



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 20, 2026 – 12:34 AM UTC

PDB ID : 2HP5 / pdb_00002hp5
Title : Crystal Structure of the OXA-10 W154G mutant at pH 7.0
Authors : Kerff, F.; Falzone, C.; Herman, R.; Sauvage, E.; Charlier, P.
Deposited on : 2006-07-17
Resolution : 2.70 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 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
Mogul : 2022.3.0, CSD as543be (2022)
Xtriage (Phenix) : 2.0
EDS : 3.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

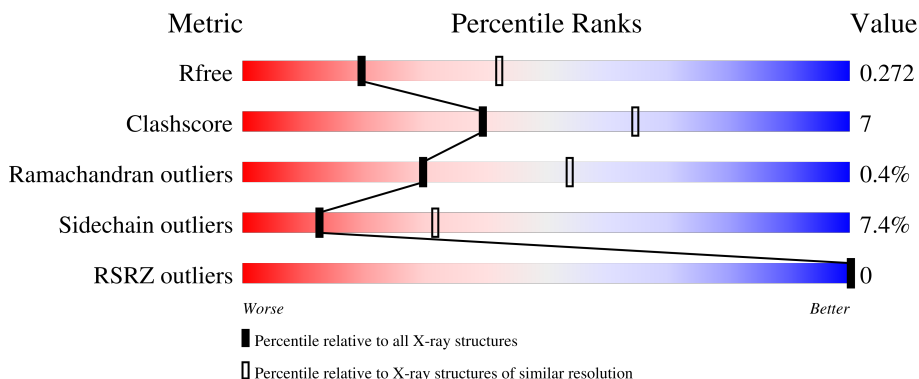
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.70 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}	180053	3538 (2.70-2.70)
Clashscore	190562	3843 (2.70-2.70)
Ramachandran outliers	187476	3778 (2.70-2.70)
Sidechain outliers	187428	3778 (2.70-2.70)
RSRZ outliers	180081	3538 (2.70-2.70)

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	A	248	
1	B	248	
1	C	248	
1	D	248	

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 7622 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 Beta-lactamase PSE-2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	246	Total 1933	C 1234	N 325	O 367	S 7	0	0	0
1	B	238	Total 1875	C 1196	N 316	O 356	S 7	0	0	0
1	C	231	Total 1825	C 1167	N 307	O 345	S 6	0	0	0
1	D	233	Total 1842	C 1178	N 309	O 349	S 6	0	0	0

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	19	MET	-	cloning artifact	UNP P14489
A	154	GLY	TRP	engineered mutation	UNP P14489
B	19	MET	-	cloning artifact	UNP P14489
B	154	GLY	TRP	engineered mutation	UNP P14489
C	19	MET	-	cloning artifact	UNP P14489
C	154	GLY	TRP	engineered mutation	UNP P14489
D	19	MET	-	cloning artifact	UNP P14489
D	154	GLY	TRP	engineered mutation	UNP P14489

- Molecule 2 is SULFATE ION (CCD ID: SO4) (formula: O₄S).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total O S 5 4 1	0	0
2	A	1	Total O S 5 4 1	0	0
2	B	1	Total O S 5 4 1	0	0
2	B	1	Total O S 5 4 1	0	0
2	B	1	Total O S 5 4 1	0	0
2	C	1	Total O S 5 4 1	0	0
2	C	1	Total O S 5 4 1	0	0
2	D	1	Total O S 5 4 1	0	0
2	D	1	Total O S 5 4 1	0	0
2	D	1	Total O S 5 4 1	0	0

- Molecule 3 is COBALT (II) ION (CCD ID: CO) (formula: Co).

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

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	C	1	Total Co 1 1	0	0
3	D	1	Total Co 1 1	0	0

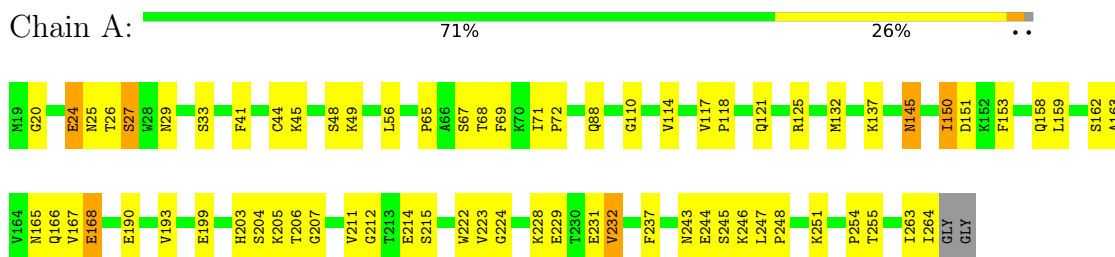
- Molecule 4 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	25	Total O 25 25	0	0
4	B	28	Total O 28 28	0	0
4	C	24	Total O 24 24	0	0
4	D	16	Total O 16 16	0	0

