



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 15, 2017 – 03:24 am GMT

PDB ID : 3NRU
Title : Ligand binding domain of EPHA7
Authors : Walker, J.R.; Yermekbayeva, L.; Seitova, A.; Kania, J.; Bountra, C.; Weigelt, J.; Arrowsmith, C.H.; Edwards, A.M.; Bochkarev, A.; Dhe-Paganon, S.
Deposited on : 2010-06-30
Resolution : 2.30 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<http://wwpdb.org/validation/2016/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
Mogul	:	1.7.2 (RC1), CSD as538be (2017)
Xtriage (Phenix)	:	1.9-1692
EDS	:	trunk28620
Percentile statistics	:	20161228.v01 (using entries in the PDB archive December 28th 2016)
Refmac	:	5.8.0135
CCP4	:	6.5.0
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	recalc28949

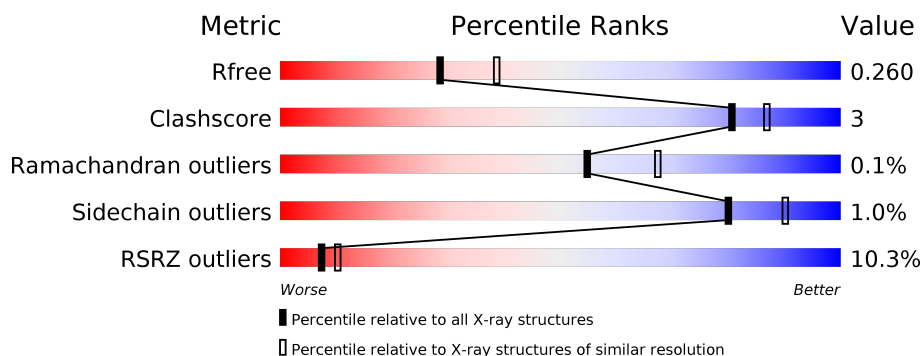
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.30 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}	100719	4130 (2.30-2.30)
Clashscore	112137	4751 (2.30-2.30)
Ramachandran outliers	110173	4705 (2.30-2.30)
Sidechain outliers	110143	4704 (2.30-2.30)
RSRZ outliers	101464	4156 (2.30-2.30)

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. 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	187	<div> <div>7%</div> <div>81%• 15%</div> </div>
1	B	187	<div> <div>8%</div> <div>77%7% 16%</div> </div>
1	C	187	<div> <div>5%</div> <div>76%9% 14%</div> </div>
1	D	187	<div> <div>11%</div> <div>78%7% • 14%</div> </div>
1	E	187	<div> <div>9%</div> <div>78%10% 13%</div> </div>
1	F	187	<div> <div>6%</div> <div>77%6% • 17%</div> </div>

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Mol	Chain	Length	Quality of chain
1	G	187	<div> <div>3%</div> <div>81%</div> <div>14%</div> </div>
1	H	187	<div> <div>4%</div> <div>74%</div> <div>10%</div> <div>16%</div> </div>
1	I	187	<div> <div>15%</div> <div>76%</div> <div>10%</div> <div>14%</div> </div>
1	J	187	<div> <div>10%</div> <div>80%</div> <div>6%</div> <div>14%</div> </div>
1	K	187	<div> <div>9%</div> <div>77%</div> <div>5%</div> <div>17%</div> </div>
1	L	187	<div> <div>17%</div> <div>74%</div> <div>7%</div> <div>18%</div> </div>

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 15958 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 Ephrin receptor.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	159	Total	C	N	O	S	0	1	0
			1285	822	209	249	5			
1	B	158	Total	C	N	O	S	0	3	0
			1294	827	212	250	5			
1	C	160	Total	C	N	O	S	0	1	0
			1292	827	213	246	6			
1	D	160	Total	C	N	O	S	0	2	0
			1297	829	216	247	5			
1	E	163	Total	C	N	O	S	0	0	0
			1310	839	216	249	6			
1	F	156	Total	C	N	O	S	0	1	0
			1270	811	213	241	5			
1	G	160	Total	C	N	O	S	0	0	0
			1296	827	214	250	5			
1	H	157	Total	C	N	O	S	0	1	0
			1251	799	201	245	6			
1	I	160	Total	C	N	O	S	0	0	0
			1264	815	205	238	6			
1	J	161	Total	C	N	O	S	0	1	0
			1307	833	217	252	5			
1	K	155	Total	C	N	O	S	0	0	0
			1215	779	200	232	4			
1	L	153	Total	C	N	O	S	0	0	0
			1213	776	195	236	6			

There are 168 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	30	ALA	-	EXPRESSION TAG	UNP B7ZLK0
A	31	ALA	-	EXPRESSION TAG	UNP B7ZLK0
A	205	GLU	-	EXPRESSION TAG	UNP B7ZLK0
A	206	PHE	-	EXPRESSION TAG	UNP B7ZLK0
A	207	VAL	-	EXPRESSION TAG	UNP B7ZLK0

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Chain	Residue	Modelled	Actual	Comment	Reference
A	208	GLU	-	EXPRESSION TAG	UNP B7ZLK0
A	209	HIS	-	EXPRESSION TAG	UNP B7ZLK0
A	210	HIS	-	EXPRESSION TAG	UNP B7ZLK0
A	211	HIS	-	EXPRESSION TAG	UNP B7ZLK0
A	212	HIS	-	EXPRESSION TAG	UNP B7ZLK0
A	213	HIS	-	EXPRESSION TAG	UNP B7ZLK0
A	214	HIS	-	EXPRESSION TAG	UNP B7ZLK0
A	215	HIS	-	EXPRESSION TAG	UNP B7ZLK0
A	216	HIS	-	EXPRESSION TAG	UNP B7ZLK0
B	30	ALA	-	EXPRESSION TAG	UNP B7ZLK0
B	31	ALA	-	EXPRESSION TAG	UNP B7ZLK0
B	205	GLU	-	EXPRESSION TAG	UNP B7ZLK0
B	206	PHE	-	EXPRESSION TAG	UNP B7ZLK0
B	207	VAL	-	EXPRESSION TAG	UNP B7ZLK0
B	208	GLU	-	EXPRESSION TAG	UNP B7ZLK0
B	209	HIS	-	EXPRESSION TAG	UNP B7ZLK0
B	210	HIS	-	EXPRESSION TAG	UNP B7ZLK0
B	211	HIS	-	EXPRESSION TAG	UNP B7ZLK0
B	212	HIS	-	EXPRESSION TAG	UNP B7ZLK0
B	213	HIS	-	EXPRESSION TAG	UNP B7ZLK0
B	214	HIS	-	EXPRESSION TAG	UNP B7ZLK0
B	215	HIS	-	EXPRESSION TAG	UNP B7ZLK0
B	216	HIS	-	EXPRESSION TAG	UNP B7ZLK0
C	30	ALA	-	EXPRESSION TAG	UNP B7ZLK0
C	31	ALA	-	EXPRESSION TAG	UNP B7ZLK0
C	205	GLU	-	EXPRESSION TAG	UNP B7ZLK0
C	206	PHE	-	EXPRESSION TAG	UNP B7ZLK0
C	207	VAL	-	EXPRESSION TAG	UNP B7ZLK0
C	208	GLU	-	EXPRESSION TAG	UNP B7ZLK0
C	209	HIS	-	EXPRESSION TAG	UNP B7ZLK0
C	210	HIS	-	EXPRESSION TAG	UNP B7ZLK0
C	211	HIS	-	EXPRESSION TAG	UNP B7ZLK0
C	212	HIS	-	EXPRESSION TAG	UNP B7ZLK0
C	213	HIS	-	EXPRESSION TAG	UNP B7ZLK0
C	214	HIS	-	EXPRESSION TAG	UNP B7ZLK0
C	215	HIS	-	EXPRESSION TAG	UNP B7ZLK0
C	216	HIS	-	EXPRESSION TAG	UNP B7ZLK0
D	30	ALA	-	EXPRESSION TAG	UNP B7ZLK0
D	31	ALA	-	EXPRESSION TAG	UNP B7ZLK0
D	205	GLU	-	EXPRESSION TAG	UNP B7ZLK0
D	206	PHE	-	EXPRESSION TAG	UNP B7ZLK0
D	207	VAL	-	EXPRESSION TAG	UNP B7ZLK0

