CG-CD2	7.53	112.33	106.30
1	C	205	TRP	CE2-CD2-CG	-7.50	101.30	107.30
2	D	309	TRP	CD1-CG-CD2	7.50	112.30	106.30
1	A	72	TRP	CE2-CD2-CG	-7.49	101.31	107.30
2	D	242	ARG	NE-CZ-NH1	-7.49	116.56	120.30
1	C	72	TRP	CE2-CD2-CG	-7.41	101.37	107.30
1	A	294	TRP	CE2-CD2-CG	-7.40	101.38	107.30
1	C	335	TRP	CD1-CG-CD2	7.39	112.21	106.30
1	A	253	TRP	O-C-N	7.39	134.52	122.70
2	D	46	TRP	CE2-CD2-CG	-7.34	101.42	107.30
2	B	402	TRP	CE2-CD2-CG	-7.34	101.43	107.30
2	D	197	TRP	CE2-CD2-CG	-7.34	101.43	107.30
2	D	370	TRP	CE2-CD2-CG	-7.31	101.45	107.30
1	A	335	TRP	CD1-CG-CD2	7.30	112.14	106.30
1	A	205	TRP	CE2-CD2-CG	-7.25	101.50	107.30
1	A	97	ARG	NE-CZ-NH2	7.21	123.91	120.30
1	C	253	TRP	CE2-CD2-CG	-7.21	101.53	107.30
2	D	238	ARG	NE-CZ-NH2	7.14	123.87	120.30
1	C	461	ARG	NE-CZ-NH1	-7.12	116.74	120.30
1	C	97	ARG	NE-CZ-NH2	7.12	123.86	120.30
1	C	417	LYS	C-N-CD	-7.12	104.95	120.60
1	C	479	TRP	CD1-CG-CD2	7.10	111.98	106.30
1	C	335	TRP	CE2-CD2-CG	-7.10	101.62	107.30
1	A	253	TRP	CD1-CG-CD2	7.10	111.98	106.30
1	A	335	TRP	CE2-CD2-CG	-7.09	101.63	107.30
2	B	309	TRP	CE2-CD2-CG	-7.08	101.64	107.30
2	D	309	TRP	CE2-CD2-CG	-7.08	101.64	107.30
1	C	461	ARG	NE-CZ-NH2	7.07	123.83	120.30
1	C	253	TRP	CD1-CG-CD2	7.05	111.94	106.30
1	C	479	TRP	CE2-CD2-CG	-7.04	101.67	107.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	253	TRP	CE2-CD2-CG	-7.03	101.67	107.30
2	B	242	ARG	NE-CZ-NH2	7.00	123.80	120.30
1	A	479	TRP	CE2-CD2-CG	-6.96	101.73	107.30
1	A	236	TRP	CE2-CD2-CG	-6.91	101.77	107.30
2	D	402	TRP	CE2-CD2-CG	-6.91	101.77	107.30
1	A	93	ARG	NE-CZ-NH2	6.90	123.75	120.30
2	B	197	TRP	CE2-CD2-CG	-6.88	101.80	107.30
1	A	343	ARG	NE-CZ-NH1	-6.75	116.92	120.30
2	B	401	ARG	NE-CZ-NH1	-6.70	116.95	120.30
2	D	401	ARG	NE-CZ-NH1	-6.70	116.95	120.30
1	A	96	ARG	NE-CZ-NH2	6.69	123.65	120.30
1	A	479	TRP	CD1-CG-CD2	6.69	111.65	106.30
1	C	236	TRP	CE2-CD2-CG	-6.68	101.95	107.30
1	C	96	ARG	NE-CZ-NH2	6.67	123.63	120.30
2	B	510	ARG	NE-CZ-NH2	6.66	123.63	120.30
1	A	248	ARG	NE-CZ-NH2	6.59	123.60	120.30
2	B	324	TRP	CE2-CD2-CG	-6.57	102.04	107.30
2	B	197	TRP	CD1-CG-CD2	6.55	111.54	106.30
2	B	105	ARG	NE-CZ-NH1	-6.55	117.03	120.30
2	B	453	ARG	NE-CZ-NH2	6.54	123.57	120.30
2	B	510	ARG	NE-CZ-NH1	-6.51	117.05	120.30
2	D	197	TRP	CD1-CG-CD2	6.47	111.47	106.30
1	C	75	ILE	CA-C-N	-6.44	103.04	117.20
2	B	28	ARG	NE-CZ-NH2	6.42	123.51	120.30
2	D	105	ARG	NE-CZ-NH1	-6.42	117.09	120.30
1	C	444	TRP	CB-CG-CD1	-6.41	118.67	127.00
1	C	248	ARG	NE-CZ-NH2	6.41	123.50	120.30
