



wwPDB X-ray Structure Validation Summary Report ⓘ

May 13, 2020 – 12:06 am BST

PDB ID : 12E8
Title : 2E8 FAB FRAGMENT
Authors : Rupp, B.; Trakhanov, S.
Deposited on : 1998-03-14
Resolution : 1.90 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	:	2.11
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)	:	2.11

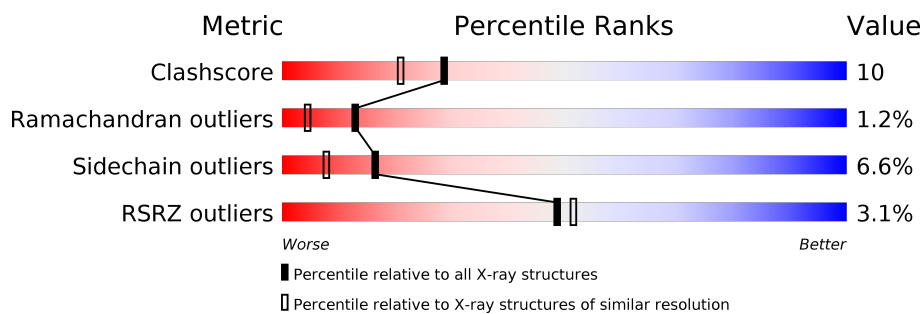
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.90 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	141614	6847 (1.90-1.90)
Ramachandran outliers	138981	6760 (1.90-1.90)
Sidechain outliers	138945	6760 (1.90-1.90)
RSRZ outliers	127900	6082 (1.90-1.90)

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 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	L	214	<div> <div>2%</div> <div>79%</div> <div>19%</div> <div>.</div> </div>
1	M	214	<div> <div>2%</div> <div>82%</div> <div>16%</div> <div>.</div> </div>
2	H	221	<div> <div>3%</div> <div>76%</div> <div>21%</div> <div>.</div> </div>
2	P	221	<div> <div>5%</div> <div>75%</div> <div>21%</div> <div>.</div> </div>

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 7429 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 IGG1-KAPPA 2E8 FAB (LIGHT CHAIN).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	L	214	Total	C	N	O	S	0	0	0
			1649	1020	277	342	10			
1	M	214	Total	C	N	O	S	0	0	0
			1649	1020	277	342	10			

There are 20 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
L	21	ILE	VAL	CONFLICT	GB 10121892
L	32	ALA	ASN	CONFLICT	GB 10121892
L	46	LEU	ALA	CONFLICT	GB 10121892
L	47	MET	LEU	CONFLICT	GB 10121892
L	53	ASN	TYR	CONFLICT	GB 10121892
L	56	THR	SER	CONFLICT	GB 10121892
L	78	MET	VAL	CONFLICT	GB 10121892
L	85	ASP	GLU	CONFLICT	GB 10121892
L	92	SER	ASN	CONFLICT	GB 10121892
L	163	ALA	TRP	CONFLICT	GB 10121892
M	21	ILE	VAL	CONFLICT	GB 10121892
M	32	ALA	ASN	CONFLICT	GB 10121892
M	46	LEU	ALA	CONFLICT	GB 10121892
M	47	MET	LEU	CONFLICT	GB 10121892
M	53	ASN	TYR	CONFLICT	GB 10121892
M	56	THR	SER	CONFLICT	GB 10121892
M	78	MET	VAL	CONFLICT	GB 10121892
M	85	ASP	GLU	CONFLICT	GB 10121892
M	92	SER	ASN	CONFLICT	GB 10121892
M	163	ALA	TRP	CONFLICT	GB 10121892

- Molecule 2 is a protein called IGG1-KAPPA 2E8 FAB (HEAVY CHAIN).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	H	221	Total 1682	C 1064	N 276	O 336	S 6	40	0	0
2	P	221	Total 1682	C 1064	N 276	O 336	S 6	40	0	0