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Chain	Residue	Modelled	Actual	Comment	Reference
D	208	GLU	-	EXPRESSION TAG	UNP B7ZLK0
D	209	HIS	-	EXPRESSION TAG	UNP B7ZLK0
D	210	HIS	-	EXPRESSION TAG	UNP B7ZLK0
D	211	HIS	-	EXPRESSION TAG	UNP B7ZLK0
D	212	HIS	-	EXPRESSION TAG	UNP B7ZLK0
D	213	HIS	-	EXPRESSION TAG	UNP B7ZLK0
D	214	HIS	-	EXPRESSION TAG	UNP B7ZLK0
D	215	HIS	-	EXPRESSION TAG	UNP B7ZLK0
D	216	HIS	-	EXPRESSION TAG	UNP B7ZLK0
E	30	ALA	-	EXPRESSION TAG	UNP B7ZLK0
E	31	ALA	-	EXPRESSION TAG	UNP B7ZLK0
E	205	GLU	-	EXPRESSION TAG	UNP B7ZLK0
E	206	PHE	-	EXPRESSION TAG	UNP B7ZLK0
E	207	VAL	-	EXPRESSION TAG	UNP B7ZLK0
E	208	GLU	-	EXPRESSION TAG	UNP B7ZLK0
E	209	HIS	-	EXPRESSION TAG	UNP B7ZLK0
E	210	HIS	-	EXPRESSION TAG	UNP B7ZLK0
E	211	HIS	-	EXPRESSION TAG	UNP B7ZLK0
E	212	HIS	-	EXPRESSION TAG	UNP B7ZLK0
E	213	HIS	-	EXPRESSION TAG	UNP B7ZLK0
E	214	HIS	-	EXPRESSION TAG	UNP B7ZLK0
E	215	HIS	-	EXPRESSION TAG	UNP B7ZLK0
E	216	HIS	-	EXPRESSION TAG	UNP B7ZLK0
F	30	ALA	-	EXPRESSION TAG	UNP B7ZLK0
F	31	ALA	-	EXPRESSION TAG	UNP B7ZLK0
F	205	GLU	-	EXPRESSION TAG	UNP B7ZLK0
F	206	PHE	-	EXPRESSION TAG	UNP B7ZLK0
F	207	VAL	-	EXPRESSION TAG	UNP B7ZLK0
F	208	GLU	-	EXPRESSION TAG	UNP B7ZLK0
F	209	HIS	-	EXPRESSION TAG	UNP B7ZLK0
F	210	HIS	-	EXPRESSION TAG	UNP B7ZLK0
F	211	HIS	-	EXPRESSION TAG	UNP B7ZLK0
F	212	HIS	-	EXPRESSION TAG	UNP B7ZLK0
F	213	HIS	-	EXPRESSION TAG	UNP B7ZLK0
F	214	HIS	-	EXPRESSION TAG	UNP B7ZLK0
F	215	HIS	-	EXPRESSION TAG	UNP B7ZLK0
F	216	HIS	-	EXPRESSION TAG	UNP B7ZLK0
G	30	ALA	-	EXPRESSION TAG	UNP B7ZLK0
G	31	ALA	-	EXPRESSION TAG	UNP B7ZLK0
G	205	GLU	-	EXPRESSION TAG	UNP B7ZLK0
G	206	PHE	-	EXPRESSION TAG	UNP B7ZLK0
G	207	VAL	-	EXPRESSION TAG	UNP B7ZLK0

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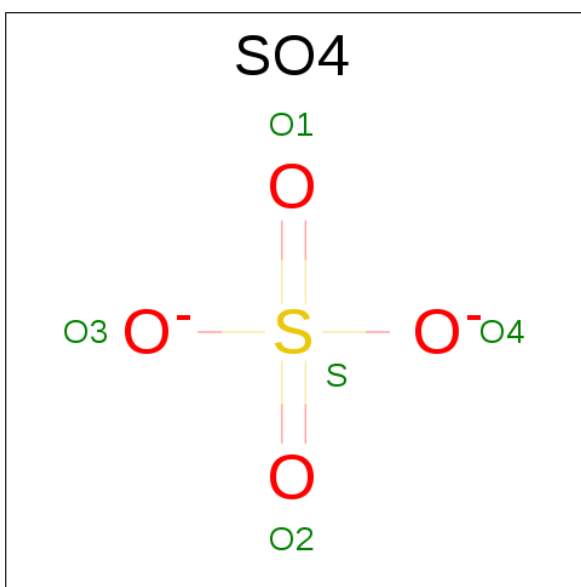
Chain	Residue	Modelled	Actual	Comment	Reference
G	208	GLU	-	EXPRESSION TAG	UNP B7ZLK0
G	209	HIS	-	EXPRESSION TAG	UNP B7ZLK0
G	210	HIS	-	EXPRESSION TAG	UNP B7ZLK0
G	211	HIS	-	EXPRESSION TAG	UNP B7ZLK0
G	212	HIS	-	EXPRESSION TAG	UNP B7ZLK0
G	213	HIS	-	EXPRESSION TAG	UNP B7ZLK0
G	214	HIS	-	EXPRESSION TAG	UNP B7ZLK0
G	215	HIS	-	EXPRESSION TAG	UNP B7ZLK0
G	216	HIS	-	EXPRESSION TAG	UNP B7ZLK0
H	30	ALA	-	EXPRESSION TAG	UNP B7ZLK0
H	31	ALA	-	EXPRESSION TAG	UNP B7ZLK0
H	205	GLU	-	EXPRESSION TAG	UNP B7ZLK0
H	206	PHE	-	EXPRESSION TAG	UNP B7ZLK0
H	207	VAL	-	EXPRESSION TAG	UNP B7ZLK0
H	208	GLU	-	EXPRESSION TAG	UNP B7ZLK0
H	209	HIS	-	EXPRESSION TAG	UNP B7ZLK0
H	210	HIS	-	EXPRESSION TAG	UNP B7ZLK0
H	211	HIS	-	EXPRESSION TAG	UNP B7ZLK0
H	212	HIS	-	EXPRESSION TAG	UNP B7ZLK0
H	213	HIS	-	EXPRESSION TAG	UNP B7ZLK0
H	214	HIS	-	EXPRESSION TAG	UNP B7ZLK0
H	215	HIS	-	EXPRESSION TAG	UNP B7ZLK0
H	216	HIS	-	EXPRESSION TAG	UNP B7ZLK0
I	30	ALA	-	EXPRESSION TAG	UNP B7ZLK0
I	31	ALA	-	EXPRESSION TAG	UNP B7ZLK0
I	205	GLU	-	EXPRESSION TAG	UNP B7ZLK0
I	206	PHE	-	EXPRESSION TAG	UNP B7ZLK0
I	207	VAL	-	EXPRESSION TAG	UNP B7ZLK0
I	208	GLU	-	EXPRESSION TAG	UNP B7ZLK0
I	209	HIS	-	EXPRESSION TAG	UNP B7ZLK0
I	210	HIS	-	EXPRESSION TAG	UNP B7ZLK0
I	211	HIS	-	EXPRESSION TAG	UNP B7ZLK0
I	212	HIS	-	EXPRESSION TAG	UNP B7ZLK0
I	213	HIS	-	EXPRESSION TAG	UNP B7ZLK0
I	214	HIS	-	EXPRESSION TAG	UNP B7ZLK0
I	215	HIS	-	EXPRESSION TAG	UNP B7ZLK0
I	216	HIS	-	EXPRESSION TAG	UNP B7ZLK0
J	30	ALA	-	EXPRESSION TAG	UNP B7ZLK0
J	31	ALA	-	EXPRESSION TAG	UNP B7ZLK0
J	205	GLU	-	EXPRESSION TAG	UNP B7ZLK0
J	206	PHE	-	EXPRESSION TAG	UNP B7ZLK0
J	207	VAL	-	EXPRESSION TAG	UNP B7ZLK0

