



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 29, 2021 – 04:08 PM EDT

PDB ID : 1PVP
Title : BASIS FOR A SWITCH IN SUBSTRATE SPECIFICITY: CRYSTAL STRUCTURE OF SELECTED VARIANT OF CRE SITE-SPECIFIC RECOMBINASE, ALSHG BOUND TO THE ENGINEERED RECOGNITION SITE LOXM7
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Deposited on : 2003-06-28
Resolution : 2.35 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

<https://www.wwpdb.org/validation/2017/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)	:	1.13
EDS	:	2.18
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.18

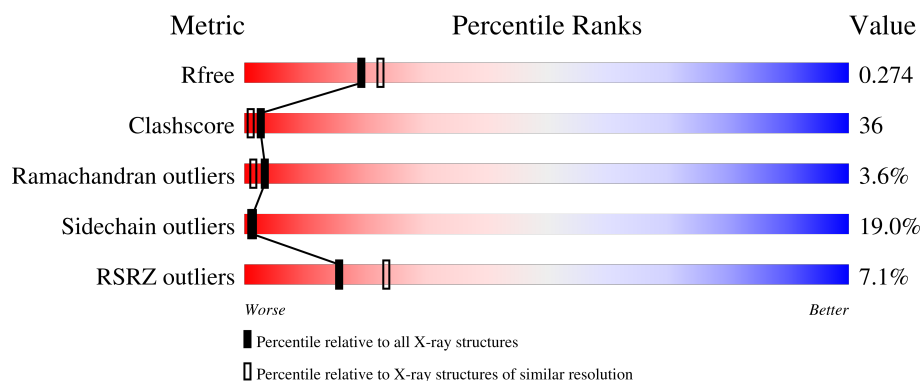
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.35 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}	130704	1164 (2.36-2.36)
Clashscore	141614	1232 (2.36-2.36)
Ramachandran outliers	138981	1211 (2.36-2.36)
Sidechain outliers	138945	1212 (2.36-2.36)
RSRZ outliers	127900	1150 (2.36-2.36)

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 $\leq 5\%$. 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	C	34	<div> <div>9%</div> <div>29%</div> <div>59%</div> <div>9%</div> <div>.</div> </div>
2	D	34	<div> <div>3%</div> <div>18%</div> <div>71%</div> <div>12%</div> </div>
3	A	349	<div> <div>11%</div> <div>39%</div> <div>40%</div> <div>11%</div> <div>.</div> <div>7%</div> </div>
3	B	349	<div> <div>2%</div> <div>38%</div> <div>45%</div> <div>9%</div> <div>9%</div> </div>

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 6738 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 DNA chain called 34-MER.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	C	33	Total	C	N	O	P	0	0	1
			655	317	115	192	31			

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	7	DC	DT	engineered mutation	GB M10145
C	8	DT	DC	engineered mutation	GB M10145
C	9	DA	DG	engineered mutation	GB M10145
C	26	DT	DC	engineered mutation	GB M10145
C	27	DA	DG	engineered mutation	GB M10145
C	28	DG	DA	engineered mutation	GB M10145

- Molecule 2 is a DNA chain called 34-MER.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	D	34	Total	C	N	O	P	0	4	0
			774	375	138	224	37			

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
D	7	DC	DT	engineered mutation	GB M10494
D	8	DT	DC	engineered mutation	GB M10494
D	9	DA	DG	engineered mutation	GB M10494
D	26	DT	DC	engineered mutation	GB M10494
D	27	DA	DG	engineered mutation	GB M10494
D	28	DG	DA	engineered mutation	GB M10494

- Molecule 3 is a protein called Recombinase cre.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	A	323	Total 2546	C 1582	N 486	O 463	S 15	34	0	0
3	B	318	Total 2507	C 1560	N 480	O 452	S 15	27	0	0

There are 24 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-5	MET	-	initiating methionine	UNP P06956
A	-4	HIS	-	expression tag	UNP P06956
A	-3	HIS	-	expression tag	UNP P06956
A	-2	HIS	-	expression tag	UNP P06956
A	-1	HIS	-	expression tag	UNP P06956
A	0	HIS	-	expression tag	UNP P06956
A	1	HIS	-	expression tag	UNP P06956
A	174	ALA	ILE	engineered mutation	UNP P06956
A	258	LEU	THR	engineered mutation	UNP P06956
A	259	SER	ARG	engineered mutation	UNP P06956
A	262	HIS	GLU	engineered mutation	UNP P06956
A	266	GLY	GLU	engineered mutation	UNP P06956
B	-5	MET	-	initiating methionine	UNP P06956
B	-4	HIS	-	expression tag	UNP P06956
B	-3	HIS	-	expression tag	UNP P06956
B	-2	HIS	-	expression tag	UNP P06956
B	-1	HIS	-	expression tag	UNP P06956
B	0	HIS	-	expression tag	UNP P06956
B	1	HIS	-	expression tag	UNP P06956
B	174	ALA	ILE	engineered mutation	UNP P06956
B	258	LEU	THR	engineered mutation	UNP P06956
B	259	SER	ARG	engineered mutation	UNP P06956
B	262	HIS	GLU	engineered mutation	UNP P06956
B	266	GLY	GLU	engineered mutation	UNP P06956

