



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 4, 2026 – 10:30 PM UTC

PDB ID : 1DT0 / pdb_00001dt0
Title : CLONING, SEQUENCE, AND CRYSTALLOGRAPHIC STRUCTURE
OF RECOMBINANT IRON SUPEROXIDE DISMUTASE FROM PSEU-
DOMONAS OVALIS
Authors : Bond, C.J.; Huang, J.; Hajduk, R.; Flick, K.; Heath, P.; Stoddard, B.L.
Deposited on : 2000-01-10
Resolution : 2.10 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
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

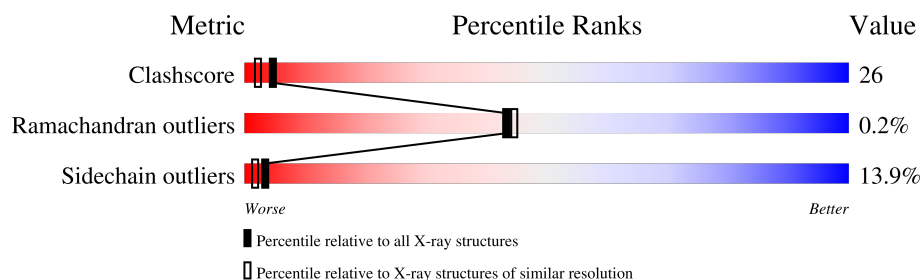
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.10 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	7164 (2.10-2.10)
Ramachandran outliers	187476	7099 (2.10-2.10)
Sidechain outliers	187428	7100 (2.10-2.10)

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	197	56% 35% 9% .
1	B	197	48% 44% 8%
1	C	197	56% 35% 8% ..

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 5217 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 SUPEROXIDE DISMUTASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	197	Total	C	N	O	S	0	0	0
			1555	1008	255	289	3			
1	B	197	Total	C	N	O	S	0	0	0
			1555	1008	255	289	3			
1	C	195	Total	C	N	O	S	0	0	0
			1538	997	252	286	3			

- Molecule 2 is FE (III) ION (CCD ID: FE) (formula: Fe).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total	Fe	0	0
			1	1		
2	C	2	Total	Fe	0	0
			2	2		

- Molecule 3 is water.

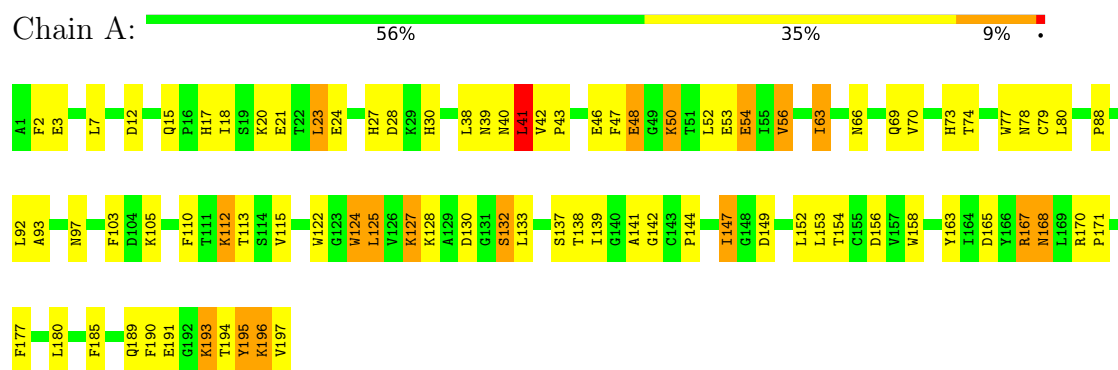
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	185	Total	O	0	0
			185	185		
3	B	257	Total	O	0	0
			257	257		
3	C	124	Total	O	0	0
			124	124		

