



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 04:33 AM UTC

PDB ID : 1NIT / pdb_00001nit
Title : CRYSTAL STRUCTURE OF ACONITASE WITH TRANS-ACONITATE
AND NITROCITRATE BOUND
Authors : Lauble, H.; Kennedy, M.C.; Beinert, H.; Stout, C.D.
Deposited on : 1993-01-17
Resolution : 2.05 Å(reported)

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

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

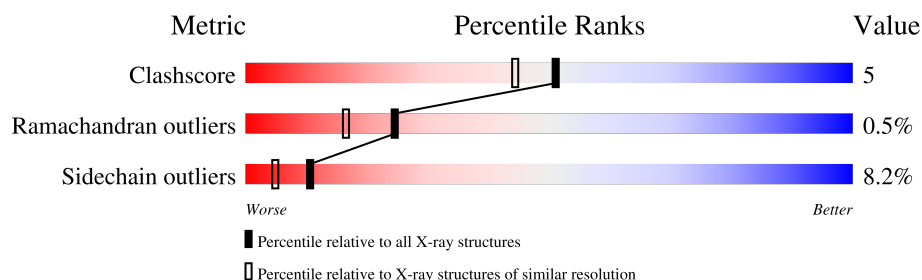
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.05 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	190562	2333 (2.04-2.04)
Ramachandran outliers	187476	2318 (2.04-2.04)
Sidechain outliers	187428	2318 (2.04-2.04)

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 $\leq 5\%$.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	754	 73% 21% . .

2 Entry composition [i](#)

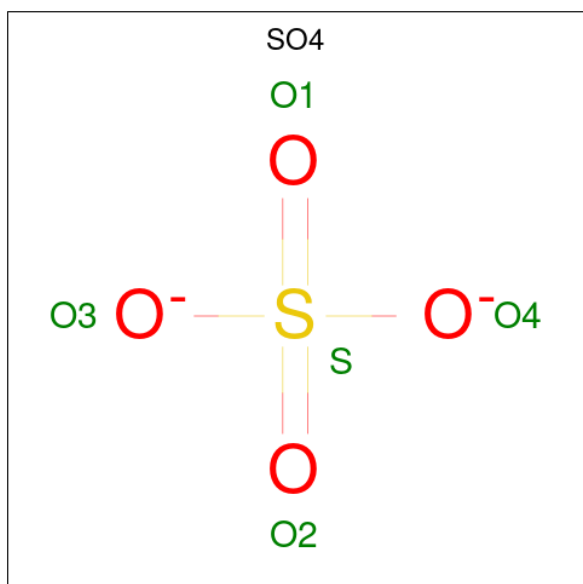
There are 4 unique types of molecules in this entry. The entry contains 6116 atoms, of which 1 is hydrogen and 0 are deuteriums.

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 ACONITASE.

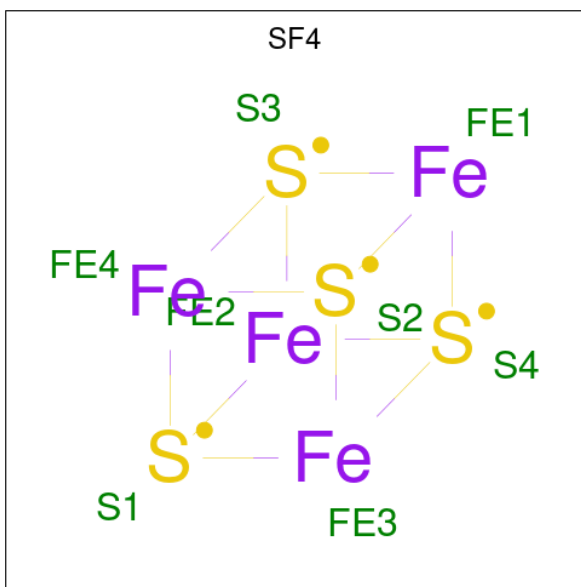
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	753	5812	3664	1031	1095	22	0	0	0

- Molecule 2 is SULFATE ION (CCD ID: SO4) (formula: O₄S).



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

- Molecule 3 is IRON/SULFUR CLUSTER (CCD ID: SF4) (formula: Fe₄S₄).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	Fe	S	0	0
			8	4	4		

- Molecule 4 is water.

