



wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 14, 2017 – 11:44 pm GMT

PDB ID : 3V98
Title : S663D Stable-5-LOX
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Deposited on : 2011-12-23
Resolution : 2.07 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
Xtriage (Phenix) : 1.9-1692
EDS : trunk28683
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : recalc28949

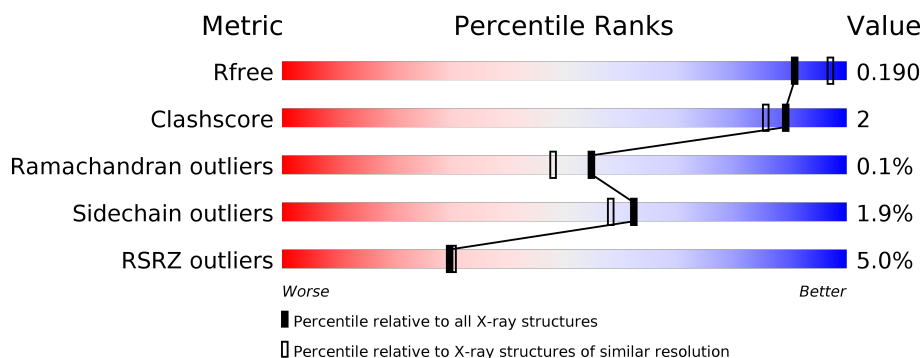
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.07 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))
R_{free}	100719	2028 (2.08-2.04)
Clashscore	112137	2143 (2.08-2.04)
Ramachandran outliers	110173	2126 (2.08-2.04)
Sidechain outliers	110143	2126 (2.08-2.04)
RSRZ outliers	101464	2035 (2.08-2.04)

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 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.

Mol	Chain	Length	Quality of chain
1	A	691	<div> <div>4%</div> <div> <div></div> <div>90%</div> <div>6%</div> <div></div> </div> </div>
1	B	691	<div> <div>5%</div> <div> <div></div> <div>92%</div> <div>5%</div> <div></div> </div> </div>

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 22560 atoms, of which 10654 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 Arachidonate 5-lipoxygenase.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	669	Total	C	H	N	O	S	0	2	0
			10766	3492	5316	922	1010	26			
1	B	676	Total	C	H	N	O	S	0	1	0
			10836	3519	5338	938	1015	26			

There are 64 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-17	MET	-	EXPRESSION TAG	UNP P09917
A	-16	GLY	-	EXPRESSION TAG	UNP P09917
A	-15	SER	-	EXPRESSION TAG	UNP P09917
A	-14	SER	-	EXPRESSION TAG	UNP P09917
A	-13	HIS	-	EXPRESSION TAG	UNP P09917
A	-12	HIS	-	EXPRESSION TAG	UNP P09917
A	-11	HIS	-	EXPRESSION TAG	UNP P09917
A	-10	HIS	-	EXPRESSION TAG	UNP P09917
A	-9	HIS	-	EXPRESSION TAG	UNP P09917
A	-8	HIS	-	EXPRESSION TAG	UNP P09917
A	-7	SER	-	EXPRESSION TAG	UNP P09917
A	-6	SER	-	EXPRESSION TAG	UNP P09917
A	-5	GLY	-	EXPRESSION TAG	UNP P09917
A	-4	LEU	-	EXPRESSION TAG	UNP P09917
A	-3	VAL	-	EXPRESSION TAG	UNP P09917
A	-2	PRO	-	EXPRESSION TAG	UNP P09917
A	-1	ARG	-	EXPRESSION TAG	UNP P09917
A	0	GLY	-	EXPRESSION TAG	UNP P09917
A	1	SER	-	EXPRESSION TAG	UNP P09917
A	2	HIS	-	EXPRESSION TAG	UNP P09917
A	16	GLU	TRP	ENGINEERED MUTATION	UNP P09917
A	17	HIS	PHE	ENGINEERED MUTATION	UNP P09917
A	43	GLY	ASN	SEE REMARK 999	UNP P09917
A	44	SER	ASP	SEE REMARK 999	UNP P09917
A	75	GLY	TRP	ENGINEERED MUTATION	UNP P09917