3 Residue-property plots

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

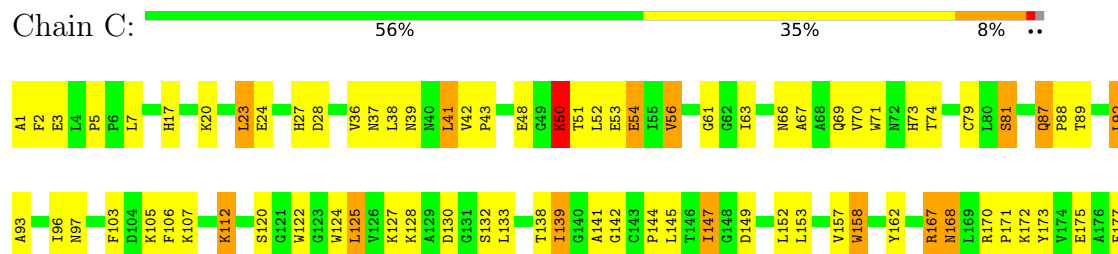
• Molecule 1: SUPEROXIDE DISMUTASE



• Molecule 1: SUPEROXIDE DISMUTASE



• Molecule 1: SUPEROXIDE DISMUTASE



W178	W179	L180	V181	N182	E191	G192	K193	T194	Y195	LYS	VAL
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4 Data and refinement statistics

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

Property	Value	Source
Space group	P 32 2 1	Depositor
Cell constants a, b, c, α , β , γ	115.03Å 115.03Å 82.50Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	50.00 – 2.10	Depositor
% Data completeness (in resolution range)	97.6 (50.00-2.10)	Depositor
R_{merge}	0.05	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	X-PLOR 3.851	Depositor
R, R_{free}	0.220 , 0.290	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	5217	wwPDB-VP
Average B, all atoms (Å ²)	32.0	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: FE

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	0.59	0/1607	0.94	8/2193 (0.4%)
1	B	0.56	0/1607	0.91	4/2193 (0.2%)
1	C	0.56	0/1590	0.90	4/2172 (0.2%)
All	All	0.57	0/4804	0.92	16/6558 (0.2%)

There are no bond length outliers.

All (16) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	158	TRP	N-CA-C	-7.99	98.64	110.23
1	B	158	TRP	N-CA-C	-7.58	99.23	110.23
1	C	158	TRP	N-CA-C	-6.98	99.95	110.28
1	B	152	LEU	N-CA-C	-5.81	106.23	113.55
1	B	124	TRP	N-CA-C	5.60	118.34	109.50
1	B	125	LEU	N-CA-C	-5.53	99.39	108.41
1	A	195	TYR	N-CA-C	5.41	117.87	110.24
1	A	48	GLU	N-CA-C	5.34	118.58	111.75
1	A	125	LEU	N-CA-C	-5.32	99.73	108.41
1	C	125	LEU	N-CA-C	-5.28	99.81	108.41
1	C	152	LEU	N-CA-C	-5.22	106.97	113.55
1	A	124	TRP	N-CA-C	5.15	117.64	109.50
1	A	110	PHE	N-CA-C	-5.09	105.81	111.36
1	A	41	LEU	N-CA-C	5.07	117.92	111.69
1	A	167	ARG	CB-CA-C	-5.07	110.71	116.54
1	C	167	ARG	CB-CA-C	-5.05	110.73	116.54

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	1555	0	1472	66	0
1	B	1555	0	1472	94	0
1	C	1538	0	1450	77	0
2	A	1	0	0	0	0
2	C	2	0	0	1	0
3	A	185	0	0	22	1
3	B	257	0	0	42	1
3	C	124	0	0	33	0
All	All	5217	0	4394	233	1

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 26.

