



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 9, 2026 – 09:34 AM UTC

PDB ID : 3IXT / pdb_00003ixt
Title : Crystal Structure of Motavizumab Fab Bound to Peptide Epitope
Authors : McLellan, J.S.; Chen, M.; Kim, A.; Yang, Y.; Graham, B.S.; Kwong, P.D.
Deposited on : 2009-09-04
Resolution : 2.75 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)
Xtrriage (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

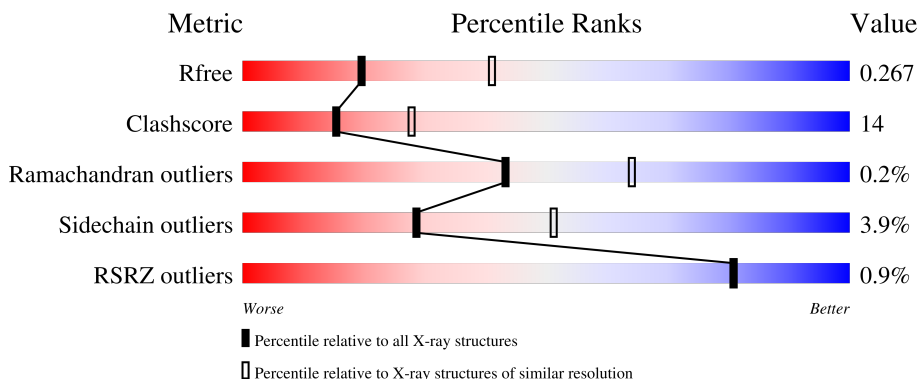
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.75 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	1009 (2.76-2.76)
Clashscore	190562	1044 (2.76-2.76)
Ramachandran outliers	187476	1024 (2.76-2.76)
Sidechain outliers	187428	1024 (2.76-2.76)
RSRZ outliers	180081	1009 (2.76-2.76)

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	B	213	 78% 19% ..
1	L	213	 79% 17% ..
2	A	225	 66% 28% 6%
2	H	225	 67% 27% 5%
3	C	26	 8% 65% 31% .

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Mol	Chain	Length	Quality of chain
3	P	26	 <p>A horizontal bar chart representing the quality of chain. The bar is divided into segments: a red segment at the beginning labeled '12%', a green segment in the middle labeled '50%', and a yellow segment at the end labeled '42%'. There are two small red dots at the far right end of the bar.</p>

2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 7010 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 Motavizumab Fab light chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	L	211	Total 1611	C 1012	N 268	O 325	S 6	0	0	0
1	B	210	Total 1607	C 1010	N 267	O 324	S 6	0	0	0

- Molecule 2 is a protein called Motavizumab Fab heavy chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	H	213	Total 1626	C 1039	N 266	O 314	S 7	0	0	0
2	A	212	Total 1620	C 1036	N 265	O 312	S 7	0	0	0

- Molecule 3 is a protein called Fusion glycoprotein F1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
3	P	26	Total 192	C 116	N 33	O 41	S 2	0	0	1
3	C	26	Total 192	C 116	N 33	O 41	S 2	0	0	1

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
P	253	ACE	-	acetylation	UNP P03420
P	278	NH2	-	amidation	UNP P03420
C	253	ACE	-	acetylation	UNP P03420
C	278	NH2	-	amidation	UNP P03420

- Molecule 4 is 1,2-ETHANEDIOL (CCD ID: EDO) (formula: C₂H₆O₂).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	P	1	Total C O 4 2 2	0	0
4	A	1	Total C O 4 2 2	0	0
4	C	1	Total C O 4 2 2	0	0


- Molecule 5 is water.

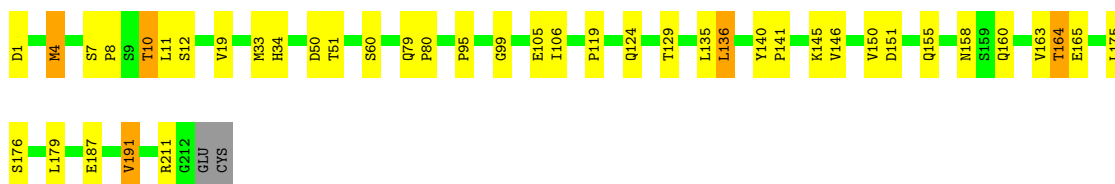
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	L	36	Total O 36 36	0	0
5	H	40	Total O 40 40	0	0
5	P	3	Total O 3 3	0	0
5	B	30	Total O 30 30	0	0
5	A	40	Total O 40 40	0	0
5	C	1	Total O 1 1	0	0

3 Residue-property plots


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.