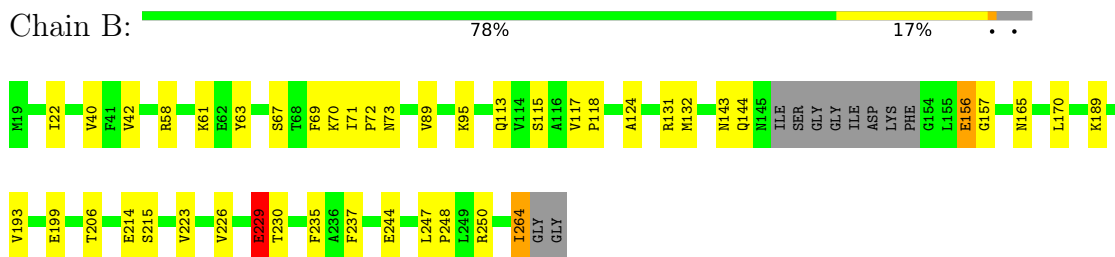
3 Residue-property plots [i](#)

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.

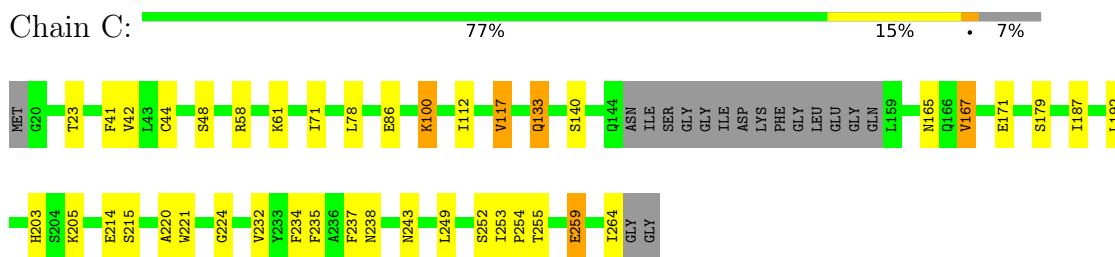
- Molecule 1: Beta-lactamase PSE-2



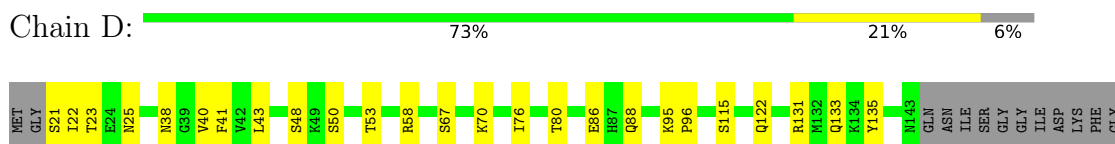
- Molecule 1: Beta-lactamase PSE-2



- Molecule 1: Beta-lactamase PSE-2



- Molecule 1: Beta-lactamase PSE-2



L155	E196	I161	Y174	Q185	V202	T206	V211	G212	T213	E214	S215	N216	P217	A220	W221	W222	V226	E227	V232	F237	N238	D242	K246	L247	P248	L249	P254	E261	G262	I263	L264	GLY	GLY
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4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	47.11Å 125.40Å 92.36Å 90.00° 99.80° 90.00°	Depositor
Resolution (Å)	46.47 – 2.70 46.47 – 2.70	Depositor EDS
% Data completeness (in resolution range)	98.8 (46.47-2.70) 98.8 (46.47-2.70)	Depositor EDS
R_{merge}	0.12	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.54 (at 2.69Å)	Xtrriage
Refinement program	REFMAC 5.2.0005	Depositor
R, R_{free}	0.210 , 0.267 0.212 , 0.272	Depositor DCC
R_{free} test set	1437 reflections (4.94%)	wwPDB-VP
Wilson B-factor (Å ²)	35.8	Xtrriage
Anisotropy	0.232	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 23.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.44$, $\langle L^2 \rangle = 0.26$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	7622	wwPDB-VP
Average B, all atoms (Å ²)	32.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.53% 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: SO4, CO

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	0.55	0/1972	0.88	0/2662
1	B	0.48	0/1912	0.81	1/2581 (0.0%)
1	C	0.48	1/1862 (0.1%)	0.83	1/2515 (0.0%)
1	D	0.47	0/1879	0.85	3/2538 (0.1%)
All	All	0.50	1/7625 (0.0%)	0.84	5/10296 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	117	VAL	CA-CB	5.77	1.57	1.54

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	261	GLU	N-CA-C	-6.19	106.95	114.75
1	D	95	LYS	CA-C-N	5.89	127.20	119.84
1	D	95	LYS	C-N-CA	5.89	127.20	119.84
1	C	214	GLU	N-CA-C	-5.82	107.99	114.62
1	B	229	GLU	CB-CA-C	-5.06	110.72	116.54

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	1933	0	1932	42	0
1	B	1875	0	1872	17	0
1	C	1825	0	1826	18	0
1	D	1842	0	1843	24	0
2	A	10	0	0	0	0
2	B	15	0	0	0	0
2	C	10	0	0	0	0
2	D	15	0	0	0	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
3	C	1	0	0	0	0
3	D	1	0	0	0	0
4	A	25	0	0	1	0
4	B	28	0	0	0	0
4	C	24	0	0	0	0
4	D	16	0	0	0	0
All	All	7622	0	7473	100	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 7.