2	B	299	GLU	CA-CB-CG	-6.41	99.30	113.40
1	A	461	ARG	NE-CZ-NH1	-6.38	117.11	120.30
1	A	467	LEU	CA-CB-CG	6.36	129.93	115.30
2	D	468	ARG	NE-CZ-NH2	6.33	123.47	120.30
2	D	324	TRP	CE2-CD2-CG	-6.28	102.28	107.30
1	A	75	ILE	CA-C-N	-6.26	103.42	117.20
1	C	284	ARG	NE-CZ-NH2	6.26	123.43	120.30
2	D	299	GLU	CA-CB-CG	-6.25	99.65	113.40
2	D	523	ARG	NE-CZ-NH2	6.24	123.42	120.30
2	D	510	ARG	NE-CZ-NH2	6.21	123.40	120.30
1	A	284	ARG	NE-CZ-NH2	6.20	123.40	120.30
2	D	361	TRP	CG-CD2-CE3	6.11	139.40	133.90
2	D	510	ARG	NE-CZ-NH1	-6.10	117.25	120.30
2	B	361	TRP	CG-CD2-CE3	6.07	139.36	133.90
2	B	324	TRP	CD1-CG-CD2	6.04	111.13	106.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	468	ARG	NE-CZ-NH2	6.03	123.32	120.30
2	D	238	ARG	NE-CZ-NH1	-6.00	117.30	120.30
2	D	453	ARG	NE-CZ-NH2	5.98	123.29	120.30
1	A	20	TYR	CB-CG-CD1	-5.97	117.42	121.00
1	A	51	LYS	N-CA-C	5.90	126.94	111.00
2	B	86	MET	CG-SD-CE	-5.90	90.76	100.20
2	D	153	CYS	CB-CA-C	-5.87	98.66	110.40
2	B	238	ARG	NE-CZ-NH1	-5.87	117.36	120.30
1	A	444	TRP	CB-CG-CD1	-5.86	119.38	127.00
2	D	86	MET	CG-SD-CE	-5.84	90.85	100.20
2	D	394	LEU	CA-CB-CG	5.80	128.65	115.30
1	C	361	ARG	NE-CZ-NH2	5.77	123.19	120.30
2	B	153	CYS	CB-CA-C	-5.72	98.96	110.40
1	C	277	ARG	NE-CZ-NH2	5.71	123.16	120.30
1	A	361	ARG	NE-CZ-NH2	5.70	123.15	120.30
1	A	100	TYR	CB-CG-CD2	-5.69	117.58	121.00
2	B	394	LEU	CA-CB-CG	5.67	128.34	115.30
2	D	453	ARG	NE-CZ-NH1	-5.64	117.48	120.30
1	C	472	TRP	CG-CD1-NE1	-5.63	104.47	110.10
2	D	426	ASP	CB-CG-OD1	5.63	123.36	118.30
1	C	20	TYR	CB-CG-CD1	-5.60	117.64	121.00
1	A	50	LYS	N-CA-C	-5.58	95.94	111.00
2	D	324	TRP	CD1-CG-CD2	5.58	110.76	106.30
2	D	197	TRP	CG-CD2-CE3	5.54	138.89	133.90
1	C	444	TRP	CG-CD2-CE3	5.52	138.87	133.90
1	C	248	ARG	NE-CZ-NH1	-5.50	117.55	120.30
2	D	28	ARG	NE-CZ-NH2	5.48	123.04	120.30
1	A	72	TRP	CG-CD2-CE3	5.47	138.82	133.90
1	C	50	LYS	N-CA-C	-5.46	96.27	111.00
2	B	28	ARG	NE-CZ-NH1	-5.44	117.58	120.30
2	D	272	TYR	CB-CG-CD1	-5.43	117.74	121.00
1	A	465	MET	CA-CB-CG	5.42	122.52	113.30
2	D	361	TRP	CB-CG-CD1	-5.41	119.97	127.00
2	B	361	TRP	CB-CG-CD1	-5.39	119.99	127.00
2	B	426	ASP	CB-CG-OD1	5.37	123.14	118.30
1	A	479	TRP	CG-CD2-CE3	5.37	138.73	133.90
1	C	465	MET	CA-CB-CG	5.36	122.42	113.30
2	D	28	ARG	NE-CZ-NH1	-5.36	117.62	120.30
2	B	197	TRP	CG-CD2-CE3	5.35	138.72	133.90
1	A	472	TRP	CG-CD1-NE1	-5.35	104.75	110.10
2	B	296	TRP	CG-CD2-CE3	5.34	138.71	133.90
2	B	361	TRP	CG-CD1-NE1	-5.33	104.77	110.10