All (233) 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:156:ASP:OD2	3:B:793:HOH:O	1.59	1.20
1:C:53:GLU:HG3	3:C:1610:HOH:O	1.46	1.12
1:C:145:LEU:HD11	3:C:1610:HOH:O	1.63	0.98
1:B:12:ASP:HB2	3:B:569:HOH:O	1.63	0.97
1:A:48:GLU:HA	3:A:1680:HOH:O	1.64	0.95
3:B:793:HOH:O	2:C:1602:FE:FE	1.18	0.95
1:C:37:ASN:HB3	3:C:1619:HOH:O	1.69	0.93
1:A:42:VAL:HB	3:A:1680:HOH:O	1.74	0.87
1:A:144:PRO:O	1:A:147:ILE:HG13	1.73	0.87
1:C:168:ASN:HD22	1:C:168:ASN:H	1.24	0.82
1:B:120:SER:HA	3:B:546:HOH:O	1.79	0.81
1:B:168:ASN:H	1:B:168:ASN:HD22	1.29	0.80
1:B:158:TRP:HA	3:B:546:HOH:O	1.84	0.77
1:A:21:GLU:OE2	1:B:167:ARG:NH1	2.18	0.77
1:C:139:ILE:HG12	3:C:1661:HOH:O	1.84	0.76
1:B:147:ILE:HD12	1:B:149:ASP:OD2	1.85	0.76
1:C:175:GLU:HB2	3:C:1658:HOH:O	1.85	0.76
1:B:144:PRO:O	1:B:147:ILE:HG13	1.84	0.76
1:C:88:PRO:HB2	3:C:1624:HOH:O	1.86	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:188:GLU:HG2	3:B:563:HOH:O	1.86	0.75
1:C:144:PRO:O	1:C:147:ILE:HG13	1.86	0.75
1:B:164:ILE:HA	3:B:654:HOH:O	1.88	0.73
1:C:41:LEU:HD22	3:C:1619:HOH:O	1.90	0.72
1:A:7:LEU:HB2	3:A:1708:HOH:O	1.91	0.71
1:B:24:GLU:O	1:B:28:ASP:HB2	1.91	0.70
1:A:48:GLU:HG2	3:A:1622:HOH:O	1.92	0.70
1:B:8:PRO:HA	3:B:539:HOH:O	1.90	0.70
1:C:194:THR:O	1:C:195:TYR:HB2	1.93	0.69
1:C:93:ALA:N	3:C:1624:HOH:O	2.25	0.69
1:B:191:GLU:HA	3:B:738:HOH:O	1.93	0.68
1:B:147:ILE:HD12	1:B:149:ASP:CG	2.20	0.67
1:B:46:GLU:HB2	3:B:661:HOH:O	1.94	0.66
1:B:121:GLY:O	3:B:675:HOH:O	2.13	0.66
1:B:160:HIS:NE2	3:B:793:HOH:O	2.28	0.66
1:B:90:GLY:HA3	3:B:652:HOH:O	1.94	0.66
1:C:73:HIS:ND1	3:C:1604:HOH:O	2.28	0.66
1:A:167:ARG:NH2	3:A:1770:HOH:O	2.28	0.65
1:A:24:GLU:O	1:A:28:ASP:HB2	1.96	0.65
1:A:42:VAL:HG22	1:A:43:PRO:HD3	1.78	0.65
1:C:66:ASN:O	1:C:70:VAL:HG23	1.97	0.65
1:B:100:PHE:O	3:B:670:HOH:O	2.14	0.64
1:A:196:LYS:O	1:A:197:VAL:HB	1.97	0.63
1:C:1:ALA:HA	3:C:1620:HOH:O	1.97	0.63
1:A:54:GLU:HG2	3:A:1756:HOH:O	1.99	0.63
1:B:193:LYS:HE2	3:B:756:HOH:O	1.98	0.62
1:B:38:LEU:O	1:B:42:VAL:HG13	1.99	0.62