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	C	31	Total 31	O 31	0	0
4	D	31	Total 31	O 31	0	0
4	A	68	Total 68	O 68	0	0
4	B	126	Total 126	O 126	0	0

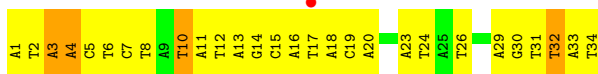
3 Residue-property plots [i](#)

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 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.

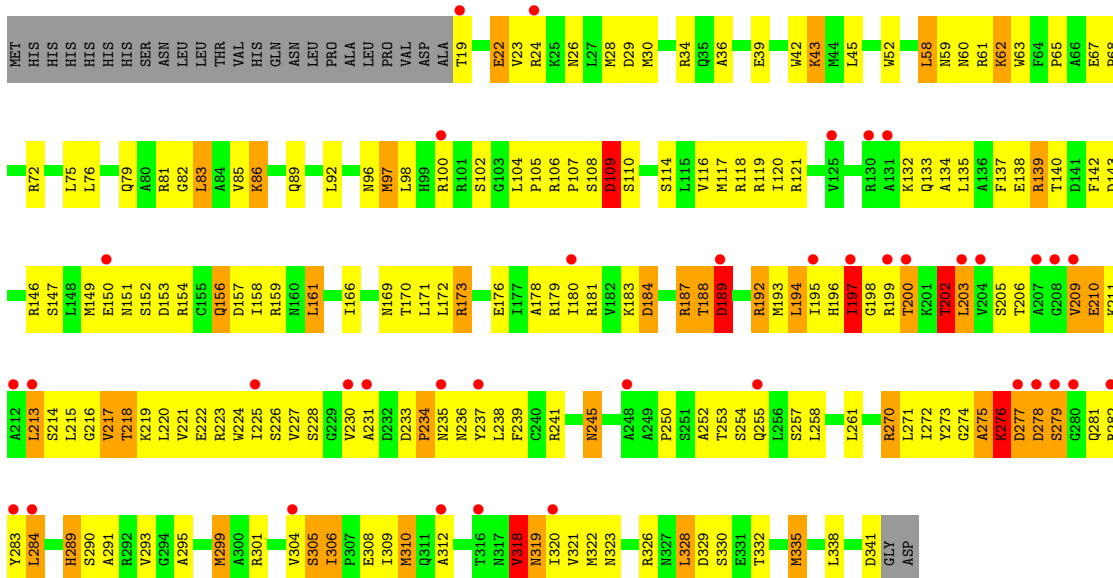
• Molecule 1: 34-MER



• Molecule 2: 34-MER

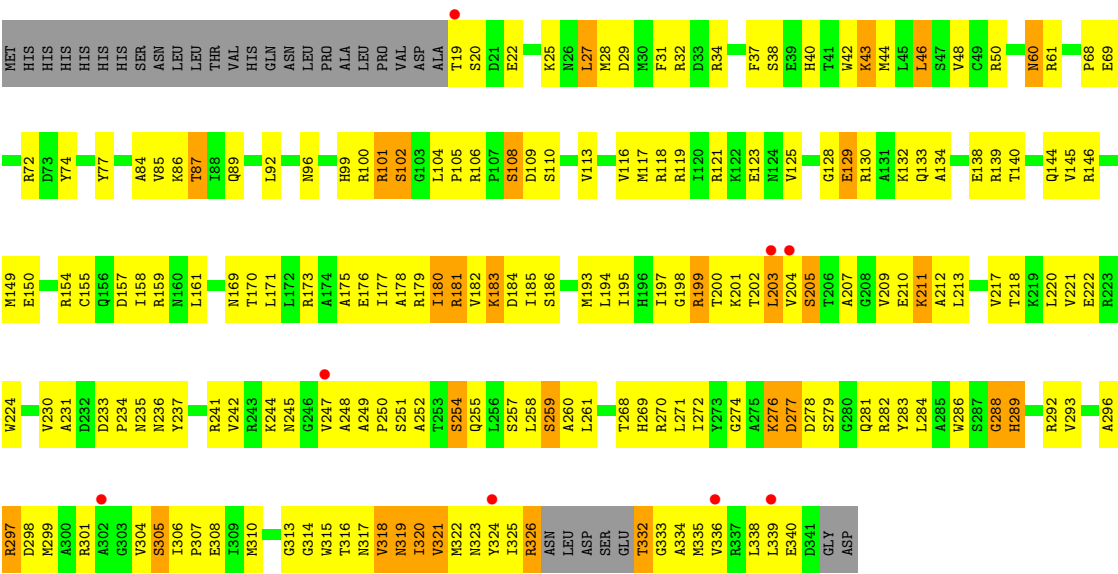


• Molecule 3: Recombinase cre



• Molecule 3: Recombinase cre





4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	107.78Å 121.47Å 180.69Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	5.00 – 2.35 80.62 – 2.35	Depositor EDS
% Data completeness (in resolution range)	95.0 (5.00-2.35) 94.6 (80.62-2.35)	Depositor EDS
R_{merge}	0.04	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.78 (at 2.34Å)	Xtriage
Refinement program	TNT	Depositor
R, R_{free}	0.232 , 0.294 0.235 , 0.274	Depositor DCC
R_{free} test set	2180 reflections (4.65%)	wwPDB-VP
Wilson B-factor (Å ²)	47.6	Xtriage
Anisotropy	0.301	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 85.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	6738	wwPDB-VP
Average B, all atoms (Å ²)	56.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.73% 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

5.1 Standard geometry

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	C	0.60	0/733	1.43	5/1129 (0.4%)
2	D	0.80	1/868 (0.1%)	1.43	11/1337 (0.8%)
3	A	0.37	0/2588	0.72	3/3490 (0.1%)
3	B	0.42	1/2548 (0.0%)	0.71	0/3434
All	All	0.49	2/6737 (0.0%)	0.96	19/9390 (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
3	A	1	0

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	10	DT	C5-C7	8.08	1.54	1.50
3	B	259	SER	CB-OG	5.91	1.50	1.42

The worst 5 of 19 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	4	DA	O4'-C1'-N9	9.59	114.71	108.00
3	A	173	ARG	NE-CZ-NH1	-8.48	116.06	120.30
2	D	3	DA	O4'-C4'-C3'	-7.90	101.26	106.00
1	C	7	DC	P-O3'-C3'	7.89	129.17	119.70
3	A	202	THR	N-CA-C	7.78	132.01	111.00

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
3	A	202	THR	CA

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	C	655	0	368	28	0
2	D	774	0	434	62	0
