



wwPDB X-ray Structure Validation Summary Report ⓘ

Jan 31, 2016 – 07:01 PM GMT

PDB ID : 1DO5
Title : HUMAN COPPER CHAPERONE FOR SUPEROXIDE DISMUTASE DOMAIN II
Authors : Lamb, A.L.; Wernimont, A.K.; Pufahl, R.A.; O'Halloran, T.V.; Rosenzweig, A.C.
Deposited on : 1999-12-18
Resolution : 2.75 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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

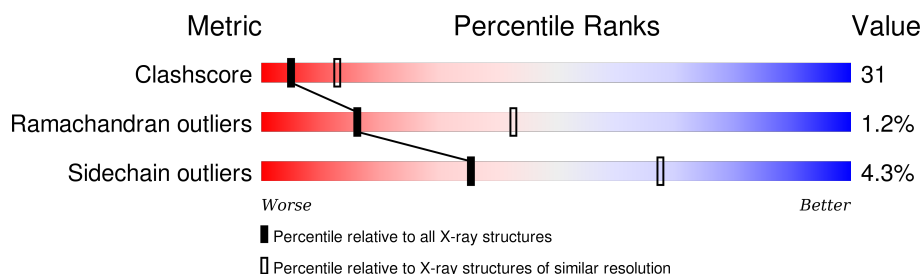
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.75 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	3829 (2.80-2.72)
Ramachandran outliers	100387	3767 (2.80-2.72)
Sidechain outliers	100360	3770 (2.80-2.72)

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	154	
1	B	154	
1	C	154	
1	D	154	

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 4495 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 HUMAN COPPER CHAPERONE FOR SUPEROXIDE DISMUTASE DOMAIN II.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	154	Total	C	N	O	S	0	0	0
			1143	696	218	224	5			
1	B	148	Total	C	N	O	S	0	0	0
			1094	664	210	215	5			
1	C	148	Total	C	N	O	S	0	0	0
			1094	664	210	215	5			
1	D	153	Total	C	N	O	S	0	0	0
			1134	691	216	222	5			

- Molecule 2 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	B	1	Total	Zn	0	0
			1	1		
2	A	1	Total	Zn	0	0
			1	1		
2	D	1	Total	Zn	0	0
			1	1		
2	C	1	Total	Zn	0	0
			1	1		

- Molecule 3 is water.

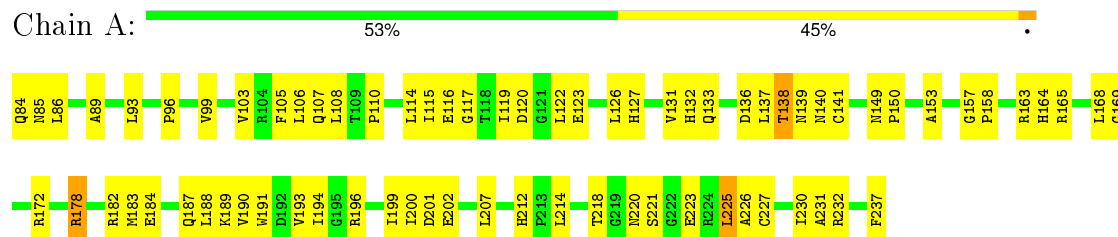
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	6	Total	O	0	0
			6	6		
3	B	7	Total	O	0	0
			7	7		
3	C	8	Total	O	0	0
			8	8		
3	D	5	Total	O	0	0
			5	5		

3 Residue-property plots

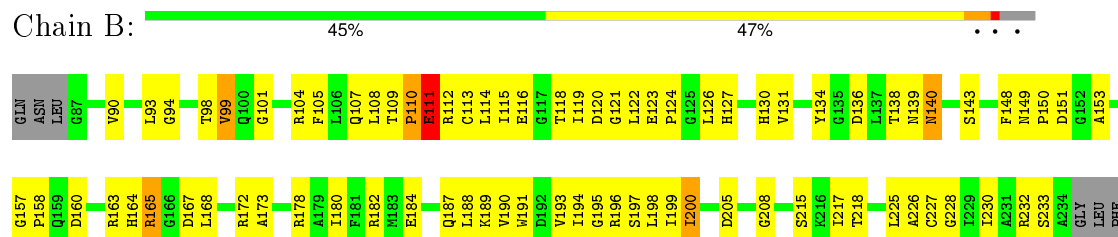
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according 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.