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	290	Total	H	O	0	0
			291	1	290		

4 Data and refinement statistics

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

Property	Value	Source
Space group	B 1 1 2	Depositor
Cell constants a, b, c, α , β , γ	185.50Å 72.00Å 73.00Å 90.00° 90.00° 77.70°	Depositor
Resolution (Å)	8.00 – 2.05	Depositor
% Data completeness (in resolution range)	(Not available) (8.00-2.05)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	X-PLOR	Depositor
R, R_{free}	0.172 , (Not available)	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	6116	wwPDB-VP
Average B, all atoms (Å ²)	20.0	wwPDB-VP

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: SF4, SO4

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	1.10	30/5938 (0.5%)	1.80	122/8044 (1.5%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	3

All (30) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	321	HIS	CD2-NE2	-7.19	1.29	1.37
1	A	626	HIS	CD2-NE2	-7.07	1.30	1.37
1	A	13	HIS	CD2-NE2	-6.66	1.30	1.37
1	A	717	HIS	CD2-NE2	-6.55	1.30	1.37
1	A	101	HIS	CD2-NE2	-6.48	1.30	1.37
1	A	298	HIS	CD2-NE2	-6.18	1.31	1.37
1	A	569	HIS	CD2-NE2	-5.99	1.31	1.37
1	A	460	HIS	CD2-NE2	-5.99	1.31	1.37
1	A	582	HIS	CD2-NE2	-5.89	1.31	1.37
1	A	379	HIS	CD2-NE2	-5.87	1.31	1.37
1	A	580	ARG	CD-NE	-5.71	1.38	1.46
1	A	692	HIS	CD2-NE2	-5.67	1.31	1.37
1	A	616	VAL	CA-CB	5.54	1.57	1.54
1	A	332	HIS	CG-ND1	-5.50	1.32	1.38
1	A	306	HIS	CD2-NE2	-5.50	1.31	1.37
1	A	646	HIS	CD2-NE2	-5.49	1.31	1.37
1	A	159	VAL	CA-CB	5.47	1.60	1.54
1	A	729	HIS	CD2-NE2	-5.47	1.31	1.37

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	167	HIS	CD2-NE2	-5.37	1.31	1.37
1	A	629	ARG	NE-CZ	5.35	1.39	1.33
1	A	332	HIS	CD2-NE2	-5.32	1.31	1.37
1	A	9	HIS	CD2-NE2	-5.31	1.32	1.37
1	A	147	HIS	CD2-NE2	-5.24	1.32	1.37
1	A	360	ASN	CA-CB	5.20	1.57	1.53
1	A	98	HIS	CD2-NE2	-5.15	1.32	1.37
1	A	274	HIS	CD2-NE2	-5.11	1.32	1.37
1	A	519	HIS	CB-CG	5.08	1.57	1.50
1	A	559	ILE	CA-CB	5.08	1.60	1.55
1	A	46	HIS	CD2-NE2	-5.08	1.32	1.37
1	A	519	HIS	CD2-NE2	-5.04	1.32	1.37

All (122) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	519	HIS	CB-CG-ND1	10.87	139.01	122.70
1	A	402	ARG	NE-CZ-NH2	-10.72	109.55	119.20
1	A	519	HIS	CB-CG-CD2	-9.44	118.93	131.20
1	A	539	GLN	CG-CD-NE2	8.48	129.13	116.40
1	A	498	GLU	CA-CB-CG	8.01	130.12	114.10
1	A	407	GLN	OE1-CD-NE2	-7.73	114.87	122.60
1	A	539	GLN	OE1-CD-NE2	-7.71	114.89	122.60
1	A	274	HIS	CB-CG-CD2	-7.27	121.75	131.20
1	A	430	ARG	NE-CZ-NH2	-7.21	112.72	119.20
1	A	384	LYS	N-CA-C	-7.11	102.94	111.69
1	A	427	GLN	OE1-CD-NE2	-7.00	115.60	122.60
1	A	666	ARG	NE-CZ-NH2	-6.92	112.97	119.20
1	A	753	GLN	N-CA-C	6.91	125.52	110.80
1	A	495	PHE	CA-CB-CG	6.84	120.64	113.80
1	A	515	ASP	CA-CB-CG	6.80	119.40	112.60
1	A	582	HIS	CB-CG-CD2	-6.76	122.41	131.20
1	A	115	ARG	NE-CZ-NH2	-6.69	113.18	119.20
1	A	360	ASN	OD1-CG-ND2	-6.65	115.95	122.60
1	A	9	HIS	CA-CB-CG	-6.59	107.21	113.80
1	A	705	PHE	CA-CB-CG	6.59	120.39	113.80
1	A	101	HIS	CB-CG-CD2	-6.52	122.72	131.20
1	A	731	PHE	CA-CB-CG	6.49	120.29	113.80
1	A	588	ASN	OD1-CG-ND2	-6.48	116.12	122.60
1	A	208	THR	N-CA-CB	-6.45	100.33	111.55
1	A	580	ARG	NE-CZ-NH2	-6.44	113.41	119.20
1	A	84	ILE	CA-C-O	-6.40	114.30	120.95