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Chain	Residue	Modelled	Actual	Comment	Reference
J	208	GLU	-	EXPRESSION TAG	UNP B7ZLK0
J	209	HIS	-	EXPRESSION TAG	UNP B7ZLK0
J	210	HIS	-	EXPRESSION TAG	UNP B7ZLK0
J	211	HIS	-	EXPRESSION TAG	UNP B7ZLK0
J	212	HIS	-	EXPRESSION TAG	UNP B7ZLK0
J	213	HIS	-	EXPRESSION TAG	UNP B7ZLK0
J	214	HIS	-	EXPRESSION TAG	UNP B7ZLK0
J	215	HIS	-	EXPRESSION TAG	UNP B7ZLK0
J	216	HIS	-	EXPRESSION TAG	UNP B7ZLK0
K	30	ALA	-	EXPRESSION TAG	UNP B7ZLK0
K	31	ALA	-	EXPRESSION TAG	UNP B7ZLK0
K	205	GLU	-	EXPRESSION TAG	UNP B7ZLK0
K	206	PHE	-	EXPRESSION TAG	UNP B7ZLK0
K	207	VAL	-	EXPRESSION TAG	UNP B7ZLK0
K	208	GLU	-	EXPRESSION TAG	UNP B7ZLK0
K	209	HIS	-	EXPRESSION TAG	UNP B7ZLK0
K	210	HIS	-	EXPRESSION TAG	UNP B7ZLK0
K	211	HIS	-	EXPRESSION TAG	UNP B7ZLK0
K	212	HIS	-	EXPRESSION TAG	UNP B7ZLK0
K	213	HIS	-	EXPRESSION TAG	UNP B7ZLK0
K	214	HIS	-	EXPRESSION TAG	UNP B7ZLK0
K	215	HIS	-	EXPRESSION TAG	UNP B7ZLK0
K	216	HIS	-	EXPRESSION TAG	UNP B7ZLK0
L	30	ALA	-	EXPRESSION TAG	UNP B7ZLK0
L	31	ALA	-	EXPRESSION TAG	UNP B7ZLK0
L	205	GLU	-	EXPRESSION TAG	UNP B7ZLK0
L	206	PHE	-	EXPRESSION TAG	UNP B7ZLK0
L	207	VAL	-	EXPRESSION TAG	UNP B7ZLK0
L	208	GLU	-	EXPRESSION TAG	UNP B7ZLK0
L	209	HIS	-	EXPRESSION TAG	UNP B7ZLK0
L	210	HIS	-	EXPRESSION TAG	UNP B7ZLK0
L	211	HIS	-	EXPRESSION TAG	UNP B7ZLK0
L	212	HIS	-	EXPRESSION TAG	UNP B7ZLK0
L	213	HIS	-	EXPRESSION TAG	UNP B7ZLK0
L	214	HIS	-	EXPRESSION TAG	UNP B7ZLK0
L	215	HIS	-	EXPRESSION TAG	UNP B7ZLK0
L	216	HIS	-	EXPRESSION TAG	UNP B7ZLK0

- Molecule 2 is SULFATE ION (three-letter code: SO4) (formula: O₄S).



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

- Molecule 3 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	B	1	Total	Cl	0	0
			1	1		
3	C	1	Total	Cl	0	0
			1	1		

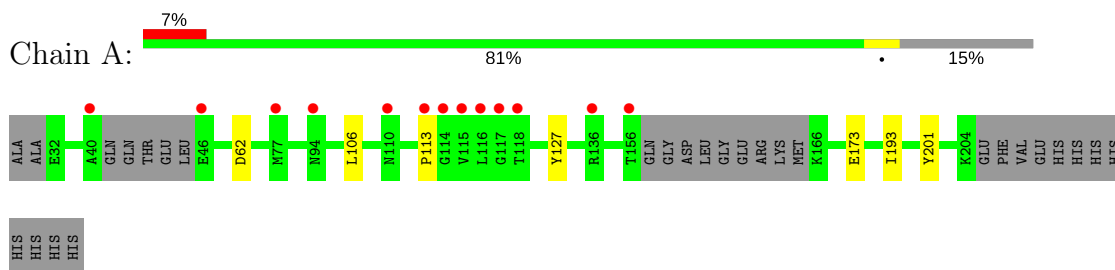
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	78	Total 78	O 78	0	0
4	B	75	Total 75	O 75	0	0
4	C	71	Total 72	O 72	0	1
4	D	49	Total 49	O 49	0	0
4	E	57	Total 57	O 57	0	0
4	F	48	Total 48	O 48	0	0
4	G	79	Total 79	O 79	0	0
4	H	45	Total 46	O 46	0	1
4	I	21	Total 21	O 21	0	0
4	J	47	Total 47	O 47	0	0
4	K	29	Total 29	O 29	0	0
4	L	11	Total 11	O 11	0	0

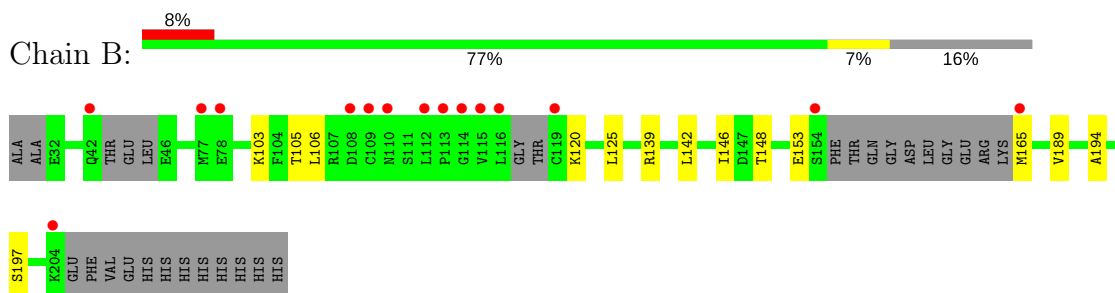
3 Residue-property plots [i](#)

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.