3	A	2546	0	2566	197	0
3	B	2507	0	2533	173	0
4	A	68	0	0	13	0
4	B	126	0	0	6	0
4	C	31	0	0	1	0
4	D	31	0	0	3	0
All	All	6738	0	5901	436	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 36.

The worst 5 of 436 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)
2:D:33:DA:H2''	2:D:34:DT:H5''	1.30	1.11
2:D:15:DC:H2'	2:D:16[B]:DA:C8	1.88	1.07
2:D:15:DC:C2'	2:D:16[B]:DA:C8	2.47	0.97
2:D:1:DA:N7	4:D:63:HOH:O	2.03	0.92
3:B:193:MET:HE1	3:B:221:VAL:HG11	1.52	0.91

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	
3	A	321/349 (92%)	269 (84%)	35 (11%)	17 (5%)	2	0
3	B	314/349 (90%)	290 (92%)	18 (6%)	6 (2%)	8	6
All	All	635/698 (91%)	559 (88%)	53 (8%)	23 (4%)	3	1

5 of 23 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	A	202	THR
3	A	210	GLU
3	A	234	PRO
3	A	275	ALA
3	A	278	ASP

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	
3	A	268/291 (92%)	209 (78%)	59 (22%)	1	0
3	B	263/291 (90%)	221 (84%)	42 (16%)	2	2
All	All	531/582 (91%)	430 (81%)	101 (19%)	1	1

5 of 101 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	A	335	MET

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Mol	Chain	Res	Type
3	B	101	ARG
3	B	332	THR
3	B	19	THR
3	B	38	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 17 such sidechains are listed below:

Mol	Chain	Res	Type
3	B	281	GLN
3	B	319	ASN
3	A	245	ASN
3	A	281	GLN
3	A	319	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 monosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
2	D	2

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	D	15:DC	O3'	16[B]:DA	P	1.84
1	D	19[B]:DC	O3'	20:DA	P	1.26

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	C	33/34 (97%)	0.27	3 (9%) 9 14	32, 54, 85, 100	0
2	D	34/34 (100%)	0.26	1 (2%) 51 62	35, 48, 76, 78	0
3	A	322/349 (92%)	0.90	38 (11%) 4 7	27, 61, 96, 99	9 (2%)
3	B	318/349 (91%)	0.51	8 (2%) 57 67	25, 45, 87, 98	7 (2%)
All	All	707/766 (92%)	0.66	50 (7%) 16 23	25, 54, 93, 100	16 (2%)

The worst 5 of 50 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	A	204	VAL	6.6
3	A	225	ILE	6.1
3	A	208	GLY	5.4
3	A	197	ILE	5.2
3	A	283	TYR	4.8

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 monosaccharides in this entry.

6.4 Ligands [i](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.