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	402	ARG	NE-CZ-NH1	6.36	127.86	121.50
1	A	724	THR	CA-CB-OG1	-6.35	100.07	109.60
1	A	666	ARG	CG-CD-NE	-6.35	98.04	112.00
1	A	321	HIS	CB-CG-CD2	-6.33	122.97	131.20
1	A	167	HIS	CA-CB-CG	-6.31	107.49	113.80
1	A	449	PHE	CA-CB-CG	6.30	120.10	113.80
1	A	522	LYS	CG-CD-CE	6.20	125.56	111.30
1	A	13	HIS	CB-CA-C	-6.17	98.92	109.65
1	A	290	ASN	OD1-CG-ND2	-6.16	116.44	122.60
1	A	717	HIS	CB-CG-CD2	-6.16	123.19	131.20
1	A	522	LYS	O-C-N	6.15	130.32	122.39
1	A	566	THR	N-CA-CB	-6.14	101.66	110.44
1	A	454	ASP	CA-CB-CG	6.13	118.73	112.60
1	A	524	SER	N-CA-C	6.11	123.82	110.80
1	A	446	ASN	OD1-CG-ND2	-6.07	116.53	122.60
1	A	589	ASN	OD1-CG-ND2	-6.07	116.53	122.60
1	A	460	HIS	CB-CG-CD2	-6.03	123.36	131.20
1	A	583	LEU	N-CA-C	6.01	117.83	111.28
1	A	13	HIS	CA-CB-CG	-6.00	107.80	113.80
1	A	139	TRP	CG-CD2-CE3	5.96	139.86	133.90
1	A	574	GLY	CA-C-N	5.95	125.62	119.56
1	A	574	GLY	C-N-CA	5.95	125.62	119.56
1	A	719	ASN	OD1-CG-ND2	-5.91	116.69	122.60
1	A	523	ASP	N-CA-C	-5.89	98.26	110.80
1	A	410	ARG	NE-CZ-NH2	-5.85	113.93	119.20
1	A	49	ASP	N-CA-CB	-5.80	103.90	111.09
1	A	147	HIS	CB-CG-CD2	-5.77	123.69	131.20
1	A	430	ARG	NE-CZ-NH1	5.72	127.22	121.50
1	A	368	ARG	CA-CB-CG	-5.68	102.75	114.10
1	A	568	ASP	N-CA-C	-5.66	105.88	112.89
1	A	374	LYS	CA-CB-CG	5.64	125.38	114.10
1	A	569	HIS	CB-CG-CD2	-5.63	123.88	131.20
1	A	596	ASN	CA-CB-CG	5.63	118.23	112.60
1	A	582	HIS	CB-CG-ND1	5.56	131.04	122.70
1	A	298	HIS	CB-CG-CD2	-5.55	123.98	131.20
1	A	729	HIS	CB-CG-CD2	-5.53	124.01	131.20
1	A	46	HIS	CB-CG-CD2	-5.52	124.02	131.20
1	A	659	ILE	N-CA-C	-5.52	99.60	107.77
1	A	195	TRP	CG-CD1-NE1	-5.52	103.03	110.20
1	A	101	HIS	CB-CG-ND1	5.51	130.97	122.70
1	A	263	ILE	N-CA-C	-5.50	106.95	112.17
1	A	626	HIS	CB-CG-CD2	-5.48	124.07	131.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	148	GLN	OE1-CD-NE2	-5.45	117.15	122.60
1	A	679	PRO	CB-CA-C	5.44	116.35	111.40
1	A	425	ILE	CB-CA-C	-5.43	102.38	111.29
1	A	618	ASP	CA-CB-CG	5.43	118.03	112.60
1	A	4	LYS	CA-CB-CG	-5.43	103.24	114.10