1:A:42:VAL:CG2	1:A:43:PRO:HD3	2.31	0.61
1:A:112:LYS:HD2	3:A:1759:HOH:O	2.01	0.61
1:A:165:ASP:HB3	3:A:1717:HOH:O	2.00	0.61
1:B:163:TYR:O	3:B:654:HOH:O	2.16	0.61
1:A:197:VAL:HG22	3:A:1733:HOH:O	2.01	0.60
1:A:74:THR:HG22	1:A:195:TYR:OH	2.02	0.60
1:A:197:VAL:HG21	3:A:1702:HOH:O	2.01	0.59
1:A:144:PRO:HA	1:A:147:ILE:HD11	1.85	0.59
1:B:168:ASN:H	1:B:168:ASN:ND2	1.98	0.59
1:A:27:HIS:HD2	1:A:28:ASP:OD1	1.87	0.58
1:A:167:ARG:NH2	3:A:1712:HOH:O	2.36	0.58
1:B:147:ILE:HG12	3:B:784:HOH:O	2.03	0.58
1:B:74:THR:HG21	1:B:195:TYR:OH	2.03	0.57
1:C:50:LYS:HB3	1:C:54:GLU:HB3	1.86	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:167:ARG:NE	3:B:654:HOH:O	2.32	0.57
1:A:20:LYS:NZ	3:A:1602:HOH:O	2.30	0.57
1:A:168:ASN:HD22	1:A:168:ASN:H	1.53	0.57
1:C:5:PRO:HB3	3:C:1611:HOH:O	2.05	0.56
1:A:66:ASN:O	1:A:70:VAL:HG23	2.05	0.56
1:A:52:LEU:O	1:A:56:VAL:HG13	2.06	0.56
1:C:168:ASN:HD22	1:C:168:ASN:N	1.99	0.56
1:B:190:PHE:C	1:B:191:GLU:HG2	2.31	0.56
1:B:11:HIS:HB2	3:B:634:HOH:O	2.06	0.56
1:C:147:ILE:HD12	1:C:149:ASP:OD2	2.06	0.56
1:B:17:HIS:HB2	1:B:180:LEU:HD11	1.87	0.56
1:C:127:LYS:HE3	1:C:191:GLU:OE2	2.06	0.55
1:A:38:LEU:O	1:A:42:VAL:HG13	2.07	0.55
1:C:138:THR:HB	1:C:142:GLY:HA3	1.87	0.55
1:A:167:ARG:NH1	1:B:21:GLU:OE2	2.40	0.55
1:B:2:PHE:H	1:B:39:ASN:HD21	1.54	0.55
1:B:197:VAL:HA	3:B:726:HOH:O	2.05	0.55
1:C:36:VAL:HG13	3:C:1612:HOH:O	2.06	0.55
1:B:15:GLN:NE2	3:B:569:HOH:O	2.39	0.55
1:C:24:GLU:O	1:C:28:ASP:HB2	2.07	0.55
1:C:69:GLN:HA	3:C:1604:HOH:O	2.06	0.55
1:B:74:THR:CG2	1:B:195:TYR:OH	2.55	0.54
1:B:66:ASN:O	1:B:70:VAL:HG23	2.07	0.54
1:A:7:LEU:HD21	1:A:23:LEU:HD13	1.89	0.54
1:B:6:PRO:HD2	3:B:619:HOH:O	2.07	0.54
1:B:149:ASP:CG	3:B:603:HOH:O	2.51	0.54
1:A:193:LYS:HD3	3:A:1634:HOH:O	2.08	0.53
1:C:17:HIS:HB2	1:C:180:LEU:HD11	1.89	0.53
1:C:73:HIS:CE1	3:C:1604:HOH:O	2.62	0.53
1:C:38:LEU:O	1:C:42:VAL:HG13	2.09	0.53
1:B:69:GLN:HG2	1:B:141:ALA:HB2	1.90	0.53
1:B:42:VAL:HG22	1:B:43:PRO:HD3	1.90	0.53
1:C:23:LEU:O	1:C:27:HIS:HB3	2.09	0.53
