



# wwPDB X-ray Structure Validation Summary Report ⓘ

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PDB ID : 6I04  
Title : Crystal structure of Sema domain of the Met receptor in complex with FAB  
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Deposited on : 2018-10-25  
Resolution : 3.10 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](mailto: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.

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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

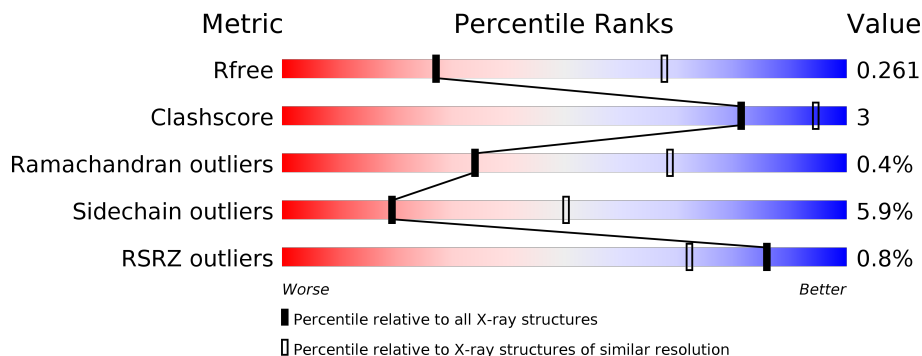
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 3.10 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	1094 (3.10-3.10)
Clashscore	141614	1184 (3.10-3.10)
Ramachandran outliers	138981	1141 (3.10-3.10)
Sidechain outliers	138945	1141 (3.10-3.10)
RSRZ outliers	127900	1067 (3.10-3.10)

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  $\geq 3$ , 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	552	
1	B	552	
2	C	230	
2	H	230	
3	D	214	
3	L	214	

## 2 Entry composition i

There are 3 unique types of molecules in this entry. The entry contains 13366 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 Hepatocyte growth factor receptor.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	442	3512	2241	588	662	21	0	0	0
1	B	432	3439	2194	576	648	21	0	0	0

There are 24 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	565	GLY	-	expression tag	UNP P08581
A	566	GLY	-	expression tag	UNP P08581
A	567	GLY	-	expression tag	UNP P08581
A	568	GLY	-	expression tag	UNP P08581
A	569	GLY	-	expression tag	UNP P08581
A	570	SER	-	expression tag	UNP P08581
A	571	HIS	-	expression tag	UNP P08581
A	572	HIS	-	expression tag	UNP P08581
A	573	HIS	-	expression tag	UNP P08581
A	574	HIS	-	expression tag	UNP P08581
A	575	HIS	-	expression tag	UNP P08581
A	576	HIS	-	expression tag	UNP P08581
B	565	GLY	-	expression tag	UNP P08581
B	566	GLY	-	expression tag	UNP P08581
B	567	GLY	-	expression tag	UNP P08581
B	568	GLY	-	expression tag	UNP P08581
B	569	GLY	-	expression tag	UNP P08581
B	570	SER	-	expression tag	UNP P08581
B	571	HIS	-	expression tag	UNP P08581
B	572	HIS	-	expression tag	UNP P08581
B	573	HIS	-	expression tag	UNP P08581
B	574	HIS	-	expression tag	UNP P08581
B	575	HIS	-	expression tag	UNP P08581
B	576	HIS	-	expression tag	UNP P08581

- Molecule 2 is a protein called Fab heavy chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	H	211	Total	C	N	O	S	0	0	0
			1588	1016	255	312	5			
2	C	214	Total	C	N	O	S	0	0	0
			1609	1028	259	317	5			