1	A	585	ASN	OD1-CG-ND2	-5.42	117.17	122.60
1	A	569	HIS	CB-CG-ND1	5.42	130.83	122.70
1	A	274	HIS	CB-CG-ND1	5.40	130.80	122.70
1	A	266	THR	CA-CB-OG1	-5.35	101.57	109.60
1	A	26	ASP	CA-C-O	-5.33	114.78	120.42
1	A	439	ASN	OD1-CG-ND2	-5.33	117.27	122.60
1	A	139	TRP	CB-CG-CD1	-5.31	118.93	126.90
1	A	637	ASN	OD1-CG-ND2	-5.31	117.29	122.60
1	A	626	HIS	CA-CB-CG	-5.30	108.50	113.80
1	A	674	LYS	N-CA-C	5.29	117.80	111.71
1	A	98	HIS	CB-CG-CD2	-5.27	124.34	131.20
1	A	668	HIS	CA-CB-CG	-5.27	108.53	113.80
1	A	346	TRP	CE2-CD2-CG	-5.27	100.88	107.20
1	A	121	GLN	CA-CB-CG	-5.27	103.56	114.10
1	A	168	THR	CA-C-N	5.27	126.42	119.84
1	A	168	THR	C-N-CA	5.27	126.42	119.84
1	A	379	HIS	CA-CB-CG	-5.26	108.54	113.80
1	A	692	HIS	CA-CB-CG	-5.26	108.54	113.80
1	A	379	HIS	CB-CG-CD2	-5.25	124.38	131.20
1	A	139	TRP	CE2-CD2-CG	-5.24	100.91	107.20
1	A	580	ARG	NE-CZ-NH1	5.24	126.74	121.50
1	A	287	ASP	CA-CB-CG	5.21	117.81	112.60
1	A	514	GLN	OE1-CD-NE2	-5.21	117.39	122.60
1	A	485	ASP	CA-CB-CG	5.20	117.80	112.60
1	A	390	THR	CA-C-N	5.20	125.11	119.76
1	A	390	THR	C-N-CA	5.20	125.11	119.76
1	A	522	LYS	N-CA-C	5.20	119.25	113.02
1	A	373	ALA	CA-C-O	-5.19	115.05	120.55
1	A	625	GLN	OE1-CD-NE2	-5.18	117.42	122.60
1	A	522	LYS	CA-C-O	5.16	125.67	119.43
1	A	360	ASN	CB-CG-ND2	5.15	124.13	116.40
1	A	349	ASP	CA-C-O	5.14	126.35	120.54
1	A	607	ASN	OD1-CG-ND2	-5.14	117.45	122.60
1	A	265	ALA	O-C-N	-5.14	116.55	122.87
1	A	536	GLN	N-CA-C	-5.14	107.01	113.28
1	A	399	THR	O-C-N	-5.13	116.30	122.15
1	A	346	TRP	CG-CD1-NE1	-5.13	103.53	110.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	732	ASN	OD1-CG-ND2	-5.12	117.48	122.60
1	A	236	ALA	N-CA-C	5.10	117.55	109.50
1	A	270	PHE	CA-C-N	5.09	124.85	119.76
1	A	270	PHE	C-N-CA	5.09	124.85	119.76
1	A	193	ILE	CA-C-N	5.09	125.09	119.90
1	A	193	ILE	C-N-CA	5.09	125.09	119.90
1	A	521	PRO	N-CA-C	-5.05	102.08	112.47
1	A	346	TRP	CD1-CG-CD2	5.04	114.36	106.30
1	A	410	ARG	NE-CZ-NH1	5.03	126.53	121.50
1	A	444	SER	N-CA-C	-5.03	105.41	112.25
1	A	752	GLN	OE1-CD-NE2	-5.02	117.58	122.60
1	A	440	THR	CA-CB-OG1	-5.01	102.08	109.60