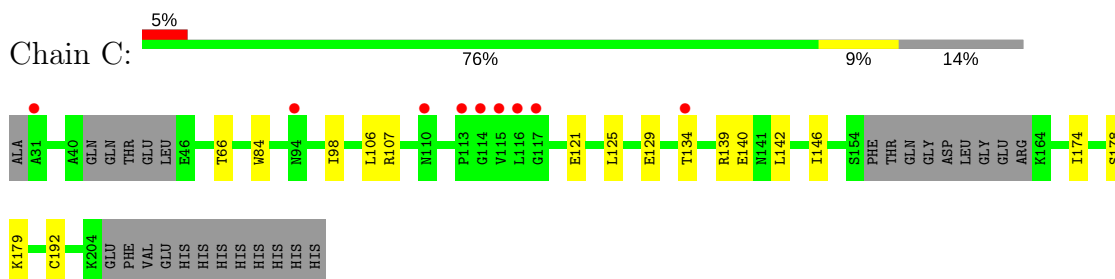
- Molecule 1: Ephrin receptor



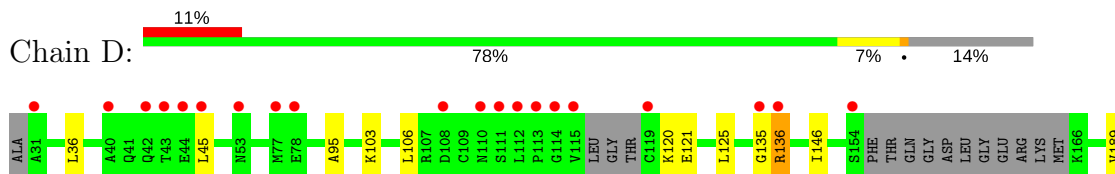
- Molecule 1: Ephrin receptor

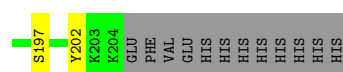


- Molecule 1: Ephrin receptor

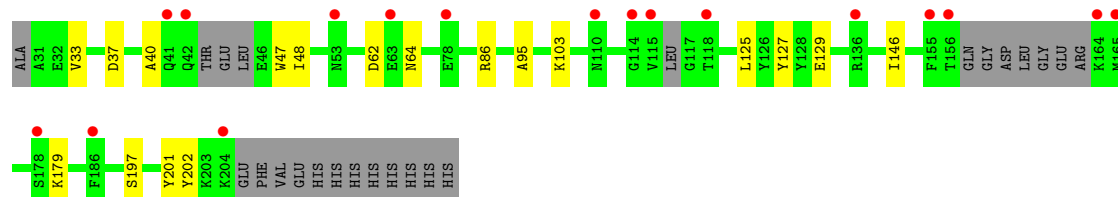
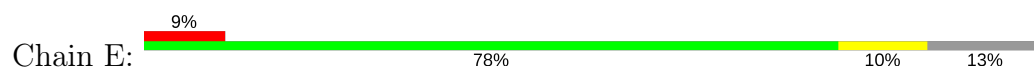


- Molecule 1: Ephrin receptor

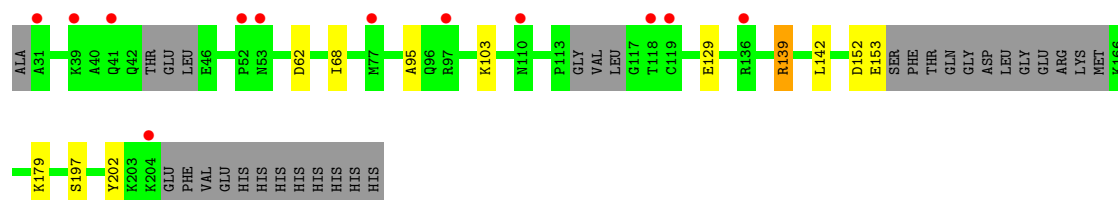




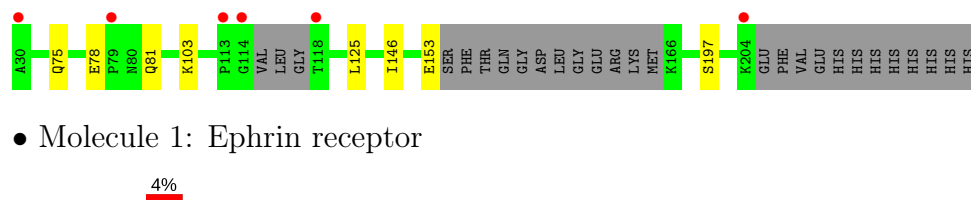
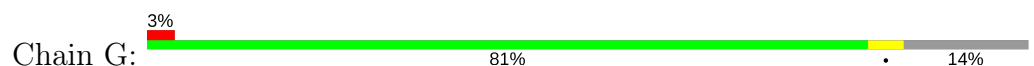
• Molecule 1: Ephrin receptor



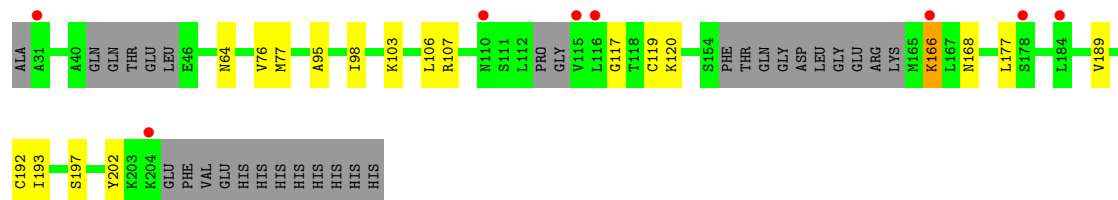
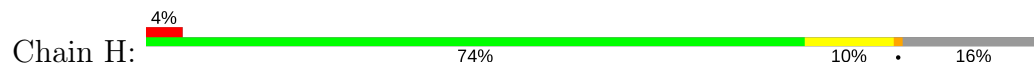
• Molecule 1: Ephrin receptor