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Chain	Residue	Modelled	Actual	Comment	Reference
A	76	SER	LEU	ENGINEERED MUTATION	UNP P09917
A	240	ALA	CYS	ENGINEERED MUTATION	UNP P09917
A	561	ALA	CYS	ENGINEERED MUTATION	UNP P09917
A	653	GLU	LYS	ENGINEERED MUTATION	UNP P09917
A	654	ASN	LYS	ENGINEERED MUTATION	UNP P09917
A	655	LEU	LYS	ENGINEERED MUTATION	UNP P09917
A	663	ASP	SER	ENGINEERED MUTATION	UNP P09917
B	-11	MET	-	EXPRESSION TAG	UNP P09917
B	-10	GLY	-	EXPRESSION TAG	UNP P09917
B	-9	SER	-	EXPRESSION TAG	UNP P09917
B	-8	SER	-	EXPRESSION TAG	UNP P09917
B	-7	HIS	-	EXPRESSION TAG	UNP P09917
B	-6	HIS	-	EXPRESSION TAG	UNP P09917
B	-5	HIS	-	EXPRESSION TAG	UNP P09917
B	-4	HIS	-	EXPRESSION TAG	UNP P09917
B	-3	HIS	-	EXPRESSION TAG	UNP P09917
B	-2	HIS	-	EXPRESSION TAG	UNP P09917
B	-1	SER	-	EXPRESSION TAG	UNP P09917
B	-1A	SER	-	EXPRESSION TAG	UNP P09917
B	-1B	GLY	-	EXPRESSION TAG	UNP P09917
B	-1C	LEU	-	EXPRESSION TAG	UNP P09917
B	-1D	VAL	-	EXPRESSION TAG	UNP P09917
B	-1E	PRO	-	EXPRESSION TAG	UNP P09917
B	-1F	ARG	-	EXPRESSION TAG	UNP P09917
B	-1G	GLY	-	EXPRESSION TAG	UNP P09917
B	-1H	SER	-	EXPRESSION TAG	UNP P09917
B	-1I	HIS	-	EXPRESSION TAG	UNP P09917
B	16	GLU	TRP	ENGINEERED MUTATION	UNP P09917
B	17	HIS	PHE	ENGINEERED MUTATION	UNP P09917
B	43	GLY	ASN	SEE REMARK 999	UNP P09917
B	44	SER	ASP	SEE REMARK 999	UNP P09917
B	75	GLY	TRP	ENGINEERED MUTATION	UNP P09917
B	76	SER	LEU	ENGINEERED MUTATION	UNP P09917
B	240	ALA	CYS	ENGINEERED MUTATION	UNP P09917
B	561	ALA	CYS	ENGINEERED MUTATION	UNP P09917
B	653	GLU	LYS	ENGINEERED MUTATION	UNP P09917
B	654	ASN	LYS	ENGINEERED MUTATION	UNP P09917
B	655	LEU	LYS	ENGINEERED MUTATION	UNP P09917
B	663	ASP	SER	ENGINEERED MUTATION	UNP P09917

- Molecule 2 is FE (II) ION (three-letter code: FE2) (formula: Fe).

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

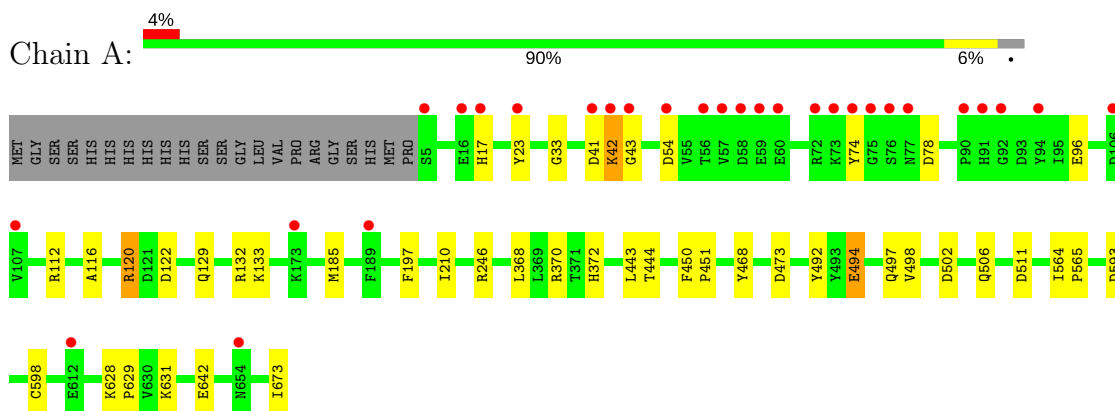
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	482	Total 482	O 482	0	0
3	B	474	Total 474	O 474	0	0

