



Full wwPDB X-ray Structure Validation Report

Feb 28, 2014 – 10:03 PM GMT

PDB ID : 2DDD
Title : Unique behavior of a histidine responsible for an engineered green-to-red photoconversion process
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Deposited on : 2006-01-27
Resolution : 1.55 Å(reported)

This is a full wwPDB 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/ValidationPDFNotes.html>

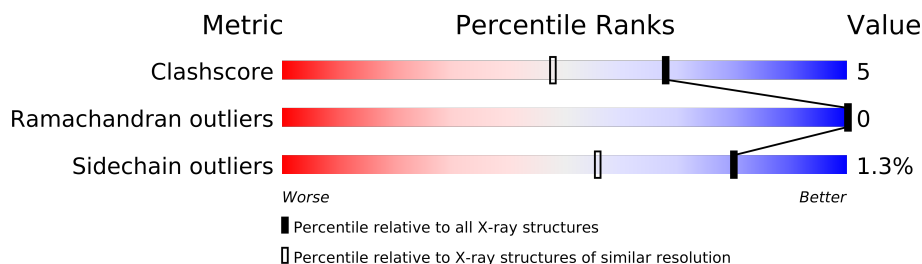
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.15 2013
Xtriage (Phenix) : **NOT EXECUTED**
EDS : **NOT EXECUTED**
Percentile statistics : 21963
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : stable22683

1 Overall quality at a glance

The reported resolution of this entry is 1.55 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	79885	1249 (1.58-1.54)
Ramachandran outliers	78287	1212 (1.58-1.54)
Sidechain outliers	78261	1210 (1.58-1.54)

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. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	225	
1	B	225	

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 4209 atoms, of which 0 are hydrogen and 0 are deuterium.

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 photoconvertible fluorescent protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	224	Total	C	N	O	S	0	0	0
			1798	1148	306	333	11			
1	B	225	Total	C	N	O	S	0	0	0
			1807	1154	308	334	11			

There are 16 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	VAL	MET	ENGINEERED MUTATION	UNP Q53UG8
A	12	VAL	LEU	ENGINEERED MUTATION	UNP Q53UG8
A	64	CR8	HIS	CHROMOPHORE	UNP Q53UG8
A	64	CR8	TYR	CHROMOPHORE	UNP Q53UG8
A	64	CR8	GLY	CHROMOPHORE	UNP Q53UG8
A	70	LYS	GLU	ENGINEERED MUTATION	UNP Q53UG8
A	144	SER	PRO	ENGINEERED MUTATION	UNP Q53UG8
A	197	LEU	GLN	ENGINEERED MUTATION	UNP Q53UG8
B	1	VAL	MET	ENGINEERED MUTATION	UNP Q53UG8
B	12	VAL	LEU	ENGINEERED MUTATION	UNP Q53UG8
B	64	CR8	HIS	CHROMOPHORE	UNP Q53UG8
B	64	CR8	TYR	CHROMOPHORE	UNP Q53UG8
B	64	CR8	GLY	CHROMOPHORE	UNP Q53UG8
B	70	LYS	GLU	ENGINEERED MUTATION	UNP Q53UG8
B	144	SER	PRO	ENGINEERED MUTATION	UNP Q53UG8
B	197	LEU	GLN	ENGINEERED MUTATION	UNP Q53UG8

- Molecule 2 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

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

- Molecule 3 is SODIUM ION (three-letter code: NA) (formula: Na).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	B	1	Total 1	Na 1	0	0
3	A	1	Total 1	Na 1	0	0

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	309	Total 309	O 309	0	0
4	B	291	Total 291	O 291	0	0

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: photoconvertible fluorescent protein

Chain A: 



- Molecule 1: photoconvertible fluorescent protein

Chain B: 



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	97.84Å 118.41Å 48.86Å 90.00° 119.96° 90.00°	Depositor
Resolution (Å)	100.00 – 1.55	Depositor
% Data completeness (in resolution range)	(Not available) (100.00-1.55)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	0.04	Depositor
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.175 , 0.190	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	4209	wwPDB-VP
Average B, all atoms (Å ²)	13.0	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: NA, CR8, MG

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	0.32	0/1814	0.66	0/2445
1	B	0.32	0/1823	0.66	0/2456
All	All	0.32	0/3637	0.66	0/4901

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1798	0	1754	22	0
1	B	1807	0	1767	17	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
4	A	309	0	0	0	0
4	B	291	0	0	0	0
All	All	4209	0	3521	35	0

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 5.