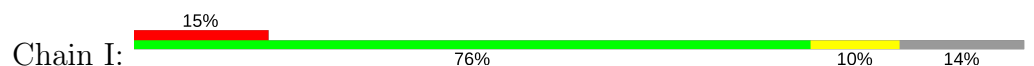
• Molecule 1: Ephrin receptor

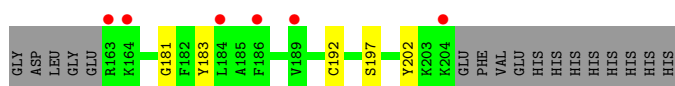


• Molecule 1: Ephrin receptor

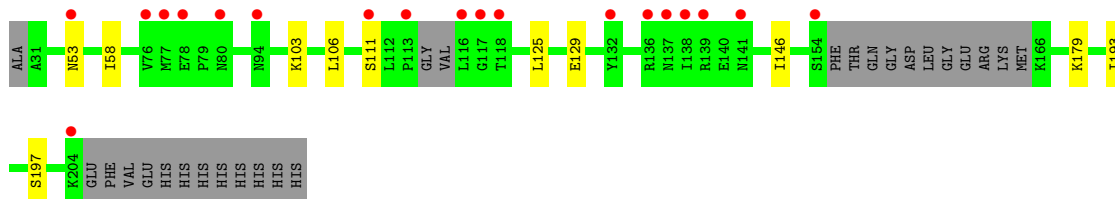
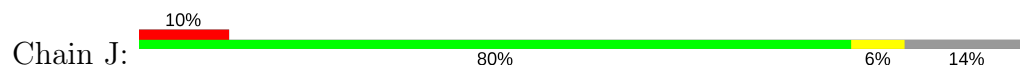


• Molecule 1: Ephrin receptor

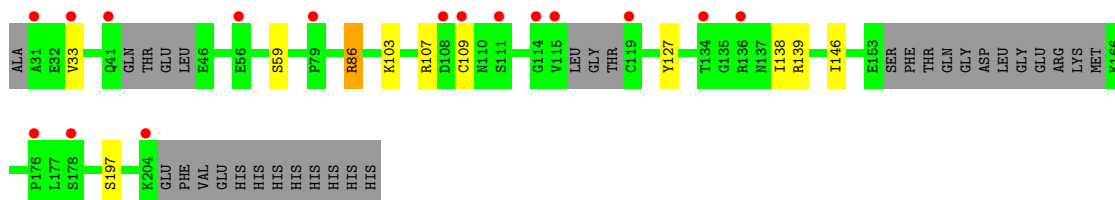
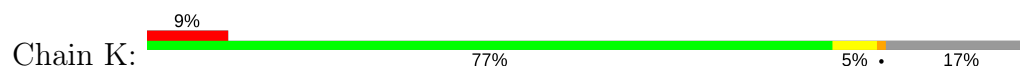




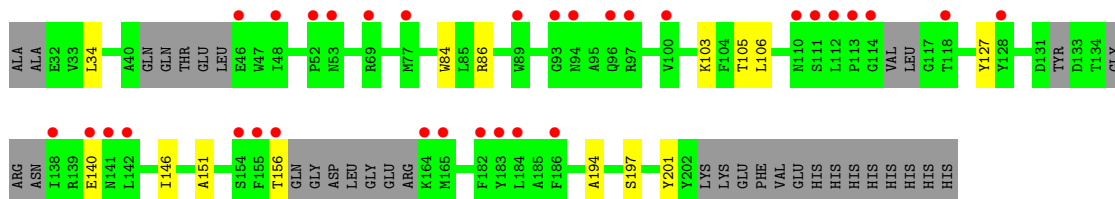
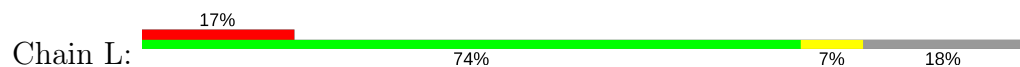
• Molecule 1: Ephrin receptor



• Molecule 1: Ephrin receptor



• Molecule 1: Ephrin receptor



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	137.62Å 140.70Å 143.78Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	19.97 – 2.30 19.97 – 2.30	Depositor EDS
% Data completeness (in resolution range)	99.8 (19.97-2.30) 99.8 (19.97-2.30)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.06	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.18 (at 2.30Å)	Xtriage
Refinement program	REFMAC 5.5.0109	Depositor
R, R_{free}	0.235 , 0.269 0.229 , 0.260	Depositor DCC
R_{free} test set	6230 reflections (5.31%)	DCC
Wilson B-factor (Å ²)	42.2	Xtriage
Anisotropy	0.037	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 39.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.35$	Xtriage
Estimated twinning fraction	0.000 for -h,l,k 0.001 for -l,-k,-h 0.002 for k,h,-l 0.000 for k,l,h 0.000 for l,h,k	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	15958	wwPDB-VP
Average B, all atoms (Å ²)	45.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.30% 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, CL

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	0.39	0/1312	0.54	0/1782
1	B	0.39	0/1319	0.53	0/1788
1	C	0.37	0/1318	0.53	0/1786
1	D	0.35	0/1323	0.49	0/1795
1	E	0.36	0/1336	0.53	0/1809
1	F	0.34	0/1295	0.50	0/1754
1	G	0.38	0/1322	0.54	0/1793
1	H	0.35	0/1275	0.52	0/1729
1	I	0.34	0/1290	0.51	0/1750
1	J	0.36	0/1333	0.53	0/1809
1	K	0.34	0/1239	0.52	0/1685
1	L	0.33	0/1236	0.49	0/1677
All	All	0.36	0/15598	0.52	0/21157

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	1285	0	1230	3	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	B	1294	0	1235	12	0
1	C	1292	0	1257	14	0
1	D	1297	0	1248	9	0
1	E	1310	0	1267	9	0
1	F	1270	0	1229	10	0
1	G	1296	0	1257	3	0
1	H	1251	0	1181	13	0
1	I	1264	0	1210	9	0
1	J	1307	0	1265	8	0
1	K	1215	0	1150	6	0
1	L	1213	0	1143	8	0
2	A	5	0	0	0	0
2	B	15	0	0	0	0
2	C	5	0	0	0	0
2	D	10	0	0	0	0
2	G	10	0	0	0	0
2	J	5	0	0	0	0
3	B	1	0	0	0	0
3	C	1	0	0	0	0
4	A	78	0	0	0	0
4	B	75	0	0	0	0
4	C	72	0	0	0	0
4	D	49	0	0	0	0
4	E	57	0	0	0	0
4	F	48	0	0	0	0
4	G	79	0	0	0	0
4	H	46	0	0	0	0
4	I	21	0	0	0	0
4	J	47	0	0	0	0
4	K	29	0	0	0	0
4	L	11	0	0	0	0
All	All	15958	0	14672	94	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.