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	428	TRP	CG-CD2-CE3	5.33	138.69	133.90
2	D	428	TRP	CG-CD2-CE3	5.32	138.69	133.90
1	C	472	TRP	CG-CD2-CE3	5.29	138.66	133.90
2	B	377	MET	CA-CB-CG	5.28	122.27	113.30
1	A	444	TRP	CG-CD2-CE3	5.27	138.65	133.90
1	A	361	ARG	CA-CB-CG	5.26	124.97	113.40
1	C	72	TRP	CG-CD2-CE3	5.24	138.62	133.90
1	C	294	TRP	CG-CD1-NE1	-5.22	104.88	110.10
2	D	377	MET	CA-CB-CG	5.21	122.16	113.30
1	C	345	ARG	NE-CZ-NH1	-5.21	117.70	120.30
1	C	294	TRP	CG-CD2-CE3	5.20	138.58	133.90
2	D	197	TRP	CB-CG-CD1	-5.20	120.25	127.00
2	D	431	ARG	NE-CZ-NH2	5.19	122.89	120.30
1	A	472	TRP	CG-CD2-CE3	5.18	138.57	133.90
2	D	361	TRP	CG-CD1-NE1	-5.18	104.92	110.10
1	C	361	ARG	CA-CB-CG	5.18	124.79	113.40
1	C	100	TYR	CB-CG-CD2	-5.17	117.90	121.00
2	B	296	TRP	CG-CD1-NE1	-5.16	104.94	110.10
1	C	359	ARG	NE-CZ-NH2	5.14	122.87	120.30
2	B	370	TRP	CG-CD2-CE3	5.14	138.52	133.90
2	D	370	TRP	CG-CD2-CE3	5.13	138.52	133.90
2	D	401	ARG	NE-CZ-NH2	5.13	122.86	120.30
2	B	401	ARG	NE-CZ-NH2	5.10	122.85	120.30
2	B	370	TRP	CB-CG-CD1	-5.09	120.39	127.00
2	B	428	TRP	CB-CG-CD1	-5.04	120.44	127.00
2	D	260	VAL	CB-CA-C	-5.04	101.82	111.40
1	A	294	TRP	CG-CD2-CE3	5.04	138.44	133.90
1	C	202	VAL	CG1-CB-CG2	-5.02	102.87	110.90
1	C	472	TRP	CB-CG-CD1	-5.01	120.49	127.00
2	D	370	TRP	CB-CG-CD1	-5.01	120.49	127.00
1	A	277	ARG	NE-CZ-NH2	5.01	122.80	120.30
2	B	197	TRP	CB-CG-CD1	-5.00	120.50	127.00