The worst 5 of 100 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:211:VAL:HG22	1:A:212:GLY:H	1.47	0.79
1:B:40:VAL:HB	1:B:58:ARG:HG2	1.65	0.77
1:D:155:LEU:HG	1:D:156:GLU:H	1.49	0.77
1:A:41:PHE:CE1	1:A:254:PRO:HB3	2.24	0.72
1:C:165:ASN:C	1:C:165:ASN:HD22	2.02	0.67

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	244/248 (98%)	220 (90%)	23 (9%)	1 (0%)	30	54
1	B	234/248 (94%)	223 (95%)	11 (5%)	0	100	100
1	C	227/248 (92%)	215 (95%)	12 (5%)	0	100	100
1	D	229/248 (92%)	207 (90%)	19 (8%)	3 (1%)	9	25
All	All	934/992 (94%)	865 (93%)	65 (7%)	4 (0%)	30	54

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	263	ILE
1	A	150	ILE
1	D	96	PRO
1	D	211	VAL

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	210/210 (100%)	192 (91%)	18 (9%)	10	25
1	B	204/210 (97%)	188 (92%)	16 (8%)	11	29
1	C	199/210 (95%)	185 (93%)	14 (7%)	14	34
1	D	201/210 (96%)	189 (94%)	12 (6%)	17	41
All	All	814/840 (97%)	754 (93%)	60 (7%)	13	32

5 of 60 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	189	LYS
1	D	161	ILE
1	C	48	SER
1	D	133	GLN
1	D	227	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 18

such sidechains are listed below:

Mol	Chain	Res	Type
1	D	25	ASN
1	D	243	ASN
1	D	158	GLN
1	C	38	ASN
1	C	216	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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 14 ligands modelled in this entry, 4 are monoatomic - leaving 10 for Mogul analysis.

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	$\# Z > 2$
2	SO4	C	267	-	4,4,4	0.24	0	6,6,6	0.15	0
2	SO4	B	269	-	4,4,4	0.22	0	6,6,6	0.11	0
2	SO4	D	268	-	4,4,4	0.24	0	6,6,6	0.20	0
2	SO4	A	267	-	4,4,4	0.24	0	6,6,6	0.19	0
2	SO4	B	268	-	4,4,4	0.22	0	6,6,6	0.13	0
2	SO4	C	268	-	4,4,4	0.23	0	6,6,6	0.14	0
2	SO4	B	267	-	4,4,4	0.26	0	6,6,6	0.14	0
2	SO4	D	267	-	4,4,4	0.26	0	6,6,6	0.13	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	SO4	A	268	-	4,4,4	0.23	0	6,6,6	0.13	0
2	SO4	D	269	-	4,4,4	0.25	0	6,6,6	0.05	0

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 [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	246/248 (99%)	-1.55	0 100 100	10, 30, 55, 80	0
1	B	238/248 (95%)	-1.58	0 100 100	13, 32, 48, 63	0
1	C	231/248 (93%)	-1.56	0 100 100	22, 32, 44, 60	0
1	D	233/248 (93%)	-1.52	0 100 100	10, 31, 45, 60	0
All	All	948/992 (95%)	-1.55	0 100 100	10, 31, 47, 80	0

There are no RSRZ outliers to report.

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 oligosaccharides 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. 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	B-factors(Å ²)	Q<0.9
2	SO4	B	269	5/5	0.98	0.08	63,64,65,65	0
2	SO4	C	268	5/5	0.98	0.09	38,38,39,39	0
2	SO4	D	269	5/5	0.98	0.07	58,59,59,60	0
2	SO4	B	268	5/5	0.99	0.04	48,48,49,49	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
2	SO4	D	268	5/5	0.99	0.05	38,39,39,39	0
2	SO4	A	268	5/5	0.99	0.06	45,46,47,47	0
2	SO4	A	267	5/5	1.00	0.04	16,16,18,20	0
2	SO4	D	267	5/5	1.00	0.03	39,39,40,40	0
2	SO4	B	267	5/5	1.00	0.05	17,21,22,22	0
2	SO4	C	267	5/5	1.00	0.03	21,21,24,24	0
3	CO	A	269	1/1	1.00	0.04	24,24,24,24	0
3	CO	B	270	1/1	1.00	0.02	27,27,27,27	0
3	CO	C	269	1/1	1.00	0.02	29,29,29,29	0
3	CO	D	270	1/1	1.00	0.04	43,43,43,43	0

6.5 Other polymers [i](#)

There are no such residues in this entry.