



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 08:02 PM UTC

PDB ID : 1GY1 / pdb_00001gy1
Title : Crystal structures of Ser86Asp and Met148Leu Rusticyanin
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Deposited on : 2002-04-16
Resolution : 1.65 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

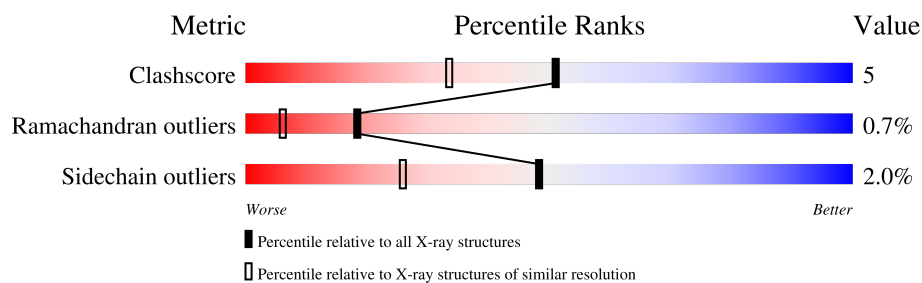
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.65 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	2662 (1.66-1.66)
Ramachandran outliers	187476	2621 (1.66-1.66)
Sidechain outliers	187428	2621 (1.66-1.66)

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	155	 84% 14% ..
1	B	155	 88% 11% ..

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 2555 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 RUSTICYANIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	154	Total	C	N	O	S	3	1	0
			1170	764	187	215	4			
1	B	154	Total	C	N	O	S	8	1	0
			1166	759	187	216	4			

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	86	ASP	SER	engineered mutation	UNP P24930
B	86	ASP	SER	engineered mutation	UNP P24930
A	20	GLN	GLU	conflict	UNP P24930
A	65	GLN	GLU	conflict	UNP P24930
A	124	ASN	ASP	conflict	UNP P24930
B	20	GLN	GLU	conflict	UNP P24930
B	65	GLN	GLU	conflict	UNP P24930
B	124	ASN	ASP	conflict	UNP P24930

- Molecule 2 is COPPER (II) ION (CCD ID: CU) (formula: Cu).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total	Cu	0	0
			1	1		
2	B	1	Total	Cu	0	0
			1	1		

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	112	Total	O	0	0
			112	112		
3	B	105	Total	O	0	0
			105	105		

3 Residue-property plots [i](#)

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: RUSTICYANIN

Chain A:  84% 14% ..



- Molecule 1: RUSTICYANIN

Chain B:  88% 11% ..



4 Data and refinement statistics

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

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	43.10Å 61.41Å 53.35Å 90.00° 96.13° 90.00°	Depositor
Resolution (Å)	52.70 – 1.65	Depositor
% Data completeness (in resolution range)	95.6 (52.70-1.65)	Depositor
R_{merge}	0.05	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	REFMAC 5.0	Depositor
R, R_{free}	0.166 , 0.190	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	2555	wwPDB-VP
Average B, all atoms (Å ²)	20.0	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: CU

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	0.76	4/1213 (0.3%)	0.97	5/1658 (0.3%)
1	B	0.66	2/1204 (0.2%)	0.94	2/1645 (0.1%)
All	All	0.71	6/2417 (0.2%)	0.95	7/3303 (0.2%)

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	2	0

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	8	LYS	CD-CE	8.69	1.78	1.52
1	A	130[A]	THR	CA-CB	-7.36	1.40	1.53
1	A	130[B]	THR	CA-CB	-7.36	1.40	1.53
1	A	130[A]	THR	CB-CG2	-6.49	1.31	1.52
1	A	130[B]	THR	CB-CG2	-6.49	1.31	1.52
1	B	81	LYS	CD-CE	6.19	1.71	1.52