1:C:81:SER:OG	1:C:182:ASN:HB2	2.09	0.52
1:B:138:THR:HB	1:B:142:GLY:HA3	1.91	0.52
1:C:42:VAL:HG22	1:C:43:PRO:HD3	1.90	0.52
1:C:93:ALA:O	1:C:97:ASN:ND2	2.39	0.52
1:B:183:TRP:HB2	3:B:720:HOH:O	2.09	0.52
1:A:78:ASN:ND2	3:A:1725:HOH:O	2.28	0.51
1:B:37:ASN:ND2	3:B:762:HOH:O	2.43	0.51
1:C:71:TRP:NE1	3:C:1610:HOH:O	2.43	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:138:THR:HB	1:A:142:GLY:HA3	1.92	0.51
1:B:52:LEU:O	1:B:56:VAL:HG13	2.10	0.51
1:B:167:ARG:NH2	3:B:654:HOH:O	2.39	0.51
1:C:37:ASN:C	3:C:1619:HOH:O	2.53	0.51
1:C:51:THR:H	1:C:54:GLU:HB2	1.75	0.51
1:C:52:LEU:O	1:C:56:VAL:HG13	2.11	0.50
1:C:88:PRO:C	3:C:1624:HOH:O	2.54	0.50
1:C:122:TRP:HZ2	3:C:1604:HOH:O	1.94	0.50
1:B:127:LYS:HE3	1:B:191:GLU:OE2	2.11	0.49
1:C:144:PRO:HA	1:C:147:ILE:HD11	1.94	0.49
1:A:18:ILE:HG21	3:A:1637:HOH:O	2.11	0.49
1:B:128:LYS:HA	3:B:603:HOH:O	2.11	0.49
1:A:168:ASN:HB3	1:B:30:HIS:NE2	2.28	0.49
1:C:2:PHE:H	1:C:39:ASN:HD21	1.61	0.49
1:A:69:GLN:HG2	1:A:141:ALA:HB2	1.94	0.49
1:C:48:GLU:HG2	3:C:1655:HOH:O	2.12	0.49
1:B:162:TYR:HB3	1:B:173:TYR:CD1	2.47	0.49
1:A:17:HIS:HB2	1:A:180:LEU:HD11	1.94	0.48
1:A:147:ILE:CD1	3:A:1685:HOH:O	2.61	0.48
1:B:105:LYS:CB	3:B:670:HOH:O	2.61	0.48
1:B:164:ILE:CA	3:B:654:HOH:O	2.54	0.48
1:B:81:SER:OG	1:B:182:ASN:HB2	2.12	0.48
1:A:115:VAL:HA	1:A:170:ARG:HD3	1.96	0.48
1:C:69:GLN:CD	3:C:1604:HOH:O	2.56	0.48
1:C:92:LEU:HB3	3:C:1624:HOH:O	2.14	0.48
1:C:170:ARG:N	1:C:171:PRO:CD	2.76	0.48
1:A:190:PHE:C	1:A:191:GLU:HG2	2.39	0.48
1:C:69:GLN:HG2	1:C:141:ALA:HB2	1.96	0.47
1:C:107:LYS:HE3	3:C:1706:HOH:O	2.13	0.47
1:A:79:CYS:HB3	1:A:153:LEU:HD12	1.95	0.47
1:A:149:ASP:O	3:A:1748:HOH:O	2.20	0.47
1:B:73:HIS:O	1:B:77:TRP:CD1	2.67	0.47
1:A:2:PHE:H	1:A:39:ASN:HD21	1.62	0.47
1:B:27:HIS:HD2	1:B:28:ASP:OD1	1.97	0.47
1:C:43:PRO:HA	3:C:1655:HOH:O	2.14	0.47
1:B:29:LYS:HA	3:B:665:HOH:O	2.14	0.47
1:C:106:PHE:HE1	1:C:125:LEU:HD13	1.80	0.47
1:C:69:GLN:CA	3:C:1604:HOH:O	2.63	0.47
1:A:163:TYR:OH	1:B:30:HIS:NE2	2.48	0.46