There are 62 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
H	3	GLN	LYS	CONFLICT	PIR S49220
H	5	GLN	LEU	CONFLICT	PIR S49220
H	6	GLN	GLU	CONFLICT	PIR S49220
H	11	VAL	LEU	CONFLICT	PIR S49220
H	13	ARG	LYS	CONFLICT	PIR S49220
H	32	TYR	THR	CONFLICT	PIR S49220
H	34	ILE	MET	CONFLICT	PIR S49220
H	43	LYS	GLN	CONFLICT	PIR S49220
H	50	TRP	ARG	CONFLICT	PIR S49220
H	53	GLU	ALA	CONFLICT	PIR S49220
H	54	ILE	ASN	CONFLICT	PIR S49220
H	56	ASP	GLU	CONFLICT	PIR S49220
H	57	THR	ILE	CONFLICT	PIR S49220
H	58	GLU	LYS	CONFLICT	PIR S49220
H	60	VAL	ASP	CONFLICT	PIR S49220
H	66	LYS	THR	CONFLICT	PIR S49220
H	69	MET	ILE	CONFLICT	PIR S49220
H	75	SER	THR	CONFLICT	PIR S49220
H	?	-	VAL	DELETION	PIR S49220
H	93	ASN	ARG	CONFLICT	PIR S49220
H	94	ALA	ARG	CONFLICT	PIR S49220
H	96	HIS	-	INSERTION	PIR S49220
H	97	ASP	-	INSERTION	PIR S49220
H	99	ASP	GLY	CONFLICT	PIR S49220
H	100	ARG	SER	CONFLICT	PIR S49220
H	100A	GLY	SER	CONFLICT	PIR S49220
H	100B	ARG	GLN	CONFLICT	PIR S49220
H	100C	PHE	GLU	CONFLICT	PIR S49220
H	108	LEU	THR	CONFLICT	PIR S49220
H	109	VAL	LEU	CONFLICT	PIR S49220
H	113	ALA	SER	CONFLICT	PIR S49220
P	3	GLN	LYS	CONFLICT	PIR S49220
P	5	GLN	LEU	CONFLICT	PIR S49220
P	6	GLN	GLU	CONFLICT	PIR S49220
P	11	VAL	LEU	CONFLICT	PIR S49220

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Chain	Residue	Modelled	Actual	Comment	Reference
P	13	ARG	LYS	CONFLICT	PIR S49220
P	32	TYR	THR	CONFLICT	PIR S49220
P	34	ILE	MET	CONFLICT	PIR S49220
P	43	LYS	GLN	CONFLICT	PIR S49220
P	50	TRP	ARG	CONFLICT	PIR S49220
P	53	GLU	ALA	CONFLICT	PIR S49220
P	54	ILE	ASN	CONFLICT	PIR S49220
P	56	ASP	GLU	CONFLICT	PIR S49220
P	57	THR	ILE	CONFLICT	PIR S49220
P	58	GLU	LYS	CONFLICT	PIR S49220
P	60	VAL	ASP	CONFLICT	PIR S49220
P	66	LYS	THR	CONFLICT	PIR S49220
P	69	MET	ILE	CONFLICT	PIR S49220
P	75	SER	THR	CONFLICT	PIR S49220
P	?	-	VAL	DELETION	PIR S49220
P	93	ASN	ARG	CONFLICT	PIR S49220
P	94	ALA	ARG	CONFLICT	PIR S49220
P	96	HIS	-	INSERTION	PIR S49220
P	97	ASP	-	INSERTION	PIR S49220
P	99	ASP	GLY	CONFLICT	PIR S49220
P	100	ARG	SER	CONFLICT	PIR S49220
P	100A	GLY	SER	CONFLICT	PIR S49220
P	100B	ARG	GLN	CONFLICT	PIR S49220
P	100C	PHE	GLU	CONFLICT	PIR S49220
P	108	LEU	THR	CONFLICT	PIR S49220
P	109	VAL	LEU	CONFLICT	PIR S49220
P	113	ALA	SER	CONFLICT	PIR S49220