All (35) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:39:ASN:HD21	1:B:213:TYR:HD1	1.29	0.79
1:A:222:LEU:HD12	1:A:223:PRO:HD2	1.72	0.71
1:A:39:ASN:HD21	1:A:213:TYR:HD1	1.37	0.69
1:B:39:ASN:ND2	1:B:213:TYR:HD1	1.99	0.60
1:A:39:ASN:ND2	1:A:213:TYR:HD1	2.01	0.58
1:A:83:PHE:HB3	1:A:84:PRO:HA	1.90	0.54
1:B:83:PHE:HB3	1:B:84:PRO:HA	1.90	0.52
1:A:74:GLU:CD	1:A:74:GLU:H	2.14	0.51
1:A:126:VAL:HB	1:B:90:GLU:HB3	1.92	0.51
1:A:202:SER:HB3	1:A:211:LYS:HD2	1.93	0.50
1:A:105:ASN:HD21	1:A:119:ASN:HB3	1.79	0.48
1:B:12:VAL:HG12	1:B:119:ASN:HB2	1.96	0.48
1:A:137:ARG:HG3	1:A:137:ARG:HH21	1.80	0.47
1:A:38:GLN:O	1:A:39:ASN:ND2	2.48	0.47
1:A:100:ILE:HD11	1:B:100:ILE:HD13	1.97	0.47
1:A:90:GLU:HB3	1:B:126:VAL:HB	1.96	0.46
1:B:197:LEU:HD23	1:B:197:LEU:C	2.35	0.46
1:B:111:LYS:NZ	1:B:111:LYS:HB3	2.30	0.45
1:B:202:SER:HB3	1:B:211:LYS:HD2	1.98	0.45
1:B:137:ARG:HG3	1:B:137:ARG:HH11	1.81	0.45
1:B:160:VAL:CG1	1:B:176:PHE:HB2	2.46	0.45
1:A:40:VAL:HG12	1:A:212:LEU:HB2	1.99	0.45
1:A:100:ILE:HD13	1:B:100:ILE:HD11	1.97	0.45
1:A:197:LEU:HD23	1:A:197:LEU:C	2.38	0.44
1:A:12:VAL:HG12	1:A:119:ASN:HB2	1.99	0.43
1:B:17:ALA:HA	1:B:21:HIS:O	2.18	0.43
1:A:160:VAL:HG13	1:A:176:PHE:HB2	2.01	0.43
1:A:17:ALA:HA	1:A:21:HIS:O	2.18	0.43
1:A:160:VAL:CG1	1:A:176:PHE:HB2	2.49	0.42
1:B:214:GLU:HG2	1:B:215:HIS:N	2.35	0.42
1:A:203:HIS:HA	1:A:209:LYS:O	2.20	0.41
1:A:131:ASN:C	1:A:131:ASN:HD22	2.22	0.41
1:B:203:HIS:HA	1:B:209:LYS:O	2.20	0.41
1:B:40:VAL:HG12	1:B:212:LEU:HB2	2.02	0.41
1:A:150:TYR:HB3	1:A:191:TYR:CD1	2.56	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	221/225 (98%)	220 (100%)	1 (0%)	0	100	100
1	B	222/225 (99%)	219 (99%)	3 (1%)	0	100	100
All	All	443/450 (98%)	439 (99%)	4 (1%)	0	100	100

There are no Ramachandran outliers to report.