1:B:12:ASP:O	1:B:15:GLN:HG3	2.14	0.46
1:B:112:LYS:NZ	3:B:748:HOH:O	2.48	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:53:GLU:OE1	1:A:197:VAL:O	2.33	0.46
1:C:147:ILE:HG13	1:C:147:ILE:H	1.58	0.46
1:B:112:LYS:HB2	3:B:598:HOH:O	2.15	0.46
1:C:27:HIS:CD2	1:C:28:ASP:OD1	2.68	0.46
1:A:93:ALA:O	1:A:97:ASN:ND2	2.37	0.46
1:B:88:PRO:HD3	1:B:103:PHE:CE1	2.50	0.46
1:B:122:TRP:CZ3	1:B:156:ASP:HB2	2.51	0.46
1:A:23:LEU:HD21	3:A:1637:HOH:O	2.15	0.45
1:B:42:VAL:N	1:B:43:PRO:CD	2.79	0.45
1:A:147:ILE:HD13	3:A:1685:HOH:O	2.16	0.45
1:B:7:LEU:HD21	1:B:23:LEU:HD13	1.99	0.45
1:B:127:LYS:HE3	1:B:191:GLU:CD	2.42	0.45
1:B:120:SER:HB3	1:B:158:TRP:CE2	2.52	0.45
1:C:61:GLY:N	3:C:1681:HOH:O	2.31	0.45
1:B:79:CYS:HB3	1:B:153:LEU:HD12	1.99	0.45
1:A:125:LEU:HG	1:A:152:LEU:HD12	1.99	0.45
1:B:176:ALA:HB2	3:B:557:HOH:O	2.17	0.45
1:A:30:HIS:NE2	1:B:163:TYR:OH	2.43	0.45
1:A:12:ASP:O	1:A:15:GLN:HG3	2.17	0.44
1:C:103:PHE:HB2	3:C:1606:HOH:O	2.17	0.44
1:B:42:VAL:HG21	3:B:680:HOH:O	2.16	0.44
1:B:185:PHE:O	1:B:189:GLN:HG2	2.17	0.44
1:B:130:ASP:OD2	1:B:132:SER:OG	2.35	0.44
1:B:167:ARG:CZ	3:B:654:HOH:O	2.64	0.44
1:C:27:HIS:HD2	1:C:28:ASP:OD1	2.00	0.44
1:A:170:ARG:HB3	1:A:171:PRO:HD3	2.00	0.44
1:B:170:ARG:HB3	1:B:171:PRO:HD3	2.00	0.44
1:A:41:LEU:HG	1:A:63:ILE:HG13	1.99	0.44
1:B:7:LEU:HD12	1:B:7:LEU:HA	1.88	0.44
1:B:105:LYS:CG	3:B:670:HOH:O	2.66	0.44
1:B:122:TRP:CE2	3:B:675:HOH:O	2.66	0.44
1:C:162:TYR:HB3	1:C:173:TYR:CD1	2.53	0.44
1:B:128:LYS:HG2	3:B:603:HOH:O	2.17	0.44
1:B:51:THR:O	1:B:52:LEU:C	2.61	0.43
1:C:112:LYS:NZ	3:C:1651:HOH:O	2.32	0.43
1:B:190:PHE:O	1:B:191:GLU:HG2	2.18	0.43
1:C:7:LEU:HD21	1:C:23:LEU:HD13	1.99	0.43
1:A:170:ARG:N	1:A:171:PRO:CD	2.82	0.43
1:B:88:PRO:O	1:B:93:ALA:HB2	2.18	0.43
1:A:73:HIS:O	1:A:77:TRP:CD1	2.71	0.43
1:B:4:LEU:HD12	1:B:5:PRO:HD2	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:63:ILE:HD12	3:C:1633:HOH:O	2.17	0.43
1:B:170:ARG:N	1:B:171:PRO:CD	2.82	0.43
1:A:122:TRP:CZ3	1:A:156:ASP:HB2	2.54	0.43