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	36	LYS	CA-CB-CG	10.95	135.99	114.10
1	B	8	LYS	CG-CD-CE	-6.82	95.62	111.30
1	A	130[A]	THR	N-CA-C	-5.39	101.38	109.95
1	A	130[B]	THR	N-CA-C	-5.39	101.38	109.95
1	A	102	ILE	N-CA-C	5.28	117.18	112.17

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	130[A]	THR	CA-CB-CG2	5.17	119.29	110.50
1	A	130[B]	THR	CA-CB-CG2	5.17	119.29	110.50

All (2) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	A	130[A]	THR	CB
1	A	130[B]	THR	CB

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	1170	0	1157	14	1
1	B	1166	0	1145	11	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
3	A	112	0	0	2	0
3	B	105	0	0	2	1
All	All	2555	0	2302	24	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 5.

All (24) 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:80:ASN:HD22	1:A:85:HIS:HE2	1.02	0.98
1:A:2:THR:HA	3:A:2001:HOH:O	1.65	0.97
1:B:80:ASN:HD22	1:B:85:HIS:HE2	1.04	0.93
1:B:75:THR:OG1	1:B:124:ASN:ND2	2.13	0.81
1:B:127:TRP:CZ2	1:B:129:PRO:HB3	2.36	0.61
1:B:80:ASN:ND2	1:B:85:HIS:HE2	1.88	0.61
1:A:127:TRP:CZ2	1:A:129:PRO:HB3	2.39	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:8:LYS:NZ	1:A:124:ASN:OD1	2.37	0.55
1:A:25:LYS:HE3	1:B:97:ALA:HA	1.89	0.55
1:B:29[A]:ASP:OD2	1:B:29[A]:ASP:OD1	2.25	0.54
1:A:99:MET:HE2	3:A:2031:HOH:O	2.08	0.52
1:B:127:TRP:CE2	1:B:129:PRO:HB3	2.49	0.48
1:B:130:THR:HG22	3:B:2091:HOH:O	2.14	0.47
1:B:136:TYR:CZ	1:B:150:GLY:HA3	2.49	0.47
1:A:75:THR:OG1	1:A:124:ASN:ND2	2.49	0.46
1:B:60:LYS:NZ	3:B:2044:HOH:O	2.46	0.45
1:B:59:LYS:HD2	1:B:59:LYS:HA	1.76	0.45
1:A:127:TRP:CE2	1:A:129:PRO:HB3	2.54	0.43
1:A:66:ILE:HA	1:A:67:PRO:HD3	1.95	0.42
1:A:51:PHE:CD1	1:A:51:PHE:C	2.97	0.42
1:A:92:LYS:C	1:A:92:LYS:HD3	2.45	0.42
1:A:9:GLU:HB3	1:A:119:LYS:HD3	2.02	0.42
1:A:78:ASN:ND2	1:A:80:ASN:H	2.19	0.41
1:A:136:TYR:CZ	1:A:150:GLY:HA3	2.56	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)
1:A:151:LYS:CE	3:B:2016:HOH:O[1_655]	1.83	0.37

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	153/155 (99%)	148 (97%)	4 (3%)	1 (1%)	18	6
1	B	153/155 (99%)	147 (96%)	5 (3%)	1 (1%)	18	6
All	All	306/310 (99%)	295 (96%)	9 (3%)	2 (1%)	18	6

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	45	VAL
1	B	45	VAL

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	126/126 (100%)	122 (97%)	4 (3%)	34	12
1	B	123/126 (98%)	121 (98%)	2 (2%)	55	34
All	All	249/252 (99%)	243 (98%)	6 (2%)	48	20

All (6) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	25	LYS
1	A	81	LYS
1	A	130[A]	THR
1	A	130[B]	THR
1	B	2	THR
1	B	36	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	78	ASN
1	A	80	ASN
1	B	78	ASN
1	B	80	ASN
1	B	124	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 2 ligands modelled in this entry, 2 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.