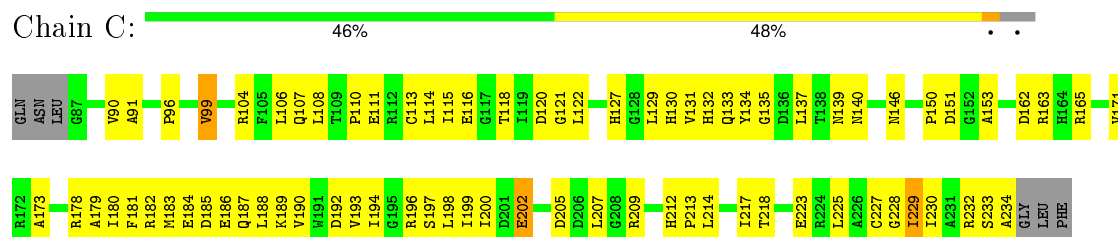
- Molecule 1: HUMAN COPPER CHAPERONE FOR SUPEROXIDE DISMUTASE DOMAIN II



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G1N	N85	L86		A89	Y90		P96	G97	T98	Y99		F105		T109	P110	E111		E116	G117	T118	I119		D120	G121	L122	E123		L126	H127	G128	L129	H130	V131	H132	Q133	Y134	G135	D136	L137	T138		N139	N140	C141	N142	S143	G144	G145	N146	H147	F148	N149	P150		A153		P158		R163	H164	R165
	L168	G169	N170	V171	R172		R178	A179		R182		D185	E186	Q187	L188	K189	V190	W191	D192	V193		R196	S197	L198	I199	D200		D205		G208		H212	P213	L214	S215	K216	L217	T218		R224	L225	A226	C227		A231	R232	S233		F237												

4 Data and refinement statistics

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

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	117.19Å 66.72Å 88.03Å 90.00° 96.63° 90.00°	Depositor
Resolution (Å)	19.21 – 2.75	Depositor
% Data completeness (in resolution range)	90.1 (19.21-2.75)	Depositor
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	CNS 0.9	Depositor
R, R_{free}	0.228 , 0.283	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	4495	wwPDB-VP
Average B, all atoms (Å ²)	32.0	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: ZN

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	0.37	0/1162	0.68	0/1568
1	B	0.35	0/1112	0.66	0/1502
1	C	0.40	0/1112	0.67	0/1502
1	D	0.35	0/1153	0.68	0/1556
All	All	0.37	0/4539	0.67	0/6128

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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	1143	0	1093	74	0
1	B	1094	0	1045	70	0
1	C	1094	0	1045	84	0
1	D	1134	0	1085	61	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
2	C	1	0	0	0	0
2	D	1	0	0	0	0
3	A	6	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	B	7	0	0	1	0
3	C	8	0	0	1	0
3	D	5	0	0	1	0
All	All	4495	0	4268	271	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 31.

The worst 5 of 271 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:150:PRO:HD2	1:B:165:ARG:HG3	1.44	0.94
1:A:212:HIS:HD2	1:A:214:LEU:H	1.17	0.88
1:C:133:GLN:HE21	1:C:146:ASN:H	0.90	0.88
1:D:149:ASN:HD21	1:D:153:ALA:H	1.21	0.87
1:C:90:VAL:HG23	1:C:233:SER:HB2	1.61	0.82

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	152/154 (99%)	141 (93%)	11 (7%)	0	100	100
1	B	146/154 (95%)	126 (86%)	16 (11%)	4 (3%)	6	18
1	C	146/154 (95%)	130 (89%)	14 (10%)	2 (1%)	14	38
1	D	151/154 (98%)	145 (96%)	5 (3%)	1 (1%)	26	59
All	All	595/616 (97%)	542 (91%)	46 (8%)	7 (1%)	16	43

5 of 7 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	111	GLU
1	C	229	ILE
1	D	196	ARG
1	B	99	VAL
1	B	110	PRO

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	118/118 (100%)	113 (96%)	5 (4%)	36	68
1	B	113/118 (96%)	109 (96%)	4 (4%)	43	75
1	C	113/118 (96%)	110 (97%)	3 (3%)	52	83
1	D	117/118 (99%)	109 (93%)	8 (7%)	20	46
All	All	461/472 (98%)	441 (96%)	20 (4%)	35	68

5 of 20 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	187	GLN
1	C	202	GLU
1	D	163	ARG
1	B	165	ARG
1	B	200	ILE

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 31 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	149	ASN
1	C	133	GLN
1	D	149	ASN
1	B	164	HIS
1	C	140	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 4 ligands modelled in this entry, 4 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 will therefore be empty.

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

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

6.3 Carbohydrates ⓘ

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

6.4 Ligands ⓘ

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

6.5 Other polymers ⓘ

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