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	3708	0	3638	70	0
1	C	3712	0	3640	61	0
2	B	4174	0	4087	67	0
2	D	4174	0	4087	59	0
3	B	1	0	0	0	0
3	D	1	0	0	0	0
4	A	14	0	6	0	0
4	C	14	0	6	0	0
5	A	17	0	0	5	0
5	C	17	0	0	6	0
6	A	15	0	0	3	0
6	C	15	0	0	2	0
7	A	102	0	0	7	0
7	B	114	0	0	2	0
7	C	74	0	0	2	0
7	D	143	0	0	2	0
All	All	16295	0	15464	232	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 7.

All (232) 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)
2:B:146:MET:HG3	2:B:180:PRO:HB2	1.62	0.82
2:D:390:PRO:HB2	2:D:393:ILE:HD11	1.63	0.81
2:B:390:PRO:HB2	2:B:393:ILE:HD11	1.64	0.80
1:C:350:ARG:NH1	1:C:416:ILE:O	2.17	0.77
2:D:146:MET:HG3	2:D:180:PRO:HB2	1.66	0.77
2:B:499:ASN:HD21	2:D:477:HIS:H	1.32	0.76
2:B:477:HIS:H	2:D:499:ASN:HD21	1.33	0.76
1:C:49:ASN:O	1:C:49:ASN:CG	2.20	0.74
1:A:85:PRO:HB2	6:A:498:CLP:S2B	2.29	0.73
1:A:49:ASN:O	1:A:49:ASN:CG	2.18	0.73
1:A:93:ARG:HG3	1:A:113:ASN:HB2	1.71	0.72
1:A:350:ARG:NH1	1:A:416:ILE:O	2.24	0.71
1:A:230:ASN:HD22	1:A:235:ALA:H	1.40	0.70
1:C:230:ASN:HD22	1:C:235:ALA:H	1.40	0.70
1:C:93:ARG:HG3	1:C:113:ASN:HB2	1.73	0.69
2:D:180:PRO:HG2	2:D:278:GLN:NE2	2.08	0.69
2:B:180:PRO:HG2	2:B:278:GLN:NE2	2.10	0.66
1:C:85:PRO:HB2	6:C:499:CLP:S2B	2.36	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:431:ARG:HG3	2:B:431:ARG:HH21	1.63	0.63
1:A:93:ARG:HD3	1:A:111:THR:O	1.99	0.62
1:C:74:PRO:HG2	1:C:254:SER:HB3	1.82	0.61
1:A:74:PRO:HG2	1:A:254:SER:HB3	1.81	0.61
2:B:499:ASN:HD21	2:D:477:HIS:N	1.98	0.61
1:C:93:ARG:HD3	1:C:111:THR:O	2.02	0.59
1:A:100:TYR:CE2	1:A:110:VAL:HB	2.37	0.59
2:D:431:ARG:HH21	2:D:431:ARG:HG3	1.68	0.59
2:D:56:ASN:O	2:D:59:ARG:HD3	2.02	0.59
1:A:94:ALA:HB3	2:D:521:LEU:HD22	1.85	0.59
1:C:355:ILE:HB	1:C:360:PRO:HD3	1.85	0.58
1:C:22:GLU:O	1:C:26:LYS:HG2	2.04	0.58
1:C:100:TYR:CE2	1:C:110:VAL:HB	2.38	0.57
2:D:209:THR:HG21	2:D:309:TRP:NE1	2.19	0.57
1:A:22:GLU:O	1:A:26:LYS:HG2	2.05	0.57
2:D:100:ARG:HD2	2:D:111:VAL:O	2.05	0.57
2:B:100:ARG:HD2	2:B:111:VAL:O	2.05	0.57
2:B:56:ASN:O	2:B:59:ARG:HD3	2.04	0.57
2:B:477:HIS:N	2:D:499:ASN:HD21	2.02	0.56
1:C:70:VAL:HG11	5:C:497:CFM:S2B	2.46	0.56
2:B:209:THR:HG21	2:B:309:TRP:NE1	2.20	0.56
1:A:70:VAL:HG11	5:A:496:CFM:S2B	2.45	0.56
1:C:53:GLN:HB3	1:C:56:LEU:HD12	1.88	0.56
2:B:55:LEU:HA	2:B:58:GLN:OE1	2.07	0.55
2:B:209:THR:HG22	2:B:213:MET:SD	2.47	0.55
2:D:21:LYS:HD2	7:D:532:HOH:O	2.06	0.55
2:D:55:LEU:HA	2:D:58:GLN:OE1	2.06	0.55
2:B:522:VAL:HG11	2:D:105:ARG:HD2	1.88	0.55
2:B:322:LEU:HD23	1:C:474:LYS:HG2	1.87	0.55
1:A:103:THR:H	1:A:107:ASN:HD21	1.55	0.54
1:A:230:ASN:HD22	1:A:235:ALA:N	2.04	0.54
2:D:209:THR:HG22	2:D:213:MET:SD	2.47	0.54
1:A:355:ILE:HB	1:A:360:PRO:HD3	1.88	0.54
2:B:369:LEU:HD13	2:B:379:LEU:HD23	1.90	0.54