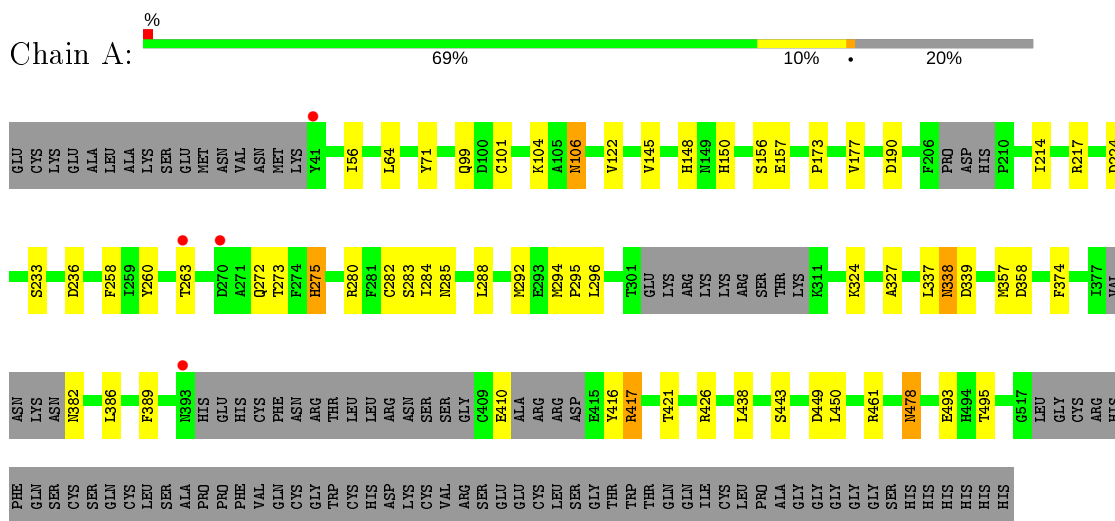
- Molecule 3 is a protein called Fab light chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
3	L	212	Total	C	N	O	S	0	0	0
			1609	1009	270	325	5			
3	D	212	Total	C	N	O	S	0	0	0
			1609	1009	270	325	5			

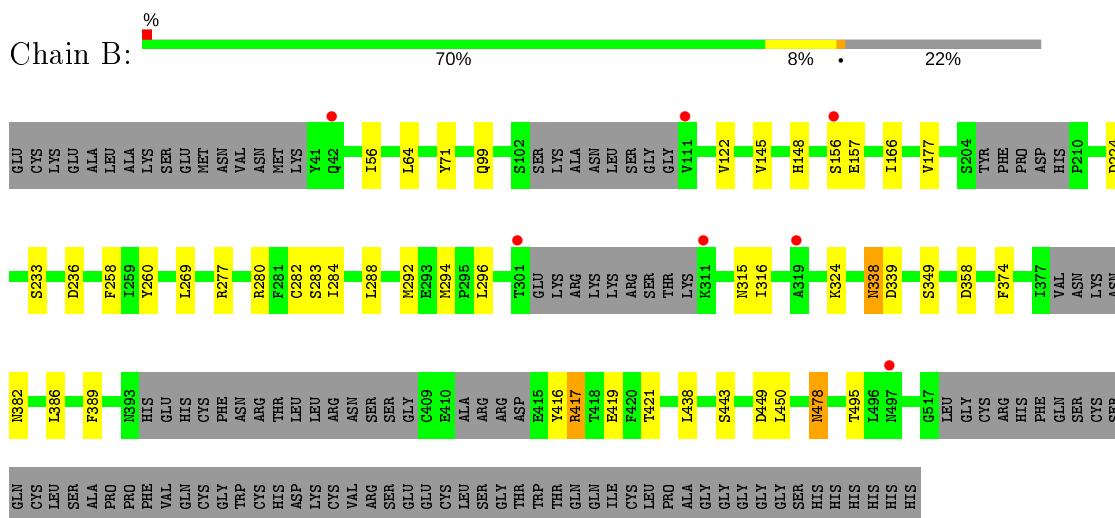
### 3 Residue-property plots i

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.

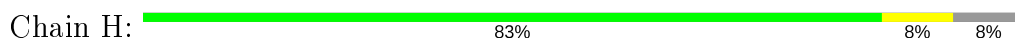
- Molecule 1: Hepatocyte growth factor receptor

