



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 10, 2018 – 04:43 am GMT

PDB ID : 5FTT
Title : Octameric complex of Latrophilin 3 (Lec, Olf) , Unc5D (Ig, Ig2, TSP1) and FLRT2 (LRR)
Authors : Jackson, V.A.; Mehmood, S.; Chavent, M.; Roversi, P.; Carrasquero, M.; del Toro, D.; Seyit-Bremer, G.; Ranaivoson, F.M.; Comoletti, D.; Sansom, M.S.P.; Robinson, C.V.; Klein, R.; Seiradake, E.
Deposited on : 2016-01-15
Resolution : 3.40 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
Mogul : 1.7.3 (157068), CSD as539be (2018)
Xtriage (Phenix) : 1.13
EDS : trunk30967
Percentile statistics : 20171227.v01 (using entries in the PDB archive December 27th 2017)
Refmac : 5.8.0158
CCP4 : 7.0 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk30967

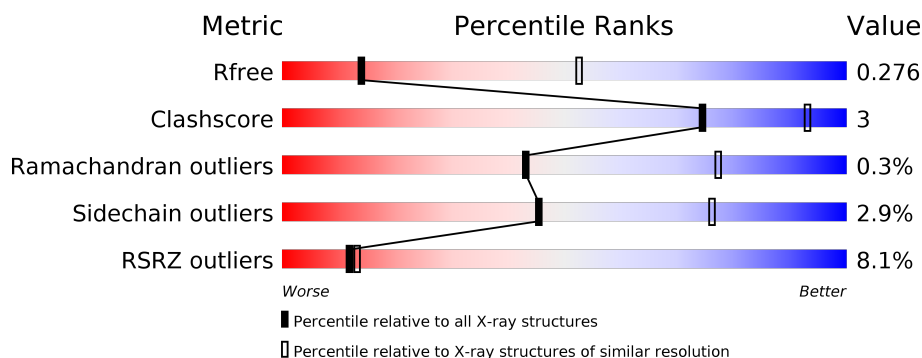
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.40 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}	111664	1928 (3.50-3.30)
Clashscore	122126	2051 (3.50-3.30)
Ramachandran outliers	120053	2006 (3.50-3.30)
Sidechain outliers	120020	2006 (3.50-3.30)
RSRZ outliers	108989	1827 (3.50-3.30)

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	285	<div> <div>4%</div> <div> <div></div> <div>82%</div> <div>10%</div> <div>8%</div> </div> </div>
1	E	285	<div> <div>5%</div> <div> <div></div> <div>80%</div> <div>10%</div> <div>9%</div> </div> </div>
2	B	339	<div> <div>12%</div> <div> <div></div> <div>82%</div> <div>14%</div> <div>•</div> </div> </div>
2	F	339	<div> <div>13%</div> <div> <div></div> <div>82%</div> <div>16%</div> <div>•</div> </div> </div>
3	C	383	<div> <div>8%</div> <div> <div></div> <div>83%</div> <div>12%</div> <div>• 5%</div> </div> </div>
3	D	383	<div> <div>%</div> <div> <div></div> <div>62%</div> <div>7%</div> <div>31%</div> </div> </div>

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Mol	Chain	Length	Quality of chain
3	G	383	<div> <div></div> <div>9%</div> <div>86%</div> <div>10%</div> <div></div> </div>
3	H	383	<div> <div></div> <div>4%</div> <div>60%</div> <div>8%</div> <div>32%</div> <div></div> </div>

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 19610 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 NETRIN RECEPTOR UNC5D.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	262	Total	C	N	O	S	0	0	0
			2060	1279	374	391	16			
1	E	259	Total	C	N	O	S	0	0	0
			2041	1268	371	386	16			