All (94) 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:H:117:GLY:HA2	1:H:119:CYS:H	0.95	1.06
1:H:117:GLY:HA2	1:H:119:CYS:N	1.72	1.01

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:136:ARG:HH21	1:D:136:ARG:HG2	1.30	0.95
1:H:117:GLY:CA	1:H:119:CYS:H	1.82	0.92
1:C:139[B]:ARG:CD	1:C:139[B]:ARG:H	1.90	0.84
1:D:136:ARG:NH2	1:D:136:ARG:HG2	1.93	0.82
1:B:139[B]:ARG:HD3	1:B:142:LEU:HD12	1.62	0.80
1:D:136:ARG:HH21	1:D:136:ARG:CG	1.95	0.78
1:B:165:MET:HG3	1:H:64:ASN:HB3	1.70	0.73
1:C:139[B]:ARG:HD3	1:C:142:LEU:HD12	1.72	0.72
1:B:105:THR:HG22	1:B:194:ALA:HB3	1.71	0.71
1:F:139:ARG:H	1:F:139:ARG:HE	1.41	0.69
1:B:139[B]:ARG:CD	1:B:139[B]:ARG:H	2.05	0.68
1:F:139:ARG:HD2	1:F:142:LEU:HD12	1.74	0.68
1:K:86:ARG:HG2	1:K:138:ILE:HG12	1.75	0.68
1:H:107:ARG:HB2	1:H:192:CYS:HB3	1.78	0.66
1:J:53[A]:ASN:OD1	1:J:53[A]:ASN:O	2.14	0.66
1:C:84:TRP:CZ2	1:C:140:GLU:HG3	2.34	0.63
1:D:120:LYS:HG3	1:D:189:VAL:HG23	1.80	0.62
1:D:36:LEU:HD11	1:D:45:LEU:HD13	1.82	0.62
1:E:103:LYS:HB2	1:E:197:SER:HB3	1.81	0.62
1:C:129:GLU:OE1	1:C:178:SER:N	2.33	0.61
1:C:139[B]:ARG:HD2	1:C:139[B]:ARG:H	1.65	0.60
1:F:139:ARG:H	1:F:139:ARG:NE	2.01	0.59
1:A:201:TYR:CZ	1:B:153:GLU:HB3	2.38	0.58
1:F:103:LYS:HB2	1:F:197:SER:HB3	1.85	0.57
1:C:139[B]:ARG:N	1:C:139[B]:ARG:HD2	2.18	0.57
1:E:37:ASP:HB3	1:E:40:ALA:HB2	1.85	0.57
1:B:125:LEU:HG	1:B:146:ILE:HD12	1.87	0.57
1:C:66:THR:HG23	1:K:107:ARG:HD3	1.86	0.57
1:J:111:SER:HB2	1:L:156:THR:HG23	1.85	0.57
1:H:120:LYS:HG3	1:H:189:VAL:HG23	1.87	0.56
1:D:103:LYS:HB2	1:D:197:SER:HB3	1.88	0.56
1:J:106:LEU:CD1	1:J:193:ILE:HG12	2.35	0.56
1:H:166:LYS:HE3	1:H:168:ASN:OD1	2.07	0.55
1:H:76:VAL:HG23	1:H:77:MET:HE2	1.88	0.55
1:I:103:LYS:HB2	1:I:197:SER:HB3	1.87	0.55
1:F:139:ARG:HE	1:F:139:ARG:N	2.05	0.55
1:H:106:LEU:HD13	1:H:193:ILE:HG12	1.87	0.55
1:I:74:CYS:HG	1:I:192:CYS:HG	1.54	0.55
1:L:127:TYR:HB3	1:L:146:ILE:HD11	1.89	0.54
1:L:84:TRP:CZ2	1:L:140:GLU:HG3	2.42	0.54
1:C:139[B]:ARG:H	1:C:139[B]:ARG:NE	2.05	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:103:LYS:HB2	1:H:197:SER:HB3	1.91	0.53
1:A:106:LEU:HD13	1:A:193:ILE:HG12	1.89	0.52
1:B:103:LYS:HB2	1:B:197:SER:HB3	1.91	0.52
1:D:106:LEU:HD21	1:D:121:GLU:HA	1.91	0.52
1:F:62:ASP:HB3	1:F:68:ILE:HD11	1.94	0.50
1:F:152:ASP:O	1:F:153:GLU:HB3	2.12	0.49
1:H:98:ILE:HD12	1:H:177:LEU:HD13	1.93	0.49
1:E:48:ILE:HD11	1:E:86:ARG:NH1	2.28	0.48
1:K:103:LYS:HB2	1:K:197:SER:HB3	1.95	0.48
1:E:62:ASP:HB3	1:E:64:ASN:H	1.78	0.48
1:G:103:LYS:HB2	1:G:197:SER:HB3	1.95	0.48
1:E:47:TRP:HB3	1:E:86:ARG:O	2.14	0.47
1:C:107:ARG:HB2	1:C:192:CYS:HB3	1.96	0.47
1:C:139[B]:ARG:HD2	1:C:139[B]:ARG:O	2.15	0.47
1:I:89:TRP:CZ2	1:I:181:GLY:HA3	2.50	0.46
1:L:106:LEU:HB3	1:L:151:ALA:HB2	1.97	0.46
1:I:112:LEU:HA	1:I:113:PRO:HD3	1.86	0.46
1:J:111:SER:HB2	1:L:156:THR:CG2	2.46	0.46
1:L:103:LYS:HB2	1:L:197:SER:HB3	1.98	0.45
1:A:173:GLU:OE1	1:B:148:THR:HG21	2.16	0.45
1:L:105:THR:OG1	1:L:194:ALA:HB3	2.16	0.45
1:I:95:ALA:HB2	1:I:202:TYR:CD2	2.52	0.45
1:B:139[B]:ARG:H	1:B:139[B]:ARG:HD2	1.80	0.44
1:E:129:GLU:HB3	1:E:179:LYS:HB2	1.98	0.44
1:B:165:MET:HG3	1:H:64:ASN:CB	2.45	0.44
1:B:139[B]:ARG:NE	1:B:139[B]:ARG:H	2.15	0.44
1:J:58:ILE:HD11	1:K:59:SER:HB2	2.00	0.44
1:L:34:LEU:HD12	1:L:201:TYR:HB3	1.99	0.44
1:D:95:ALA:HB2	1:D:202:TYR:CD2	2.54	0.43
1:I:125:LEU:HG	1:I:146:ILE:HD12	2.01	0.43
1:I:47:TRP:HB3	1:I:86:ARG:O	2.17	0.43
1:G:125:LEU:HG	1:G:146:ILE:HD12	1.99	0.43
1:I:134:THR:HA	1:I:183:TYR:OH	2.18	0.43
1:G:78:GLU:HG3	1:G:81:GLN:NE2	2.33	0.43
1:J:125:LEU:HG	1:J:146:ILE:HD12	2.00	0.43
1:J:129:GLU:HB3	1:J:179:LYS:HB2	2.01	0.42
1:D:125:LEU:HG	1:D:146:ILE:HD12	2.01	0.42
1:H:95:ALA:HB2	1:H:202:TYR:CD2	2.54	0.42
1:C:98:ILE:HB	1:C:174:ILE:HG13	2.02	0.42
1:B:120:LYS:HD2	1:B:189:VAL:HG23	2.02	0.42
1:E:125:LEU:HG	1:E:146:ILE:HD12	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:103:LYS:HB2	1:J:197:SER:HB3	2.02	0.42
1:F:95:ALA:HB2	1:F:202:TYR:CD2	2.55	0.41
1:C:129:GLU:HG2	1:C:179:LYS:HB2	2.02	0.41
1:F:129:GLU:HB2	1:F:179:LYS:HB2	2.03	0.41
1:F:139:ARG:HD3	1:K:139:ARG:HH12	1.85	0.41
1:E:201:TYR:CZ	1:I:153:GLU:HB3	2.55	0.41
1:C:125:LEU:HG	1:C:146:ILE:HD12	2.02	0.41
1:C:106:LEU:HD21	1:C:121:GLU:HA	2.02	0.41
1:K:127:TYR:HB3	1:K:146:ILE:HD11	2.03	0.41
1:E:95:ALA:HB2	1:E:202:TYR:CD2	2.55	0.40