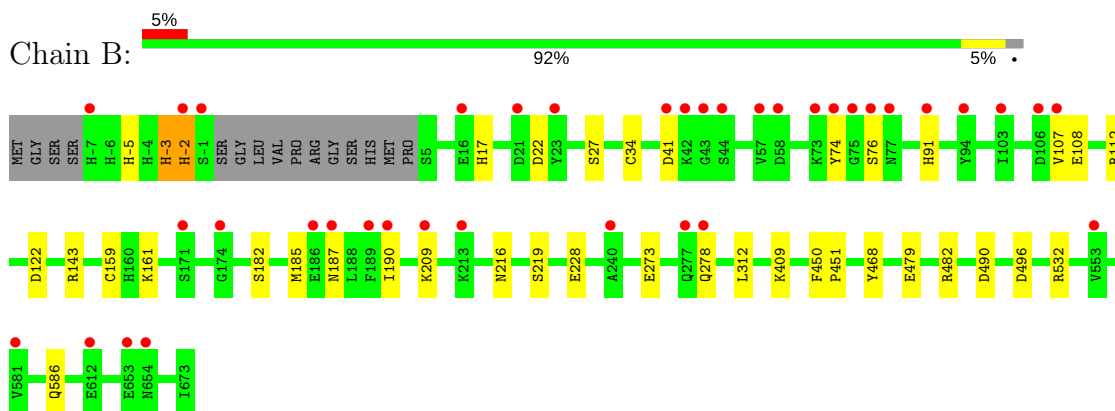
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA 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 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.

• Molecule 1: Arachidonate 5-lipoxygenase



• Molecule 1: Arachidonate 5-lipoxygenase



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	55.41Å 202.50Å 76.97Å 90.00° 109.82° 90.00°	Depositor
Resolution (Å)	41.49 – 2.07 45.81 – 2.07	Depositor EDS
% Data completeness (in resolution range)	94.3 (41.49-2.07) 94.3 (45.81-2.07)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.11 (at 2.07Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.7.2_869)	Depositor
R, R_{free}	0.166 , 0.197 0.161 , 0.190	Depositor DCC
R_{free} test set	1986 reflections (2.18%)	DCC
Wilson B-factor (Å ²)	19.1	Xtriage
Anisotropy	0.390	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.46 , 51.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.029 for h,-k,-h-l	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	22560	wwPDB-VP
Average B, all atoms (Å ²)	28.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.35% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

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: FE2

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	0.24	0/5591	0.41	0/7586
1	B	0.22	0/5642	0.41	0/7654
All	All	0.23	0/11233	0.41	0/15240

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	1
1	B	0	1
All	All	0	2

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	33	GLY	Mainchain
1	B	34	CYS	Mainchain

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	5450	5316	5335	29	0
1	B	5498	5338	5368	18	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
3	A	482	0	0	9	0
3	B	474	0	0	9	0
All	All	11906	10654	10703	47	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 2.

The worst 5 of 47 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:96:GLU:OE1	3:A:1194:HOH:O	1.87	0.91
1:B:-3:HIS:ND1	1:B:-3:HIS:N	2.36	0.73
1:B:228:GLU:OE2	3:B:1121:HOH:O	2.07	0.71
1:B:532:ARG:NH1	3:B:1214:HOH:O	2.04	0.70
1:B:-2:HIS:ND1	1:B:-2:HIS:N	2.37	0.69

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	669/691 (97%)	649 (97%)	19 (3%)	1 (0%)	55	48
1	B	673/691 (97%)	655 (97%)	18 (3%)	0	100	100
All	All	1342/1382 (97%)	1304 (97%)	37 (3%)	1 (0%)	55	48

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	42	LYS

5.3.2 Protein sidechains [i](#)

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	591/608 (97%)	583 (99%)	8 (1%)	71	69
1	B	595/608 (98%)	579 (97%)	16 (3%)	50	44
All	All	1186/1216 (98%)	1162 (98%)	24 (2%)	62	56

5 of 24 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	-2	HIS
1	B	74	TYR
1	B	490	ASP
1	B	27	SER
1	B	41	ASP

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

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

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

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 [i](#)

6.1 Protein, DNA and RNA chains [i](#)

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	669/691 (96%)	-0.00	29 (4%) 36 37	12, 21, 55, 91	0
1	B	676/691 (97%)	0.07	38 (5%) 25 26	11, 21, 54, 94	0
All	All	1345/1382 (97%)	0.03	67 (4%) 30 30	11, 21, 55, 94	0

The worst 5 of 67 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	74	TYR	11.1
1	B	189	PHE	7.2
1	A	74	TYR	7.2
1	B	76	SER	5.6
1	B	42	LYS	5.5

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

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

6.3 Carbohydrates [i](#)

There are no carbohydrates in this entry.

6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled ‘Q< 0.9’ lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
2	FE2	A	701	1/1	1.00	0.16	1.63	12,12,12,12	0
2	FE2	B	701	1/1	1.00	0.14	-0.46	11,11,11,11	0

6.5 Other polymers [i](#)

There are no such residues in this entry.