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	324	GLY	Peptide
1	A	580	ARG	Sidechain
1	A	68	ARG	Sidechain

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	5812	0	5793	60	0
2	A	5	0	0	1	0
3	A	8	0	0	0	0
4	A	290	1	0	4	0
All	All	6115	1	5793	60	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 5.

All (60) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:430:ARG:HH22	1:A:439:ASN:HD21	1.29	0.78
1:A:566:THR:HG22	1:A:568:ASP:H	1.53	0.73
1:A:228:LEU:HD23	1:A:263:ILE:HD12	1.74	0.70
1:A:250:CYS:HA	1:A:253:MET:HE3	1.74	0.70
1:A:430:ARG:HH22	1:A:439:ASN:ND2	1.91	0.69
1:A:384:LYS:HD3	1:A:476:GLY:HA3	1.78	0.65
1:A:546:LYS:HD3	1:A:741:ALA:O	2.01	0.60
1:A:277:LYS:HG3	1:A:289:ALA:HB1	1.85	0.59
1:A:49:ASP:OD2	1:A:52:ASN:HB2	2.03	0.57
1:A:336:GLU:O	1:A:340:VAL:HG23	2.04	0.57
1:A:430:ARG:HD2	1:A:432:ASP:OD1	2.04	0.57
1:A:402:ARG:HD2	1:A:403:ASP:OD1	2.05	0.56
1:A:2:ARG:HE	1:A:3:ALA:N	2.04	0.55
1:A:752:GLN:O	1:A:754:LYS:HG3	2.08	0.53
1:A:17:ARG:NH2	1:A:20:LEU:HD23	2.24	0.53
1:A:754:LYS:HZ2	1:A:754:LYS:C	2.18	0.52
1:A:552:LEU:HD23	1:A:629:ARG:HH21	1.75	0.51
1:A:428:TRP:CZ2	1:A:430:ARG:HD3	2.47	0.50
1:A:2:ARG:HE	1:A:3:ALA:H	1.59	0.50
1:A:384:LYS:NZ	4:A:1209:HOH:O	2.45	0.50
1:A:275:ARG:NH2	4:A:1055:HOH:O	2.44	0.49
1:A:644:ARG:HB3	2:A:998:SO4:O1	2.13	0.49
1:A:233:GLY:O	1:A:265:ALA:HA	2.12	0.49
1:A:622:TYR:O	1:A:626:HIS:HD2	1.96	0.49
1:A:2:ARG:NE	1:A:3:ALA:H	2.10	0.48
1:A:244:GLY:O	1:A:247:SER:HB3	2.14	0.48
1:A:374:LYS:HD2	1:A:375:GLN:HG3	1.96	0.48
1:A:341:ALA:HA	1:A:346:TRP:CE3	2.49	0.48
1:A:145:ILE:HG21	1:A:358:CYS:HB3	1.96	0.48
1:A:110:GLU:O	1:A:114:ARG:HG3	2.15	0.47
1:A:230:VAL:HA	1:A:263:ILE:HA	1.97	0.47
1:A:444:SER:HA	1:A:464:THR:O	2.15	0.47
1:A:13:HIS:CD2	1:A:13:HIS:H	2.31	0.47
1:A:717:HIS:HD2	1:A:721:THR:HB	1.80	0.46
1:A:447:ARG:NH2	4:A:1059:HOH:O	2.36	0.46
1:A:430:ARG:NH2	1:A:439:ASN:HD21	2.05	0.46
1:A:69:VAL:O	1:A:95:SER:HA	2.16	0.46
1:A:589:ASN:C	1:A:589:ASN:HD22	2.24	0.46
1:A:121:GLN:O	1:A:125:ASN:HB2	2.15	0.45
1:A:182:GLY:HA3	1:A:671:ASN:HD21	1.80	0.45
1:A:452:ARG:NH2	4:A:1288:HOH:O	2.49	0.45
1:A:143:SER:HB3	1:A:516:THR:HB	1.97	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:652:ARG:HD3	1:A:677:LEU:HG	1.98	0.45
1:A:208:THR:O	1:A:315:LEU:HB2	2.17	0.45
1:A:522:LYS:CE	1:A:522:LYS:HA	2.48	0.43
1:A:2:ARG:CD	1:A:3:ALA:H	2.32	0.42
1:A:522:LYS:HA	1:A:522:LYS:HE3	2.01	0.42
1:A:675:GLN:NE2	1:A:675:GLN:HA	2.34	0.42
1:A:576:TRP:CE2	1:A:589:ASN:HB3	2.55	0.41
1:A:438:LYS:HZ2	1:A:458:GLU:CD	2.26	0.41
1:A:376:ALA:HB2	1:A:474:ILE:HD13	2.03	0.41
1:A:26:ASP:O	1:A:30:LYS:HD3	2.21	0.41
1:A:181:VAL:HB	1:A:185:ASP:HB2	2.03	0.41
1:A:201:LYS:HA	1:A:201:LYS:HD2	1.90	0.41
1:A:330:LEU:HD22	1:A:332:HIS:CE1	2.56	0.41
1:A:334:VAL:O	1:A:337:VAL:HG12	2.20	0.41
1:A:90:LYS:HD2	1:A:134:TYR:O	2.21	0.40
1:A:221:ILE:HG12	1:A:259:MET:HB3	2.02	0.40
1:A:517:TYR:OH	1:A:519:HIS:HD2	2.05	0.40
1:A:364:GLU:HB2	1:A:504:GLU:HA	2.04	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
1	A	751/754 (100%)	714 (95%)	33 (4%)	4 (0%)	24 16