2:D:369:LEU:HD13	2:D:379:LEU:HD23	1.89	0.53
1:C:230:ASN:HD22	1:C:235:ALA:N	2.05	0.53
1:C:96:ARG:NH2	5:C:497:CFM:S5	2.82	0.53
1:C:186:PHE:HD1	2:D:120:GLU:HG2	1.73	0.53
1:C:104:THR:HA	1:C:108:ALA:O	2.09	0.53
1:C:30:LYS:HB3	1:C:47:ILE:HG12	1.91	0.53
1:A:53:GLN:HB3	1:A:56:LEU:HD12	1.91	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:A:498:CLP:S2A	2:B:92:SER:HB3	2.49	0.52
1:C:64:TYR:CZ	1:C:68:LYS:HG2	2.45	0.52
2:B:264:PRO:HG2	2:B:270:ARG:NH1	2.24	0.52
1:C:361:ARG:HB2	1:C:379:TYR:OH	2.10	0.52
1:A:104:THR:HA	1:A:108:ALA:O	2.09	0.52
1:C:473:LYS:HD2	1:C:473:LYS:N	2.25	0.52
2:B:47:THR:HG22	2:B:52:TYR:CZ	2.45	0.52
2:B:403:LYS:HE2	2:B:421:VAL:O	2.09	0.52
1:A:144:LEU:CD1	2:B:43:VAL:HG21	2.39	0.51
2:D:403:LYS:HE2	2:D:421:VAL:O	2.10	0.51
1:A:103:THR:H	1:A:107:ASN:ND2	2.09	0.51
1:C:422:GLY:HA2	1:C:439:ARG:O	2.11	0.51
2:D:95:CYS:HB3	2:D:99:PHE:CZ	2.46	0.50
1:A:361:ARG:HB2	1:A:379:TYR:OH	2.11	0.50
1:A:64:TYR:CZ	1:A:68:LYS:HG2	2.46	0.50
1:C:103:THR:H	1:C:107:ASN:HD21	1.58	0.50
2:D:264:PRO:HG2	2:D:270:ARG:NH1	2.26	0.50
1:A:27:ASP:HA	1:A:30:LYS:HE3	1.94	0.50
1:C:27:ASP:HA	1:C:30:LYS:HE3	1.93	0.50
1:C:226:ILE:HA	1:C:253:TRP:HB2	1.93	0.50
1:A:119:GLN:HA	2:B:189:PHE:O	2.11	0.50
1:A:239:ARG:HE	1:A:252:GLN:HE21	1.60	0.50
1:A:229:TYR:CE1	5:A:496:CFM:S2A	3.04	0.50
1:A:422:GLY:HA2	1:A:439:ARG:O	2.11	0.50
1:A:144:LEU:HD13	2:B:43:VAL:HG21	1.94	0.50
2:D:124:VAL:HG23	2:D:125:PHE:CD1	2.46	0.49
2:B:105:ARG:HD2	2:D:522:VAL:HG11	1.95	0.49
2:B:124:VAL:HG23	2:B:125:PHE:CD1	2.47	0.49
1:A:68:LYS:HB2	1:A:151:GLN:HG3	1.94	0.49
2:B:247:MET:HB3	2:B:249:VAL:HG23	1.94	0.49
1:C:68:LYS:HB2	1:C:151:GLN:HG3	1.95	0.49
2:B:95:CYS:HB3	2:B:99:PHE:CZ	2.47	0.49
2:D:264:PRO:HG2	2:D:270:ARG:HH11	1.78	0.49
2:B:352:VAL:O	2:B:356:THR:HG23	2.13	0.49
1:C:275:CYS:HA	1:C:358:LEU:HD22	1.95	0.49
1:A:387:TYR:O	1:A:391:MET:HG2	2.13	0.49
2:B:264:PRO:HG2	2:B:270:ARG:HH11	1.78	0.48
1:C:387:TYR:O	1:C:391:MET:HG2	2.13	0.48
2:D:47:THR:HG22	2:D:52:TYR:CZ	2.48	0.48
1:A:226:ILE:HA	1:A:253:TRP:HB2	1.94	0.48
2:B:475:ASP:HB3	2:D:521:LEU:O	2.13	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:352:VAL:O	2:D:356:THR:HG23	2.13	0.48
1:A:141:LEU:CD1	2:B:59:ARG:HD2	2.44	0.48
1:A:193:LEU:HD13	1:A:197:ILE:HD11	1.95	0.47
1:A:275:CYS:HA	1:A:358:LEU:HD22	1.97	0.47
1:C:17:LEU:O	1:C:25:ARG:HG2	2.14	0.47
1:A:17:LEU:O	1:A:25:ARG:HG2	2.14	0.47
2:D:426:ASP:O	2:D:429:HIS:HB2	2.15	0.47
1:C:417:LYS:N	1:C:418:PRO:HD3	2.30	0.47
1:A:96:ARG:NH2	5:A:496:CFM:S5	2.88	0.47
1:C:239:ARG:HE	1:C:252:GLN:HE21	1.61	0.47
1:C:355:ILE:HG22	1:C:356:GLY:H	1.78	0.47
1:A:63:ALA:O	1:A:194:GLY:HA3	2.15	0.47
1:C:229:TYR:CE1	5:C:497:CFM:S2A	3.08	0.47
2:B:521:LEU:O	2:D:475:ASP:HB3	2.15	0.47