There are 18 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	308	GLY	-	expression tag	UNP F1LW30
A	309	THR	-	expression tag	UNP F1LW30
A	310	LYS	-	expression tag	UNP F1LW30
A	311	HIS	-	expression tag	UNP F1LW30
A	312	HIS	-	expression tag	UNP F1LW30
A	313	HIS	-	expression tag	UNP F1LW30
A	314	HIS	-	expression tag	UNP F1LW30
A	315	HIS	-	expression tag	UNP F1LW30
A	316	HIS	-	expression tag	UNP F1LW30
E	308	GLY	-	expression tag	UNP F1LW30
E	309	THR	-	expression tag	UNP F1LW30
E	310	LYS	-	expression tag	UNP F1LW30
E	311	HIS	-	expression tag	UNP F1LW30
E	312	HIS	-	expression tag	UNP F1LW30
E	313	HIS	-	expression tag	UNP F1LW30
E	314	HIS	-	expression tag	UNP F1LW30
E	315	HIS	-	expression tag	UNP F1LW30
E	316	HIS	-	expression tag	UNP F1LW30

- Molecule 2 is a protein called LEUCINE-RICH REPEAT TRANSMEMBRANE PROTEIN FLRT2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	326	Total	C	N	O	S	0	0	0
			2587	1634	461	478	14			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	F	332	Total	C	N	O	S	0	0	0
			2641	1666	475	486	14			

There are 22 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	33	THR	-	expression tag	UNP Q8BLU0
B	34	GLY	-	expression tag	UNP Q8BLU0
B	363	ARG	-	expression tag	UNP Q8BLU0
B	364	THR	-	expression tag	UNP Q8BLU0
B	365	LYS	-	expression tag	UNP Q8BLU0
B	366	HIS	-	expression tag	UNP Q8BLU0
B	367	HIS	-	expression tag	UNP Q8BLU0
B	368	HIS	-	expression tag	UNP Q8BLU0
B	369	HIS	-	expression tag	UNP Q8BLU0
B	370	HIS	-	expression tag	UNP Q8BLU0
B	371	HIS	-	expression tag	UNP Q8BLU0
F	33	THR	-	expression tag	UNP Q8BLU0
F	34	GLY	-	expression tag	UNP Q8BLU0
F	363	ARG	-	expression tag	UNP Q8BLU0
F	364	THR	-	expression tag	UNP Q8BLU0
F	365	LYS	-	expression tag	UNP Q8BLU0
F	366	HIS	-	expression tag	UNP Q8BLU0
F	367	HIS	-	expression tag	UNP Q8BLU0
F	368	HIS	-	expression tag	UNP Q8BLU0
F	369	HIS	-	expression tag	UNP Q8BLU0
F	370	HIS	-	expression tag	UNP Q8BLU0
F	371	HIS	-	expression tag	UNP Q8BLU0

- Molecule 3 is a protein called ADHESION G PROTEIN-COUPLED RECEPTOR L3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	365	Total	C	N	O	S	0	0	0
			2943	1867	485	575	16			
3	D	263	Total	C	N	O	S	0	0	0
			2131	1360	351	415	5			
3	G	368	Total	C	N	O	S	0	0	0
			2968	1883	491	578	16			
3	H	261	Total	C	N	O	S	0	0	0
			2119	1354	349	411	5			

There are 44 discrepancies between the modelled and reference sequences:

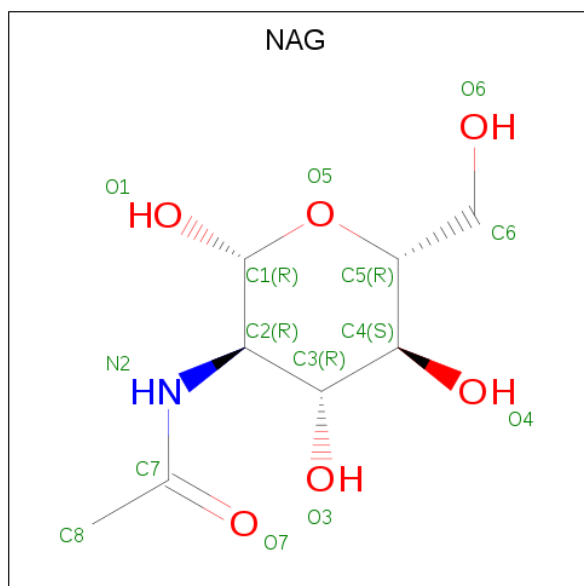
Chain	Residue	Modelled	Actual	Comment	Reference
C	90	THR	-	expression tag	UNP Q80TS3
C	91	GLY	-	expression tag	UNP Q80TS3
C	464	GLY	-	expression tag	UNP Q80TS3
C	465	THR	-	expression tag	UNP Q80TS3
C	466	LYS	-	expression tag	UNP Q80TS3
C	467	HIS	-	expression tag	UNP Q80TS3
C	468	HIS	-	expression tag	UNP Q80TS3
C	469	HIS	-	expression tag	UNP Q80TS3
C	470	HIS	-	expression tag	UNP Q80TS3
C	471	HIS	-	expression tag	UNP Q80TS3
C	472	HIS	-	expression tag	UNP Q80TS3
D	90	THR	-	expression tag	UNP Q80TS3
D	91	GLY	-	expression tag	UNP Q80TS3
D	464	GLY	-	expression tag	UNP Q80TS3
D	465	THR	-	expression tag	UNP Q80TS3
D	466	LYS	-	expression tag	UNP Q80TS3
D	467	HIS	-	expression tag	UNP Q80TS3
D	468	HIS	-	expression tag	UNP Q80TS3
D	469	HIS	-	expression tag	UNP Q80TS3
D	470	HIS	-	expression tag	UNP Q80TS3
D	471	HIS	-	expression tag	UNP Q80TS3
D	472	HIS	-	expression tag	UNP Q80TS3
G	90	THR	-	expression tag	UNP Q80TS3
G	91	GLY	-	expression tag	UNP Q80TS3
G	464	GLY	-	expression tag	UNP Q80TS3
G	465	THR	-	expression tag	UNP Q80TS3
G	466	LYS	-	expression tag	UNP Q80TS3
G	467	HIS	-	expression tag	UNP Q80TS3
G	468	HIS	-	expression tag	UNP Q80TS3
G	469	HIS	-	expression tag	UNP Q80TS3
G	470	HIS	-	expression tag	UNP Q80TS3
G	471	HIS	-	expression tag	UNP Q80TS3
G	472	HIS	-	expression tag	UNP Q80TS3
H	90	THR	-	expression tag	UNP Q80TS3
H	91	GLY	-	expression tag	UNP Q80TS3
H	464	GLY	-	expression tag	UNP Q80TS3
H	465	THR	-	expression tag	UNP Q80TS3
H	466	LYS	-	expression tag	UNP Q80TS3
H	467	HIS	-	expression tag	UNP Q80TS3
H	468	HIS	-	expression tag	UNP Q80TS3
H	469	HIS	-	expression tag	UNP Q80TS3
H	470	HIS	-	expression tag	UNP Q80TS3
H	471	HIS	-	expression tag	UNP Q80TS3

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Chain	Residue	Modelled	Actual	Comment	Reference
H	472	HIS	-	expression tag	UNP Q80TS3

- Molecule 4 is N-ACETYL-D-GLUCOSAMINE (three-letter code: NAG) (formula: $C_8H_{15}NO_6$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	1	Total	C	N	O	0	0
			14	8	1	5		
4	A	1	Total	C	N	O	0	0
			14	8	1	5		
4	B	1	Total	C	N	O	14	0
			14	8	1	5		
4	C	1	Total	C	N	O	14	0
			14	8	1	5		
4	E	1	Total	C	N	O	0	0
			14	8	1	5		
4	E	1	Total	C	N	O	0	0
			14	8	1	5		
4	F	1	Total	C	N	O	14	0
			14	8	1	5		
4	G	1	Total	C	N	O	14	0
			14	8	1	5		

- Molecule 5 is SODIUM ION (three-letter code: NA) (formula: Na).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	H	1	Total	Na	0	0
			1	1		

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	G	1	Total 1	Na 1	0	0
5	D	1	Total 1	Na 1	0	0
5	C	1	Total 1	Na 1	0	0