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	524	SER
1	A	525	SER
1	A	753	GLN

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Mol	Chain	Res	Type
1	A	109	GLY

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	A	621/622 (100%)	570 (92%)	51 (8%)	10 5

All (51) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	2	ARG
1	A	13	HIS
1	A	20	LEU
1	A	107	LEU
1	A	110	GLU
1	A	121	GLN
1	A	125	ASN
1	A	169	PRO
1	A	174	LEU
1	A	201	LYS
1	A	208	THR
1	A	228	LEU
1	A	247	SER
1	A	303	SER
1	A	310	LEU
1	A	315	LEU
1	A	317	GLU
1	A	319	LYS
1	A	325	PRO
1	A	327	THR
1	A	330	LEU
1	A	344	GLU
1	A	374	LYS
1	A	382	LYS
1	A	384	LYS

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Mol	Chain	Res	Type
1	A	412	VAL
1	A	425	ILE
1	A	430	ARG
1	A	433	ILE
1	A	435	LYS
1	A	442	VAL
1	A	487	LEU
1	A	490	LYS
1	A	496	LYS
1	A	497	LEU
1	A	498	GLU
1	A	514	GLN
1	A	522	LYS
1	A	550	LYS
1	A	553	GLU
1	A	562	LYS
1	A	578	LYS
1	A	589	ASN
1	A	631	VAL
1	A	636	GLU
1	A	657	ARG
1	A	702	LEU
1	A	704	ASP
1	A	721	THR
1	A	747	ARG
1	A	754	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (15) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	53	GLN
1	A	77	GLN
1	A	106	GLN
1	A	148	GLN
1	A	321	HIS
1	A	395	GLN
1	A	419	ASN
1	A	439	ASN
1	A	514	GLN
1	A	519	HIS
1	A	536	GLN
1	A	585	ASN

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Mol	Chain	Res	Type
1	A	589	ASN
1	A	637	ASN
1	A	671	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 oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

2 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	$\# Z > 2$
3	SF4	A	999	1,4	0,12,12	-	-	-		
2	SO4	A	998	-	4,4,4	0.69	0	6,6,6	0.49	0

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
3	SF4	A	999	1,4	-	-	0/6/5/5

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.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	998	SO4	1	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

6.1 Protein, DNA and RNA chains

EDS was not executed - this section is therefore empty.

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

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates

EDS was not executed - this section is therefore empty.

6.4 Ligands

EDS was not executed - this section is therefore empty.

6.5 Other polymers

EDS was not executed - this section is therefore empty.