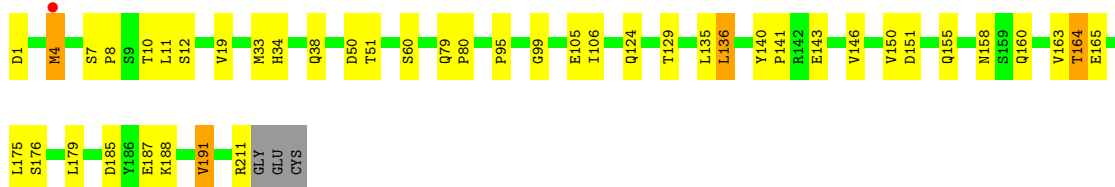
- Molecule 1: Motavizumab Fab light chain

Chain L: 



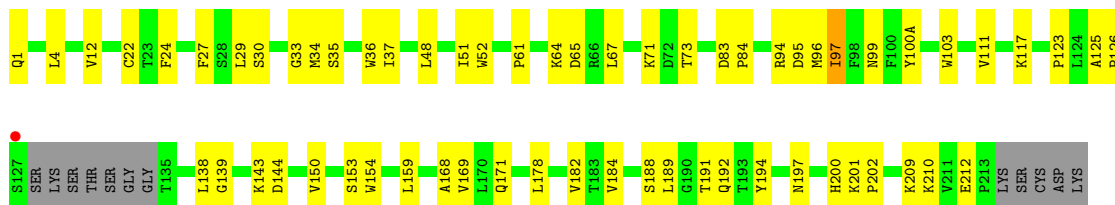
- Molecule 1: Motavizumab Fab light chain

Chain B: 



- Molecule 2: Motavizumab Fab heavy chain

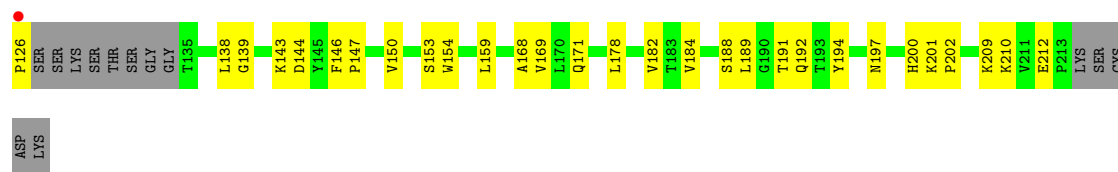
Chain H: 



- Molecule 2: Motavizumab Fab heavy chain

Chain A: 

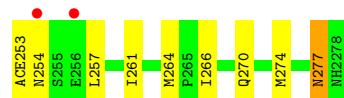




- Molecule 3: Fusion glycoprotein F1



- Molecule 3: Fusion glycoprotein F1



4 Data and refinement statistics

Property	Value	Source
Space group	P 43 21 2	Depositor
Cell constants a, b, c, α , β , γ	90.75Å 90.75Å 232.06Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	33.26 – 2.75 33.26 – 2.75	Depositor EDS
% Data completeness (in resolution range)	89.7 (33.26-2.75) 89.9 (33.26-2.75)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.26 (at 2.76Å)	Xtrriage
Refinement program	PHENIX (phenix.refine)	Depositor
R, R_{free}	0.213 , 0.274 0.209 , 0.267	Depositor DCC
R_{free} test set	1195 reflections (4.85%)	wwPDB-VP
Wilson B-factor (Å ²)	54.1	Xtrriage
Anisotropy	0.127	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 56.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.46$, $\langle L^2 \rangle = 0.29$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	7010	wwPDB-VP
Average B, all atoms (Å ²)	58.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 21.28 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 7.2550e-03. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

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: ACE, NH2, EDO

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	B	0.29	0/1644	0.74	0/2230
1	L	0.31	0/1648	0.73	0/2235
2	A	0.30	0/1663	0.69	0/2275
2	H	0.30	0/1669	0.70	0/2283
3	C	0.39	0/189	0.82	0/254
3	P	0.36	0/189	0.87	1/254 (0.4%)
All	All	0.30	0/7002	0.72	1/9531 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	P	277	ASN	CA-CB-CG	5.62	118.22	112.60

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	B	1607	0	1561	41	0
1	L	1611	0	1564	42	0
2	A	1620	0	1605	51	0
2	H	1626	0	1610	52	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	C	192	0	194	6	0
3	P	192	0	194	10	0
4	A	4	0	6	0	0
4	C	4	0	6	0	0
4	P	4	0	6	1	0
5	A	40	0	0	0	0
5	B	30	0	0	2	0
5	C	1	0	0	0	0
5	H	40	0	0	1	0
5	L	36	0	0	1	0
5	P	3	0	0	0	0
All	All	7010	0	6746	184	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 14.