2:B:493:ILE:O	2:B:497:LEU:HG	2.15	0.47
2:D:72:PRO:O	2:D:76:VAL:HG23	2.15	0.47
2:D:88:TYR:O	2:D:149:VAL:HA	2.15	0.47
1:C:193:LEU:HD13	1:C:197:ILE:HD11	1.96	0.46
2:D:180:PRO:HG2	2:D:278:GLN:HE21	1.77	0.46
2:B:457:HIS:CD2	2:D:512:MET:HB2	2.51	0.46
2:D:305:VAL:HG23	2:D:309:TRP:CE3	2.51	0.46
1:A:345:ARG:HB3	7:A:596:HOH:O	2.14	0.46
1:C:132:ALA:O	1:C:170:LYS:HE3	2.16	0.46
1:A:62:CYS:HB3	2:B:94:GLY:HA3	1.98	0.46
2:B:499:ASN:ND2	2:D:477:HIS:H	2.06	0.46
1:A:30:LYS:HB3	1:A:47:ILE:HG12	1.97	0.46
1:C:63:ALA:O	1:C:194:GLY:HA3	2.16	0.46
2:B:494:LEU:O	2:B:498:VAL:HG23	2.16	0.45
1:C:103:THR:H	1:C:107:ASN:ND2	2.13	0.45
1:A:186:PHE:HD1	2:B:120:GLU:HG2	1.80	0.45
2:D:509:THR:O	2:D:516:ASP:HA	2.16	0.45
1:A:53:GLN:HA	1:A:54:PRO:HD3	1.88	0.45
1:C:13:ILE:O	1:C:17:LEU:HG	2.16	0.45
2:B:426:ASP:O	2:B:429:HIS:HB2	2.16	0.45
1:A:355:ILE:HG22	1:A:356:GLY:H	1.82	0.45
2:D:247:MET:HB3	2:D:249:VAL:HG23	1.99	0.45
2:B:305:VAL:HG23	2:B:309:TRP:CE3	2.51	0.45
2:B:209:THR:HG21	2:B:309:TRP:HE1	1.81	0.45
1:A:472:TRP:HB2	7:A:543:HOH:O	2.16	0.45
2:D:438:LYS:HE3	2:D:461:GLU:O	2.17	0.45
2:B:180:PRO:HG2	2:B:278:GLN:HE21	1.80	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:209:LYS:HE3	1:C:209:LYS:HB2	1.83	0.45
2:D:494:LEU:O	2:D:498:VAL:HG23	2.18	0.45
2:B:438:LYS:HE3	2:B:461:GLU:O	2.17	0.44
1:A:13:ILE:O	1:A:17:LEU:HG	2.18	0.44
2:B:47:THR:HB	2:B:431:ARG:HH11	1.82	0.44
1:A:132:ALA:O	1:A:170:LYS:HE3	2.17	0.44
6:A:498:CLP:S2B	2:B:188:SER:HB3	2.57	0.44
1:C:359:ARG:HB2	5:C:497:CFM:S3A	2.57	0.44
1:A:96:ARG:HD2	5:A:496:CFM:S3B	2.57	0.44
1:A:229:TYR:CD2	1:A:254:SER:HB2	2.53	0.44
1:A:359:ARG:HB2	5:A:496:CFM:S3A	2.58	0.44
2:D:487:TYR:O	2:D:491:MET:HG3	2.18	0.44
2:D:71:GLN:O	2:D:196:GLY:HA3	2.17	0.44
2:B:231:GLU:HB3	2:B:237:PHE:CZ	2.53	0.44
1:C:186:PHE:CD1	2:D:120:GLU:HG2	2.51	0.44
2:D:86:MET:HG3	2:D:138:CYS:SG	2.57	0.44
1:C:163:ILE:HG12	1:C:182:ARG:NH2	2.32	0.44
2:B:86:MET:HG3	2:B:138:CYS:SG	2.57	0.44
1:A:218:SER:HB2	7:A:501:HOH:O	2.18	0.44
2:B:88:TYR:O	2:B:149:VAL:HA	2.18	0.44
2:D:202:GLU:O	2:D:206:ARG:HG3	2.17	0.44
2:B:72:PRO:O	2:B:76:VAL:HG23	2.18	0.44
2:D:47:THR:HB	2:D:431:ARG:HH11	1.83	0.43
2:B:405:ALA:O	2:B:409:ILE:HG23	2.18	0.43
2:D:493:ILE:O	2:D:497:LEU:HG	2.18	0.43
1:C:20:TYR:CE1	1:C:28:ARG:HG3	2.53	0.43
2:B:192:SER:OG	2:B:194:VAL:HG22	2.18	0.43
1:C:304:LYS:HA	1:C:307:GLU:HG2	2.00	0.43
1:C:97:ARG:O	1:C:231:ILE:HA	2.19	0.43
2:B:487:TYR:O	2:B:491:MET:HG3	2.18	0.43
1:C:417:LYS:HA	1:C:418:PRO:HD2	1.48	0.43
1:A:209:LYS:HE3	1:A:209:LYS:HB2	1.79	0.43
2:D:4:GLN:HG2	7:D:580:HOH:O	2.18	0.43
1:A:64:TYR:CE2	1:A:88:CYS:HB3	2.53	0.43
1:C:229:TYR:CD2	1:C:254:SER:HB2	2.54	0.43
2:D:209:THR:HG21	2:D:309:TRP:HE1	1.81	0.43