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	154/187 (82%)	146 (95%)	7 (4%)	1 (1%)	28	34
1	B	153/187 (82%)	139 (91%)	14 (9%)	0	100	100
1	C	155/187 (83%)	147 (95%)	8 (5%)	0	100	100
1	D	156/187 (83%)	149 (96%)	6 (4%)	1 (1%)	28	34
1	E	155/187 (83%)	146 (94%)	9 (6%)	0	100	100
1	F	149/187 (80%)	140 (94%)	9 (6%)	0	100	100
1	G	154/187 (82%)	147 (96%)	7 (4%)	0	100	100
1	H	150/187 (80%)	143 (95%)	7 (5%)	0	100	100
1	I	152/187 (81%)	141 (93%)	11 (7%)	0	100	100
1	J	156/187 (83%)	148 (95%)	8 (5%)	0	100	100
1	K	147/187 (79%)	138 (94%)	9 (6%)	0	100	100
1	L	141/187 (75%)	131 (93%)	10 (7%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
All	All	1822/2244 (81%)	1715 (94%)	105 (6%)	2 (0%)	55 67

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	135	GLY
1	A	113	PRO

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	139/167 (83%)	137 (99%)	2 (1%)	71 85
1	B	139/167 (83%)	138 (99%)	1 (1%)	87 94
1	C	140/167 (84%)	139 (99%)	1 (1%)	87 94
1	D	139/167 (83%)	138 (99%)	1 (1%)	87 94
1	E	141/167 (84%)	139 (99%)	2 (1%)	71 85
1	F	137/167 (82%)	136 (99%)	1 (1%)	87 94
1	G	141/167 (84%)	139 (99%)	2 (1%)	71 85
1	H	133/167 (80%)	132 (99%)	1 (1%)	85 93
1	I	133/167 (80%)	132 (99%)	1 (1%)	85 93
1	J	143/167 (86%)	143 (100%)	0	100 100
1	K	127/167 (76%)	124 (98%)	3 (2%)	54 72
1	L	131/167 (78%)	130 (99%)	1 (1%)	85 93
All	All	1643/2004 (82%)	1627 (99%)	16 (1%)	80 90

All (16) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	62	ASP
1	A	127	TYR

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Mol	Chain	Res	Type
1	B	106	LEU
1	C	134	THR
1	D	136	ARG
1	E	33	VAL
1	E	127	TYR
1	F	139	ARG
1	G	75	GLN
1	G	153	GLU
1	H	166	LYS
1	I	77	MET
1	K	33	VAL
1	K	86	ARG
1	K	109	CYS
1	L	86	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

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](#)

Of 12 ligands modelled in this entry, 2 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	A	301	-	4,4,4	0.14	0	6,6,6	0.14	0
2	SO4	B	301	-	4,4,4	0.14	0	6,6,6	0.19	0
2	SO4	B	302	-	4,4,4	0.11	0	6,6,6	0.13	0
2	SO4	B	303	-	4,4,4	0.12	0	6,6,6	0.07	0
2	SO4	C	302	-	4,4,4	0.13	0	6,6,6	0.10	0
2	SO4	D	301	-	4,4,4	0.12	0	6,6,6	0.15	0
2	SO4	D	302	-	4,4,4	0.16	0	6,6,6	0.12	0
2	SO4	G	217	-	4,4,4	0.13	0	6,6,6	0.08	0
2	SO4	G	301	-	4,4,4	0.15	0	6,6,6	0.08	0
2	SO4	J	301	-	4,4,4	0.14	0	6,6,6	0.13	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
2	SO4	A	301	-	-	0/0/0/0	0/0/0/0
2	SO4	B	301	-	-	0/0/0/0	0/0/0/0
2	SO4	B	302	-	-	0/0/0/0	0/0/0/0
2	SO4	B	303	-	-	0/0/0/0	0/0/0/0
2	SO4	C	302	-	-	0/0/0/0	0/0/0/0
2	SO4	D	301	-	-	0/0/0/0	0/0/0/0
2	SO4	D	302	-	-	0/0/0/0	0/0/0/0
2	SO4	G	217	-	-	0/0/0/0	0/0/0/0
2	SO4	G	301	-	-	0/0/0/0	0/0/0/0
2	SO4	J	301	-	-	0/0/0/0	0/0/0/0

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 ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

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	159/187 (85%)	0.34	13 (8%) 12 17	20, 33, 58, 73	0
1	B	158/187 (84%)	0.39	15 (9%) 9 12	20, 31, 57, 83	0
1	C	160/187 (85%)	0.37	9 (5%) 25 32	24, 35, 60, 74	0
1	D	160/187 (85%)	0.47	20 (12%) 4 6	24, 40, 66, 90	0
1	E	163/187 (87%)	0.50	17 (10%) 7 10	25, 40, 65, 79	0
1	F	156/187 (83%)	0.49	12 (7%) 14 19	24, 44, 72, 80	0
1	G	160/187 (85%)	0.11	6 (3%) 41 48	19, 33, 54, 64	0
1	H	157/187 (83%)	0.35	8 (5%) 29 36	26, 44, 70, 76	0
1	I	160/187 (85%)	0.95	28 (17%) 2 2	37, 65, 95, 105	0
1	J	161/187 (86%)	0.51	19 (11%) 5 7	26, 44, 77, 91	0
1	K	155/187 (82%)	0.58	16 (10%) 7 10	31, 55, 85, 94	0
1	L	153/187 (81%)	1.07	32 (20%) 1 1	43, 65, 101, 115	0
All	All	1902/2244 (84%)	0.51	195 (10%) 7 10	19, 43, 80, 115	0

All (195) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	116	LEU	6.8
1	I	114	GLY	6.7
1	C	114	GLY	6.2
1	K	108	ASP	6.2
1	B	115	VAL	6.2
1	I	163	ARG	5.9
1	L	165	MET	5.9
1	A	115	VAL	5.8
1	A	117	GLY	5.7
1	L	164	LYS	5.6
1	A	116	LEU	5.5