The worst 5 of 184 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:A:99:ASN:HB2	2:A:100(A):TYR:CE1	2.09	0.88
2:A:126:PRO:HG3	2:A:138:LEU:HB3	1.56	0.87
2:H:4:LEU:HD23	2:H:24:PHE:HB3	1.58	0.86
2:H:99:ASN:HB2	2:H:100(A):TYR:CE1	2.11	0.85
2:H:126:PRO:HG3	2:H:138:LEU:HB3	1.56	0.85

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	B	208/213 (98%)	199 (96%)	9 (4%)	0	100 100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	L	209/213 (98%)	199 (95%)	10 (5%)	0	100	100
2	A	208/225 (92%)	195 (94%)	13 (6%)	0	100	100
2	H	209/225 (93%)	198 (95%)	11 (5%)	0	100	100
3	C	24/26 (92%)	21 (88%)	3 (12%)	0	100	100
3	P	24/26 (92%)	21 (88%)	1 (4%)	2 (8%)	0	0
All	All	882/928 (95%)	833 (94%)	47 (5%)	2 (0%)	43	64

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	P	277	ASN
3	P	254	ASN

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	B	183/185 (99%)	175 (96%)	8 (4%)	25	47
1	L	183/185 (99%)	175 (96%)	8 (4%)	25	47
2	A	186/197 (94%)	179 (96%)	7 (4%)	29	52
2	H	187/197 (95%)	180 (96%)	7 (4%)	30	54
3	C	24/24 (100%)	23 (96%)	1 (4%)	26	49
3	P	24/24 (100%)	24 (100%)	0	100	100
All	All	787/812 (97%)	756 (96%)	31 (4%)	28	51

5 of 31 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	H	169	VAL
2	A	97	ILE
1	B	60	SER
2	A	169	VAL

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Mol	Chain	Res	Type
2	A	29	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 6 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	138	ASN
1	B	160	GLN
2	A	39	GLN
1	L	160	GLN
1	L	138	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](#)

3 ligands 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	$\# Z > 2$
4	EDO	C	2	-	3,3,3	0.45	0	2,2,2	0.30	0
4	EDO	A	219	-	3,3,3	0.44	0	2,2,2	0.32	0
4	EDO	P	1	-	3,3,3	0.38	0	2,2,2	0.51	0

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
4	EDO	C	2	-	-	0/1/1/1	-
4	EDO	A	219	-	-	0/1/1/1	-
4	EDO	P	1	-	-	0/1/1/1	-

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.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	P	1	EDO	1	0

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	B	210/213 (98%)	-0.19	1 (0%) 87 87	34, 55, 84, 105	0
1	L	211/213 (99%)	-0.10	0 100 100	32, 53, 84, 105	0
2	A	212/225 (94%)	-0.15	1 (0%) 87 87	34, 54, 84, 111	0
2	H	213/225 (94%)	-0.17	1 (0%) 87 87	33, 54, 85, 111	0
3	C	24/26 (92%)	0.60	2 (8%) 17 18	57, 82, 123, 138	0
3	P	24/26 (92%)	0.75	3 (12%) 8 6	57, 82, 123, 138	0
All	All	894/928 (96%)	-0.11	8 (0%) 81 81	32, 55, 90, 138	0

The worst 5 of 8 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	H	127	SER	2.8
3	C	254	ASN	2.8
3	C	256	GLU	2.6
1	B	4	MET	2.5
2	A	126	PRO	2.5

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 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
4	EDO	A	219	4/4	0.76	0.14	54,55,70,73	0
4	EDO	C	2	4/4	0.89	0.17	47,57,61,62	0
4	EDO	P	1	4/4	0.95	0.17	37,41,59,62	0

6.5 Other polymers [i](#)

There are no such residues in this entry.