1:A:130:ASP:OD2	1:A:132:SER:OG	2.35	0.43
1:B:115:VAL:HA	1:B:170:ARG:HD3	1.99	0.43
1:B:150:THR:HA	1:B:151:PRO:HD3	1.89	0.43
1:C:167:ARG:NH2	3:C:1686:HOH:O	2.45	0.43
1:C:127:LYS:HE3	1:C:191:GLU:CD	2.44	0.43
1:C:145:LEU:CD1	3:C:1610:HOH:O	2.42	0.43
1:C:194:THR:O	1:C:195:TYR:CB	2.66	0.43
1:A:74:THR:CG2	1:A:195:TYR:OH	2.67	0.43
1:A:88:PRO:HD3	1:A:103:PHE:CE1	2.53	0.43
1:C:38:LEU:HD22	1:C:67:ALA:HA	2.01	0.43
1:A:23:LEU:O	1:A:27:HIS:HB3	2.19	0.42
1:C:124:TRP:CZ2	1:C:144:PRO:HD3	2.54	0.42
1:B:144:PRO:HA	1:B:147:ILE:HD11	2.01	0.42
1:C:42:VAL:CG2	1:C:43:PRO:HD3	2.49	0.42
1:C:53:GLU:OE2	1:C:195:TYR:HE1	2.01	0.42
1:C:74:THR:HG23	3:C:1691:HOH:O	2.19	0.42
1:C:178:TRP:HA	1:C:178:TRP:CE3	2.55	0.42
1:A:42:VAL:CG2	3:A:1680:HOH:O	2.67	0.42
1:A:124:TRP:CE2	1:A:144:PRO:HD3	2.54	0.42
1:C:96:ILE:HA	1:C:133:LEU:HD12	2.02	0.42
1:A:113:THR:HG23	1:A:137:SER:HB2	2.00	0.42
1:B:47:PHE:HA	1:B:50:LYS:HG3	2.01	0.42
1:A:185:PHE:O	1:A:189:GLN:HG2	2.20	0.42
1:B:106:PHE:HE1	1:B:125:LEU:HD13	1.83	0.42
1:B:113:THR:HG23	1:B:137:SER:HB2	2.01	0.42
1:C:124:TRP:CE2	1:C:144:PRO:HD3	2.55	0.41
1:A:47:PHE:HA	1:A:50:LYS:HG3	2.03	0.41
1:A:127:LYS:HE3	1:A:191:GLU:CD	2.45	0.41
1:C:79:CYS:HB3	1:C:153:LEU:HD12	2.02	0.41
1:A:46:GLU:CG	3:A:1674:HOH:O	2.68	0.41
1:B:5:PRO:O	1:B:27:HIS:HE1	2.02	0.41
1:C:120:SER:HB3	1:C:158:TRP:CE2	2.56	0.41
1:A:147:ILE:HG13	1:A:147:ILE:H	1.56	0.41
1:B:176:ALA:CB	3:B:557:HOH:O	2.69	0.41
1:C:88:PRO:CB	1:C:92:LEU:HD13	2.51	0.41
1:A:40:ASN:ND2	3:A:1631:HOH:O	2.52	0.41
1:C:7:LEU:HD13	1:C:27:HIS:CG	2.56	0.41
1:C:89:THR:N	3:C:1624:HOH:O	2.54	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:128:LYS:HB2	1:C:130:ASP:OD2	2.21	0.41
1:B:109:GLU:HA	3:B:598:HOH:O	2.20	0.41
1:C:87:GLN:CG	3:C:1622:HOH:O	2.69	0.40
1:B:1:ALA:N	3:B:581:HOH:O	2.54	0.40
1:B:148:GLY:HA3	3:B:626:HOH:O	2.20	0.40
1:B:160:HIS:CD2	1:B:160:HIS:C	2.99	0.40
1:C:50:LYS:H	1:C:50:LYS:HG2	1.65	0.40
1:C:88:PRO:HD3	1:C:103:PHE:CE1	2.56	0.40
1:B:24:GLU:O	1:B:28:ASP:CB	2.67	0.40