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Mol	Chain	Res	Type	RSRZ
1	E	156	THR	5.3
1	D	114	GLY	5.2
1	F	31	ALA	5.1
1	E	118	THR	5.1
1	C	116	LEU	4.8
1	D	110	ASN	4.7
1	F	118	THR	4.7
1	L	142	LEU	4.7
1	J	139	ARG	4.6
1	J	154	SER	4.6
1	F	110	ASN	4.6
1	D	111	SER	4.5
1	E	115	VAL	4.5
1	B	114	GLY	4.5
1	D	115	VAL	4.5
1	K	111	SER	4.5
1	A	118	THR	4.5
1	C	117	GLY	4.5
1	L	113	PRO	4.5
1	J	113	PRO	4.5
1	I	137	ASN	4.4
1	J	116	LEU	4.3
1	K	41	GLN	4.3
1	K	115	VAL	4.3
1	H	31	ALA	4.2
1	L	184	LEU	4.2
1	D	42	GLN	4.2
1	E	165	MET	4.2
1	J	80	ASN	4.2
1	I	133	ASP	4.1
1	L	118	THR	4.1
1	A	114	GLY	4.1
1	D	45	LEU	4.1
1	G	113	PRO	4.0
1	I	204	LYS	4.0
1	K	134	THR	4.0
1	I	113	PRO	4.0
1	I	141	ASN	4.0
1	A	113	PRO	3.9
1	C	115	VAL	3.9
1	E	42	GLN	3.9
1	D	44	GLU	3.9

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Mol	Chain	Res	Type	RSRZ
1	I	134	THR	3.9
1	E	110	ASN	3.9
1	K	31	ALA	3.9
1	I	156	THR	3.8
1	E	155	PHE	3.8
1	A	46	GLU	3.8
1	B	113	PRO	3.7
1	B	165	MET	3.7
1	L	46	GLU	3.7
1	J	118	THR	3.7
1	D	77	MET	3.7
1	L	114	GLY	3.6
1	C	110	ASN	3.6
1	E	114	GLY	3.6
1	J	117	GLY	3.6
1	J	78	GLU	3.6
1	L	93	GLY	3.5
1	L	52	PRO	3.5
1	L	156	THR	3.5
1	K	119	CYS	3.4
1	D	31	ALA	3.4
1	E	164	LYS	3.4
1	D	119	CYS	3.4
1	I	119	CYS	3.4
1	B	42	GLN	3.3
1	L	53	ASN	3.3
1	I	39	LYS	3.3
1	G	30	ALA	3.3
1	H	204	LYS	3.3
1	J	136	ARG	3.3
1	I	79	PRO	3.3
1	J	77	MET	3.3
1	E	41	GLN	3.2
1	A	40	ALA	3.2
1	L	96	GLN	3.1
1	I	31	ALA	3.1
1	K	109	CYS	3.1
1	B	154	SER	3.1
1	E	204	LYS	3.1
1	G	118	THR	3.1
1	I	184	LEU	3.1
1	C	113	PRO	3.1

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Mol	Chain	Res	Type	RSRZ
1	J	132	TYR	3.0
1	I	77	MET	3.0
1	L	94	ASN	3.0
1	L	141	ASN	3.0
1	H	110	ASN	3.0
1	J	137	ASN	3.0
1	K	114	GLY	3.0
1	L	97	ARG	3.0
1	I	56	GLU	2.9
1	E	136	ARG	2.9
1	I	76	VAL	2.9
1	J	138	ILE	2.9
1	D	43	THR	2.9
1	E	178	SER	2.8
1	D	135	GLY	2.8
1	I	136	ARG	2.8
1	L	183	TYR	2.8
1	H	115	VAL	2.8
1	L	77	MET	2.8
1	D	108	ASP	2.8
1	K	136	ARG	2.8
1	B	119	CYS	2.7
1	D	113	PRO	2.7
1	I	135	GLY	2.7
1	I	164	LYS	2.7
1	C	134	THR	2.7
1	C	94	ASN	2.7
1	F	204	LYS	2.7
1	H	184	LEU	2.7
1	I	138	ILE	2.6
1	D	136	ARG	2.6
1	G	114	GLY	2.6
1	L	155	PHE	2.6
1	E	186	PHE	2.6
1	L	100	VAL	2.6
1	A	77	MET	2.6
1	A	156	THR	2.6
1	J	76	VAL	2.6
1	L	138	ILE	2.6
1	L	89	TRP	2.6
1	B	112	LEU	2.6
1	I	40	ALA	2.6

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Mol	Chain	Res	Type	RSRZ
1	E	63	GLU	2.5
1	D	53[A]	ASN	2.5
1	F	41	GLN	2.5
1	B	108	ASP	2.5
1	K	204	LYS	2.5
1	E	53	ASN	2.5
1	D	154	SER	2.5
1	F	77	MET	2.5
1	I	189	VAL	2.5
1	C	31	ALA	2.5
1	L	154	SER	2.5
1	L	128	TYR	2.5
1	L	110	ASN	2.5
1	J	94	ASN	2.4
1	L	48	ILE	2.4
1	J	111	SER	2.4
1	B	110	ASN	2.4
1	B	109	CYS	2.4
1	J	53[A]	ASN	2.4
1	K	178	SER	2.4
1	L	112	LEU	2.3
1	F	39	LYS	2.3
1	J	141	ASN	2.3
1	B	204	LYS	2.3
1	I	139	ARG	2.3
1	D	78	GLU	2.3
1	K	176	PRO	2.3
1	F	97	ARG	2.3
1	G	79	PRO	2.3
1	I	186	PHE	2.3
1	F	136	ARG	2.3
1	K	56	GLU	2.3
1	G	204	LYS	2.3
1	L	182	PHE	2.2
1	A	136	ARG	2.2
1	K	79	PRO	2.2
1	I	46	GLU	2.2
1	D	40	ALA	2.2
1	E	78	GLU	2.2
1	A	110	ASN	2.1
1	F	53	ASN	2.1
1	H	166	LYS	2.1

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Mol	Chain	Res	Type	RSRZ
1	L	111	SER	2.1
1	H	178	SER	2.1
1	L	140	GLU	2.1
1	B	78	GLU	2.1
1	H	116	LEU	2.1
1	F	119	CYS	2.1
1	L	186	PHE	2.1
1	D	112	LEU	2.1
1	I	80	ASN	2.1
1	B	77	MET	2.1
1	I	130	THR	2.1
1	K	33	VAL	2.1
1	F	52	PRO	2.1
1	J	204	LYS	2.0
1	L	69	ARG	2.0
1	A	94	ASN	2.0

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](#)

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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	LLDF	B-factors(Å ²)	Q<0.9
2	SO4	D	302	5/5	0.95	0.27	1.68	76,77,79,80	0
2	SO4	J	301	5/5	0.96	0.13	-0.60	58,61,62,64	0
2	SO4	B	301	5/5	0.95	0.12	-0.82	48,51,52,52	0
2	SO4	D	301	5/5	0.99	0.10	-0.96	39,41,42,44	0
2	SO4	A	301	5/5	0.97	0.12	-0.99	62,65,66,67	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
2	SO4	B	303	5/5	0.96	0.10	-1.05	52,54,55,56	0
2	SO4	G	217	5/5	0.98	0.09	-1.45	40,42,43,44	0
2	SO4	B	302	5/5	0.98	0.09	-1.46	43,44,46,47	0
2	SO4	C	302	5/5	0.97	0.11	-1.77	63,63,65,67	0
3	CL	B	300	1/1	0.97	0.09	-	73,73,73,73	0
2	SO4	G	301	5/5	0.95	0.17	-	78,78,80,81	0
3	CL	C	300	1/1	0.97	0.05	-	74,74,74,74	0

6.5 Other polymers [i](#)

There are no such residues in this entry.