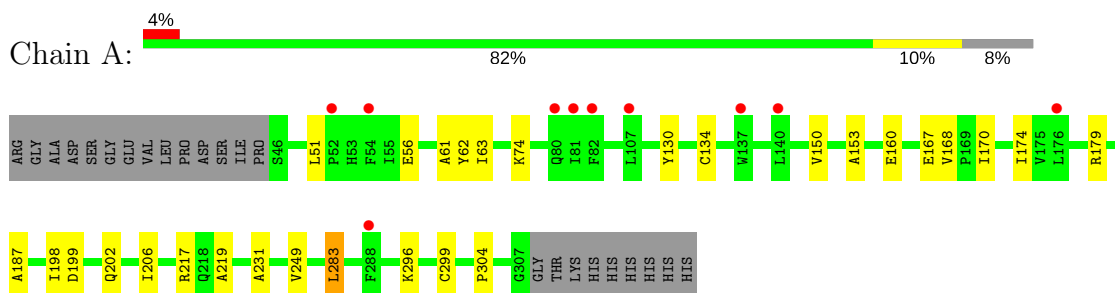
- Molecule 6 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	H	1	Total 1	Ca 1	0	0
6	G	1	Total 1	Ca 1	0	0
6	D	1	Total 1	Ca 1	0	0
6	C	1	Total 1	Ca 1	0	0

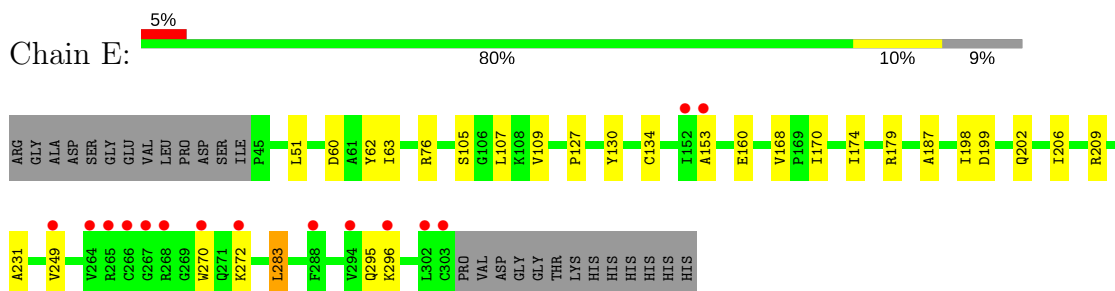
3 Residue-property plots [i](#)

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.