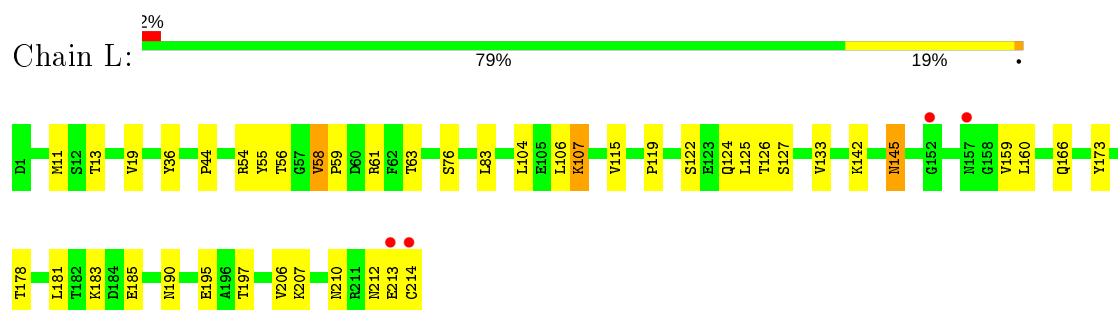
- Molecule 3 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	L	202	Total O 202 202	0	0
3	H	194	Total O 194 194	0	0
3	M	191	Total O 191 191	0	0
3	P	180	Total O 180 180	0	0

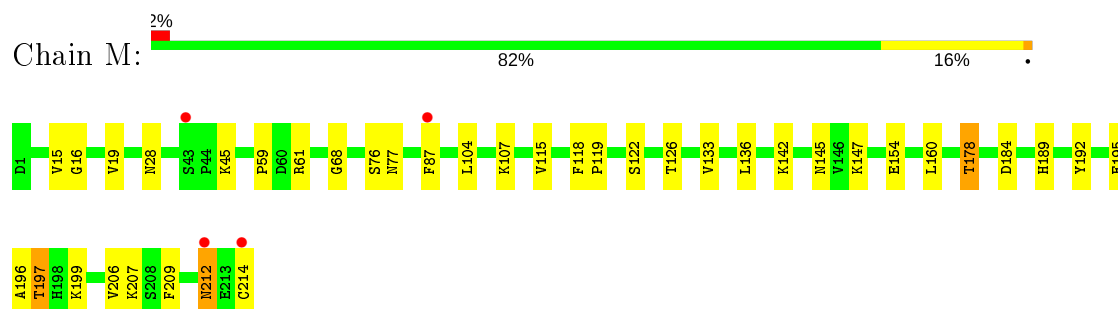
3 Residue-property plots [i](#)

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.

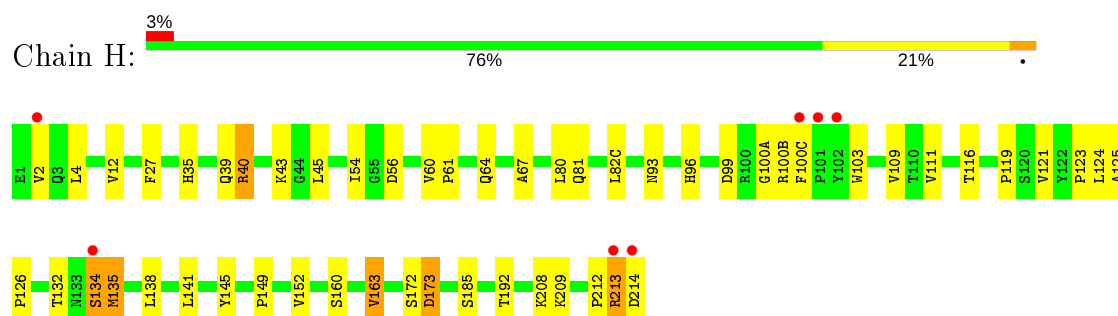
- Molecule 1: IGG1-KAPPA 2E8 FAB (LIGHT CHAIN)



- Molecule 1: IGG1-KAPPA 2E8 FAB (LIGHT CHAIN)

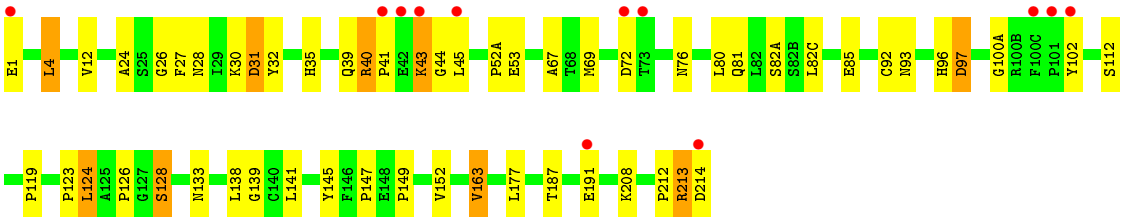


- Molecule 2: IGG1-KAPPA 2E8 FAB (HEAVY CHAIN)