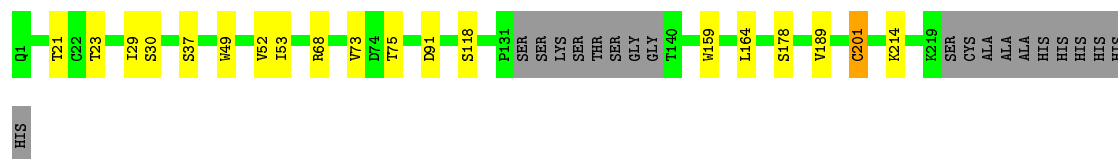


- Molecule 1: Hepatocyte growth factor receptor



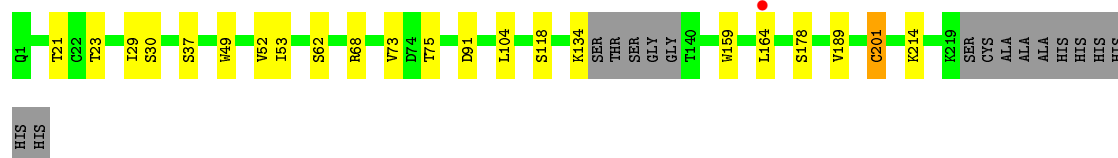
- Molecule 2: Fab heavy chain





- Molecule 2: Fab heavy chain

Chain C: 83% 9% 7%



- Molecule 3: Fab light chain

Chain L: 91% 8%



- Molecule 3: Fab light chain

Chain D: 90% 9%



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	73.93Å 85.50Å 101.30Å 77.49° 88.58° 68.76°	Depositor
Resolution (Å)	29.56 – 3.10 29.56 – 3.10	Depositor EDS
% Data completeness (in resolution range)	96.9 (29.56-3.10) 97.1 (29.56-3.10)	Depositor EDS
$R_{merge}$	0.17	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.29 (at 3.11Å)	Xtrriage
Refinement program	REFMAC 5.8.0232	Depositor
R, $R_{free}$	0.202 , 0.261 0.206 , 0.261	Depositor DCC
$R_{free}$ test set	1983 reflections (5.02%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	83.1	Xtrriage
Anisotropy	0.067	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.31 , 45.0	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.47$ , $\langle L^2 \rangle = 0.30$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
$F_o, F_c$ correlation	0.93	EDS
Total number of atoms	13366	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	90.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.45% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical 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	A	0.65	0/3594	0.74	0/4875
1	B	0.64	0/3518	0.74	0/4772
2	C	0.65	0/1650	0.78	0/2256
2	H	0.64	0/1629	0.77	0/2229
3	D	0.66	0/1645	0.75	0/2235
3	L	0.65	0/1645	0.76	0/2235
All	All	0.65	0/13681	0.75	0/18602

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	A	3512	0	3406	21	0
1	B	3439	0	3336	22	0
2	C	1609	0	1603	11	0
2	H	1588	0	1580	9	0
3	D	1609	0	1570	4	0
3	L	1609	0	1570	4	0
All	All	13366	0	13065	69	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 3.



The worst 5 of 69 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:B:338:ASN:C	1:B:338:ASN:HD22	1.81	0.84
1:A:338:ASN:C	1:A:338:ASN:HD22	1.83	0.82
1:A:338:ASN:HD22	1:A:339:ASP:N	1.84	0.75
1:B:338:ASN:HD22	1:B:339:ASP:N	1.90	0.68
2:H:29:ILE:HD11	2:H:75:THR:HA	1.79	0.65

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	430/552 (78%)	406 (94%)	21 (5%)	3 (1%)	22	57
1	B	418/552 (76%)	399 (96%)	18 (4%)	1 (0%)	47	79
2	C	210/230 (91%)	201 (96%)	9 (4%)	0	100	100
2	H	207/230 (90%)	198 (96%)	9 (4%)	0	100	100
3	D	210/214 (98%)	198 (94%)	11 (5%)	1 (0%)	29	64
3	L	210/214 (98%)	195 (93%)	14 (7%)	1 (0%)	29	64
All	All	1685/1992 (85%)	1597 (95%)	82 (5%)	6 (0%)	34	69

5 of 6 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	106	ASN
1	A	104	LYS
1	A	478	ASN
1	B	478	ASN
3	L	30	SER

### 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	399/495 (81%)	367 (92%)	32 (8%)	12	40
1	B	392/495 (79%)	373 (95%)	19 (5%)	25	58
2	C	188/199 (94%)	179 (95%)	9 (5%)	25	58
2	H	185/199 (93%)	177 (96%)	8 (4%)	29	62
3	D	183/185 (99%)	172 (94%)	11 (6%)	19	49
3	L	183/185 (99%)	172 (94%)	11 (6%)	19	49
All	All	1530/1758 (87%)	1440 (94%)	90 (6%)	19	50

5 of 90 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	L	1	ASP
3	L	202	SER
3	D	72	THR
3	L	31	SER
3	L	136	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	338	ASN
1	B	338	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, 95<sup>th</sup> 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 <sup>2</sup> )	Q < 0.9
1	A	442/552 (80%)	-0.13	4 (0%) 84 69	60, 94, 131, 163	0
1	B	432/552 (78%)	-0.08	7 (1%) 72 51	68, 97, 131, 160	0
2	C	214/230 (93%)	-0.36	1 (0%) 91 81	52, 77, 116, 137	0
2	H	211/230 (91%)	-0.47	0 100 100	53, 76, 104, 134	0
3	D	212/214 (99%)	-0.34	1 (0%) 91 81	62, 85, 108, 120	0
3	L	212/214 (99%)	-0.46	1 (0%) 91 81	55, 82, 105, 116	0
All	All	1723/1992 (86%)	-0.25	14 (0%) 86 72	52, 88, 123, 163	0

The worst 5 of 14 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	270	ASP	3.6
1	A	393	ASN	3.0
1	B	319	ALA	2.9
1	B	111	VAL	2.9
1	A	41	TYR	2.6

### 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

There are no such residues in this entry.