1:A:163:ILE:HG12	1:A:182:ARG:NH2	2.34	0.43
2:D:502:LEU:HD22	2:D:523:ARG:HD3	2.01	0.42
1:A:304:LYS:HA	1:A:307:GLU:HG2	2.00	0.42
1:A:412:PHE:O	1:A:416:ILE:HG13	2.19	0.42
1:C:96:ARG:HD2	5:C:497:CFM:S3B	2.59	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:479:TRP:O	1:A:480:GLU:HB2	2.19	0.42
2:D:313:VAL:HA	2:D:314:PRO:HD3	1.85	0.42
2:B:509:THR:O	2:B:516:ASP:HA	2.18	0.42
2:B:71:GLN:O	2:B:196:GLY:HA3	2.19	0.42
1:A:97:ARG:O	1:A:231:ILE:HA	2.19	0.42
2:B:502:LEU:HD22	2:B:523:ARG:HD3	2.01	0.42
2:B:505:LEU:HD13	2:B:523:ARG:CZ	2.50	0.42
1:A:475:LEU:O	2:B:266:ASP:HA	2.19	0.41
2:B:202:GLU:O	2:B:206:ARG:HG3	2.20	0.41
1:C:227:GLY:CA	1:C:279:MET:HG3	2.51	0.41
1:C:23:LYS:HG3	7:C:552:HOH:O	2.20	0.41
2:B:96:VAL:O	2:B:100:ARG:HG3	2.20	0.41
1:A:415:ARG:HG3	7:A:508:HOH:O	2.21	0.41
7:B:581:HOH:O	1:C:474:LYS:HA	2.20	0.41
2:B:368:ALA:O	2:B:442:MET:HA	2.20	0.41
2:D:192:SER:OG	2:D:194:VAL:HG22	2.21	0.41
1:C:355:ILE:O	1:C:380:GLU:HG3	2.20	0.41
1:A:20:TYR:CE1	1:A:28:ARG:HG3	2.55	0.41
1:C:154:CYS:HB2	1:C:155:PRO:HD3	2.03	0.41
1:C:277:ARG:NH1	1:C:383:HIS:HB2	2.35	0.41
2:D:221:ASN:OD1	2:D:287:ALA:HA	2.21	0.41
1:A:277:ARG:NH1	1:A:383:HIS:HB2	2.36	0.41
6:C:499:CLP:S2A	2:D:92:SER:HB3	2.61	0.41
2:B:431:ARG:HG3	2:B:431:ARG:NH2	2.33	0.41
1:A:141:LEU:HD13	2:B:59:ARG:HD2	2.03	0.41
1:A:140:THR:HG22	7:A:525:HOH:O	2.20	0.41
2:D:362:LEU:O	2:D:365:LYS:HB2	2.21	0.41
1:C:381:PHE:CZ	5:C:497:CFM:S2B	3.14	0.41
1:C:302:PRO:HD2	1:C:369:ASP:OD2	2.21	0.41
1:A:94:ALA:HB3	2:D:521:LEU:CD2	2.49	0.41
2:D:505:LEU:HD13	2:D:523:ARG:CZ	2.50	0.41
1:A:136:ASP:O	1:A:140:THR:HG23	2.20	0.41
2:D:405:ALA:O	2:D:409:ILE:HG23	2.21	0.41
2:D:368:ALA:O	2:D:442:MET:HA	2.21	0.41
1:C:64:TYR:CE2	1:C:88:CYS:HB3	2.56	0.41
2:D:231:GLU:HB3	2:D:237:PHE:CZ	2.56	0.41
1:C:20:TYR:HB2	1:C:25:ARG:HG3	2.03	0.40
1:A:227:GLY:CA	1:A:279:MET:HG3	2.50	0.40
1:C:21:PRO:HG3	7:C:509:HOH:O	2.20	0.40
2:B:272:TYR:HB2	7:B:530:HOH:O	2.20	0.40
1:A:96:ARG:HA	7:A:512:HOH:O	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:226:ILE:HG22	1:C:279:MET:HB3	2.04	0.40
2:B:74:GLY:HA3	2:B:193:HIS:O	2.21	0.40
1:A:332:LYS:HE2	7:A:575:HOH:O	2.21	0.40
1:A:302:PRO:HD2	1:A:369:ASP:OD2	2.21	0.40
2:B:209:THR:CG2	2:B:213:MET:SD	3.10	0.40
1:A:20:TYR:HB2	1:A:25:ARG:HG3	2.04	0.40
1:A:186:PHE:CD1	2:B:120:GLU:HG2	2.56	0.40
1:A:426:LYS:HA	2:B:104:ASN:ND2	2.37	0.40
1:C:136:ASP:O	1:C:140:THR:HG23	2.21	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	463/492 (94%)	433 (94%)	28 (6%)	2 (0%)	39	61
1	C	464/492 (94%)	437 (94%)	26 (6%)	1 (0%)	52	75
2	B	520/523 (99%)	508 (98%)	11 (2%)	1 (0%)	52	75
2	D	520/523 (99%)	507 (98%)	12 (2%)	1 (0%)	52	75
All	All	1967/2030 (97%)	1885 (96%)	77 (4%)	5 (0%)	46	68