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	193/194 (100%)	190 (98%)	3 (2%)	75	45
1	B	194/194 (100%)	192 (99%)	2 (1%)	85	66
All	All	387/388 (100%)	382 (99%)	5 (1%)	80	56

All (5) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	105	ASN
1	A	131	ASN
1	A	148	LYS
1	B	105	ASN
1	B	148	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (17) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	32	GLN

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Mol	Chain	Res	Type
1	A	39	ASN
1	A	105	ASN
1	A	115	ASN
1	A	119	ASN
1	A	127	ASN
1	A	131	ASN
1	A	161	ASN
1	A	167	GLN
1	B	32	GLN
1	B	39	ASN
1	B	105	ASN
1	B	115	ASN
1	B	127	ASN
1	B	161	ASN
1	B	167	GLN
1	B	187	GLN

5.3.3 RNA ⓘ

There are no RNA chains in this entry.

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

2 non-standard protein/DNA/RNA residues 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	$\# Z > 2$
1	CR8	A	64	1	27,27,28	3.93	9 (33%)	29,37,39	2.80	8 (27%)
1	CR8	B	64	1	27,27,28	3.93	9 (33%)	29,37,39	2.83	8 (27%)

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
1	CR8	A	64	1	-	0/9/25/26	0/3/3/3
1	CR8	B	64	1	-	0/9/25/26	0/3/3/3

All (18) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	64	CR8	O19-C	17.48	1.23	1.11
1	B	64	CR8	O19-C	17.39	1.23	1.11
1	A	64	CR8	C20-C21	-5.89	1.42	1.49
1	B	64	CR8	C20-C21	-5.81	1.42	1.49
1	B	64	CR8	O3-C1	3.47	1.34	1.24
1	A	64	CR8	O3-C1	3.45	1.34	1.24
1	B	64	CR8	C14-N13	2.89	1.40	1.36
1	A	64	CR8	C14-N13	2.81	1.39	1.36
1	B	64	CR8	C14-C16	-2.80	1.45	1.50
1	A	64	CR8	C6-C2	2.78	1.41	1.35
1	B	64	CR8	C14-N15	-2.77	1.29	1.34
1	B	64	CR8	C6-C2	2.73	1.41	1.35
1	B	64	CR8	C5-C4	2.66	1.41	1.35
1	A	64	CR8	C14-C16	-2.66	1.46	1.50
1	A	64	CR8	C5-C4	2.61	1.41	1.35
1	A	64	CR8	C14-N15	-2.61	1.29	1.34
1	A	64	CR8	C20-C16	-2.54	1.34	1.55
1	B	64	CR8	C20-C16	-2.54	1.34	1.55

All (16) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	64	CR8	C20-C16-C14	11.76	123.82	111.18
1	A	64	CR8	C20-C16-C14	11.57	123.62	111.18
1	A	64	CR8	C21-C20-C16	6.20	125.79	113.19
1	B	64	CR8	C21-C20-C16	6.05	125.49	113.19
1	A	64	CR8	C8-C9-N15	2.64	128.52	123.96
1	B	64	CR8	C8-C9-N15	2.55	128.38	123.96
1	B	64	CR8	C9-N15-C14	2.44	109.44	105.99
1	A	64	CR8	C9-N15-C14	2.43	109.42	105.99
1	B	64	CR8	C17-N13-C14	2.34	129.92	126.62
1	A	64	CR8	C17-N13-C14	2.33	129.90	126.62
1	A	64	CR8	C17-N13-C12	-2.17	120.12	124.24
1	B	64	CR8	C9-C12-N13	-2.16	102.11	104.65
1	B	64	CR8	C17-N13-C12	-2.15	120.17	124.24
1	B	64	CR8	C23-N11-C10	2.12	108.99	105.76
1	A	64	CR8	C23-N11-C10	2.08	108.93	105.76

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	64	CR8	C9-C12-N13	-2.07	102.22	104.65

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

5.5 Carbohydrates

There are no carbohydrates in this entry.

5.6 Ligand geometry

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.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

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.