All (1) 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)
3:A:1714:HOH:O	3:B:629:HOH:O[2_654]	1.96	0.24

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	195/197 (99%)	189 (97%)	6 (3%)	0	100	100
1	B	195/197 (99%)	188 (96%)	7 (4%)	0	100	100
1	C	193/197 (98%)	185 (96%)	7 (4%)	1 (0%)	24	22
All	All	583/591 (99%)	562 (96%)	20 (3%)	1 (0%)	43	44

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	50	LYS

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	161/161 (100%)	138 (86%)	23 (14%)	3	1
1	B	161/161 (100%)	138 (86%)	23 (14%)	3	1
1	C	159/161 (99%)	138 (87%)	21 (13%)	4	2
All	All	481/483 (100%)	414 (86%)	67 (14%)	3	2

All (67) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	3	GLU
1	A	23	LEU
1	A	41	LEU
1	A	50	LYS
1	A	54	GLU
1	A	56	VAL
1	A	63	ILE
1	A	80	LEU
1	A	92	LEU
1	A	105	LYS
1	A	112	LYS
1	A	127	LYS
1	A	128	LYS
1	A	132	SER
1	A	133	LEU
1	A	139	ILE
1	A	147	ILE
1	A	154	THR
1	A	168	ASN
1	A	177	PHE
1	A	193	LYS
1	A	194	THR
1	A	196	LYS
1	B	3	GLU
1	B	9	TYR
1	B	41	LEU

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Mol	Chain	Res	Type
1	B	42	VAL
1	B	50	LYS
1	B	54	GLU
1	B	56	VAL
1	B	81	SER
1	B	87	GLN
1	B	92	LEU
1	B	105	LYS
1	B	106	PHE
1	B	112	LYS
1	B	113	THR
1	B	132	SER
1	B	139	ILE
1	B	147	ILE
1	B	168	ASN
1	B	177	PHE
1	B	193	LYS
1	B	194	THR
1	B	196	LYS
1	B	197	VAL
1	C	3	GLU
1	C	20	LYS
1	C	23	LEU
1	C	41	LEU
1	C	50	LYS
1	C	54	GLU
1	C	56	VAL
1	C	81	SER
1	C	87	GLN
1	C	92	LEU
1	C	105	LYS
1	C	112	LYS
1	C	132	SER
1	C	139	ILE
1	C	147	ILE
1	C	157	VAL
1	C	168	ASN
1	C	172	LYS
1	C	177	PHE
1	C	193	LYS
1	C	194	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (34)

such sidechains are listed below:

Mol	Chain	Res	Type
1	A	17	HIS
1	A	27	HIS
1	A	32	ASN
1	A	37	ASN
1	A	39	ASN
1	A	66	ASN
1	A	72	ASN
1	A	78	ASN
1	A	87	GLN
1	A	168	ASN
1	A	179	ASN
1	A	182	ASN
1	B	17	HIS
1	B	27	HIS
1	B	37	ASN
1	B	39	ASN
1	B	66	ASN
1	B	72	ASN
1	B	78	ASN
1	B	87	GLN
1	B	168	ASN
1	B	179	ASN
1	B	182	ASN
1	C	17	HIS
1	C	27	HIS
1	C	37	ASN
1	C	39	ASN
1	C	66	ASN
1	C	72	ASN
1	C	78	ASN
1	C	87	GLN
1	C	168	ASN
1	C	179	ASN
1	C	182	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 3 ligands modelled in this entry, 3 are monoatomic - leaving 0 for Mogul analysis.

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.

No monomer is involved in short contacts.

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.