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	6	ARG
2	B	255	SER
2	D	255	SER
1	A	355	ILE
1	C	355	ILE

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	397/415 (96%)	367 (92%)	30 (8%)	16	30
1	C	396/415 (95%)	369 (93%)	27 (7%)	20	36
2	B	454/455 (100%)	426 (94%)	28 (6%)	23	41
2	D	454/455 (100%)	427 (94%)	27 (6%)	24	44
All	All	1701/1740 (98%)	1589 (93%)	112 (7%)	21	38

All (112) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	10	GLU
1	A	12	LEU
1	A	14	GLN
1	A	49	ASN
1	A	51	LYS
1	A	93	ARG
1	A	98	ASN
1	A	107	ASN
1	A	133	LYS
1	A	150	VAL
1	A	193	LEU
1	A	199	ASN
1	A	202	VAL
1	A	223	VAL
1	A	264	LEU
1	A	350	ARG
1	A	362	HIS
1	A	372	MET
1	A	385	ASP
1	A	389	ARG
1	A	396	ASP
1	A	401	TYR
1	A	404	VAL
1	A	409	PHE

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Mol	Chain	Res	Type
1	A	414	LYS
1	A	420	LEU
1	A	445	ASP
1	A	467	LEU
1	A	475	LEU
1	A	480	GLU
2	B	7	LYS
2	B	13	PRO
2	B	34	LYS
2	B	38	ASP
2	B	47	THR
2	B	86	MET
2	B	88	TYR
2	B	153	CYS
2	B	154	MET
2	B	171	LYS
2	B	172	GLU
2	B	177	ASP
2	B	178	GLU
2	B	188	SER
2	B	244	LEU
2	B	258	GLU
2	B	260	VAL
2	B	279	GLU
2	B	315	LYS
2	B	334	GLU
2	B	338	GLN
2	B	348	ARG
2	B	350	ARG
2	B	431	ARG
2	B	453	ARG
2	B	461	GLU
2	B	505	LEU
2	B	512	MET
1	C	12	LEU
1	C	14	GLN
1	C	49	ASN
1	C	51	LYS
1	C	93	ARG
1	C	98	ASN
1	C	107	ASN
1	C	133	LYS

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Mol	Chain	Res	Type
1	C	150	VAL
1	C	193	LEU
1	C	199	ASN
1	C	202	VAL
1	C	223	VAL
1	C	264	LEU
1	C	350	ARG
1	C	362	HIS
1	C	372	MET
1	C	385	ASP
1	C	389	ARG
1	C	396	ASP
1	C	401	TYR
1	C	404	VAL
1	C	409	PHE
1	C	414	LYS
1	C	420	LEU
1	C	445	ASP
1	C	461	ARG
2	D	7	LYS
2	D	13	PRO
2	D	34	LYS
2	D	38	ASP
2	D	47	THR
2	D	86	MET
2	D	88	TYR
2	D	153	CYS
2	D	154	MET
2	D	171	LYS
2	D	172	GLU
2	D	177	ASP
2	D	178	GLU
2	D	188	SER
2	D	244	LEU
2	D	258	GLU
2	D	260	VAL
2	D	279	GLU
2	D	315	LYS
2	D	338	GLN
2	D	348	ARG
2	D	350	ARG
2	D	431	ARG

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Mol	Chain	Res	Type
2	D	453	ARG
2	D	461	GLU
2	D	505	LEU
2	D	512	MET

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (31) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	49	ASN
1	A	107	ASN
1	A	230	ASN
1	A	252	GLN
1	A	271	ASN
1	A	362	HIS
1	A	383	HIS
2	B	37	GLN
2	B	104	ASN
2	B	168	ASN
2	B	278	GLN
2	B	286	ASN
2	B	457	HIS
2	B	499	ASN
2	B	518	ASN
2	B	519	HIS
1	C	107	ASN
1	C	230	ASN
1	C	252	GLN
1	C	271	ASN
1	C	362	HIS
1	C	383	HIS
2	D	104	ASN
2	D	168	ASN
2	D	278	GLN
2	D	286	ASN
2	D	457	HIS
2	D	499	ASN
2	D	513	GLN
2	D	518	ASN
2	D	519	HIS

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 ⓘ

Of 8 ligands modelled in this entry, 2 are monoatomic - leaving 6 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
4	HCA	A	494	-	4,13,13	0.44	0	3,18,18	0.35	0
5	CFM	A	496	1	0,24,24	0.00	-	0,45,45	0.00	-
6	CLP	A	498	1,2	0,21,25	0.00	-	0,39,54	0.00	-
4	HCA	C	495	-	4,13,13	0.57	0	3,18,18	0.50	0
5	CFM	C	497	1	0,24,24	0.00	-	0,45,45	0.00	-
6	CLP	C	499	1,2	0,21,25	0.00	-	0,39,54	0.00	-

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	HCA	A	494	-	-	0/7/17/17	0/0/0/0
5	CFM	A	496	1	-	0/0/84/84	0/0/8/8
6	CLP	A	498	1,2	-	0/0/72/117	0/6/7/10
4	HCA	C	495	-	-	0/7/17/17	0/0/0/0

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	CFM	C	497	1	-	0/0/84/84	0/0/8/8
6	CLP	C	499	1,2	-	0/0/72/117	0/6/7/10

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

4 monomers are involved in 16 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	A	496	CFM	5	0
6	A	498	CLP	3	0
5	C	497	CFM	6	0
6	C	499	CLP	2	0

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 [i](#)

6.1 Protein, DNA and RNA chains [i](#)

EDS was not executed - this section will therefore be empty.

6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

EDS was not executed - this section will therefore be empty.

6.3 Carbohydrates [i](#)

EDS was not executed - this section will therefore be empty.

6.4 Ligands [i](#)

EDS was not executed - this section will therefore be empty.

6.5 Other polymers [i](#)

EDS was not executed - this section will therefore be empty.