- Molecule 2: IGG1-KAPPA 2E8 FAB (HEAVY CHAIN)





4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	66.56 Å 65.57 Å 103.22 Å 90.00° 97.04° 90.00°	Depositor
Resolution (Å)	20.00 – 1.90 43.82 – 1.85	Depositor EDS
% Data completeness (in resolution range)	84.4 (20.00-1.90) 80.5 (43.82-1.85)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	0.07	Depositor
$\langle I/\sigma(I) \rangle$ ¹	0.55 (at 1.84 Å)	Xtriage
Refinement program	X-PLOR 3.851	Depositor
R, R_{free}	0.221 , 0.271 0.223 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å ²)	10.9	Xtriage
Anisotropy	0.503	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 52.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	7429	wwPDB-VP
Average B, all atoms (Å ²)	16.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 11.38% 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](#)

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	L	0.52	0/1682	0.73	0/2278
1	M	0.55	0/1682	0.72	0/2278
2	H	0.50	0/1728	0.78	0/2366
2	P	0.51	0/1728	0.78	0/2366
All	All	0.52	0/6820	0.75	0/9288

There are no bond length outliers.

There are no bond angle outliers.

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	L	1649	0	1578	25	0
1	M	1649	0	1578	24	0
2	H	1682	0	1625	33	0
2	P	1682	0	1625	50	0
3	H	194	0	0	10	0
3	L	202	0	0	9	0
3	M	191	0	0	6	0
3	P	180	0	0	22	0
All	All	7429	0	6406	125	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 10.

The worst 5 of 125 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:P:32:TYR:HA	3:P:378:HOH:O	1.66	0.93
1:L:63:THR:HG23	3:L:398:HOH:O	1.76	0.84
2:H:39:GLN:HB2	2:H:45:LEU:HD23	1.58	0.83
2:P:39:GLN:HB2	2:P:45:LEU:HD23	1.60	0.83
2:P:92:CYS:SG	3:P:376:HOH:O	2.38	0.80

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	L	212/214 (99%)	208 (98%)	4 (2%)	0	100	100
1	M	212/214 (99%)	208 (98%)	4 (2%)	0	100	100
2	H	219/221 (99%)	209 (95%)	3 (1%)	7 (3%)	4	0
2	P	219/221 (99%)	207 (94%)	9 (4%)	3 (1%)	11	3
All	All	862/870 (99%)	832 (96%)	20 (2%)	10 (1%)	13	4

5 of 10 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	H	132	THR
2	H	213	ARG
2	P	128	SER
2	P	213	ARG
2	H	100(A)	GLY

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	L	189/189 (100%)	176 (93%)	13 (7%)	15	7
1	M	189/189 (100%)	176 (93%)	13 (7%)	15	7
2	H	189/189 (100%)	179 (95%)	10 (5%)	22	13
2	P	189/189 (100%)	175 (93%)	14 (7%)	13	6
All	All	756/756 (100%)	706 (93%)	50 (7%)	16	8

5 of 50 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	H	173	ASP
1	M	133	VAL
2	P	147	PRO
1	M	15	VAL
1	M	59	PRO

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 11 such sidechains are listed below:

Mol	Chain	Res	Type
2	H	81	GLN
2	H	96	HIS
1	M	212	ASN
2	H	64	GLN
1	M	137	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 carbohydrates 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](#)

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	L	214/214 (100%)	-0.10	4 (1%) 66 69	4, 13, 31, 59	0
1	M	214/214 (100%)	-0.14	4 (1%) 66 69	4, 12, 26, 62	0
2	H	215/221 (97%)	-0.08	7 (3%) 46 49	5, 12, 30, 49	0
2	P	215/221 (97%)	0.08	12 (5%) 24 27	5, 15, 36, 51	0
All	All	858/870 (98%)	-0.06	27 (3%) 49 51	4, 13, 32, 62	0

The worst 5 of 27 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	M	214	CYS	8.3
1	L	214	CYS	6.4
2	H	214	ASP	5.3
2	H	102	TYR	5.0
2	P	214	ASP	4.7

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](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.