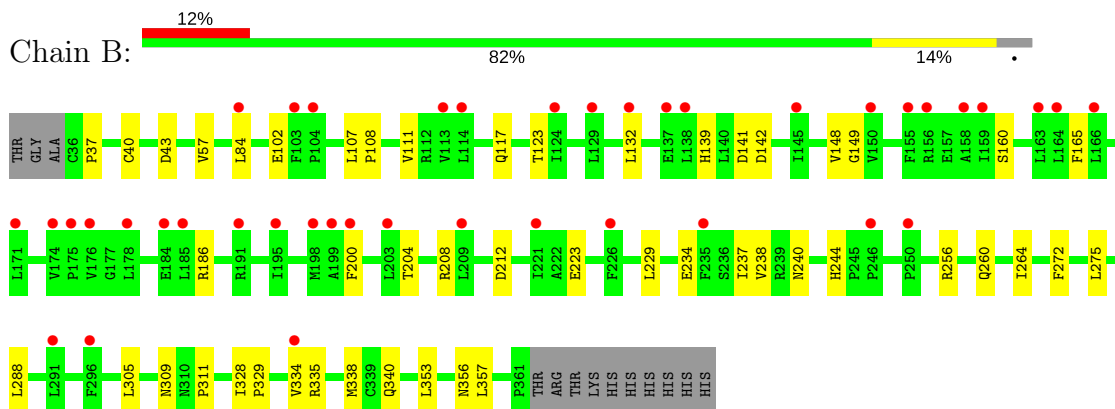
• Molecule 1: NETRIN RECEPTOR UNC5D



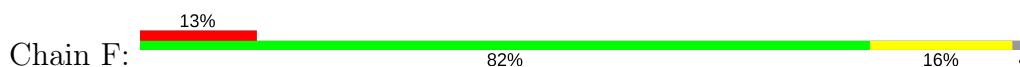
• Molecule 1: NETRIN RECEPTOR UNC5D

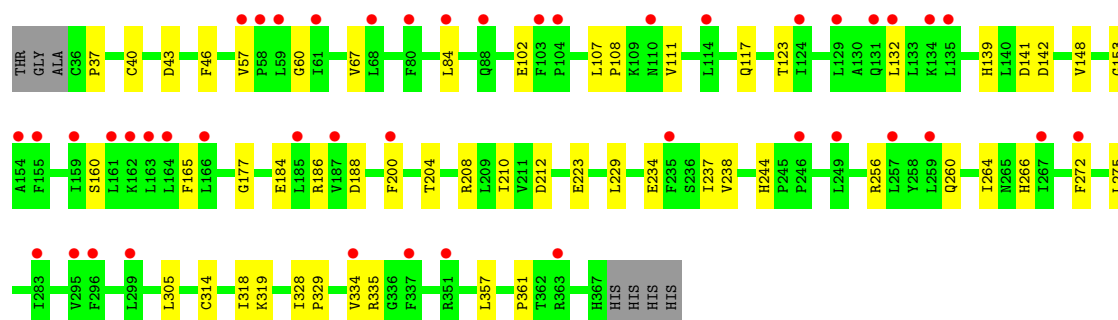


• Molecule 2: LEUCINE-RICH REPEAT TRANSMEMBRANE PROTEIN FLRT2

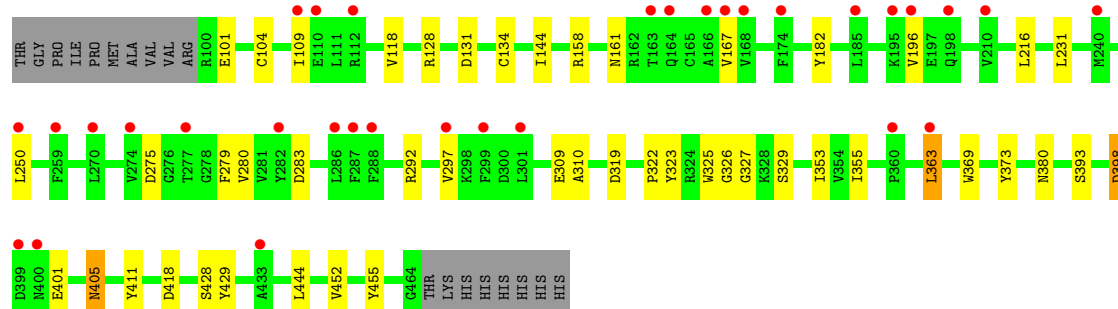
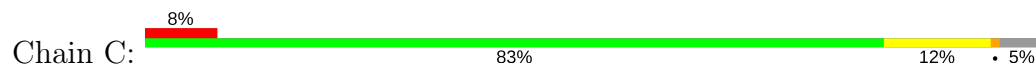


• Molecule 2: LEUCINE-RICH REPEAT TRANSMEMBRANE PROTEIN FLRT2

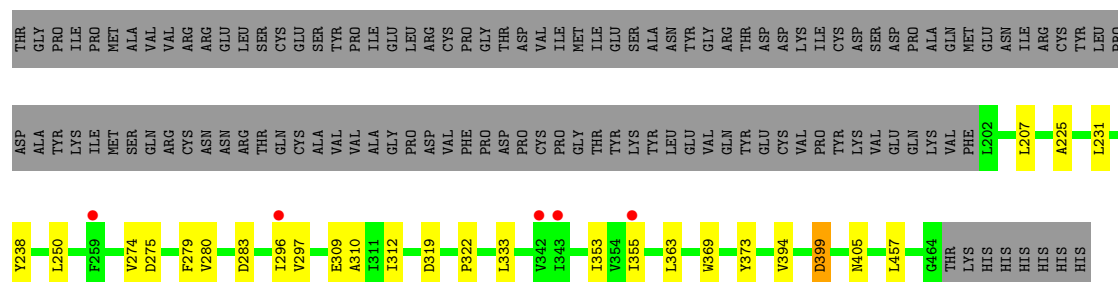




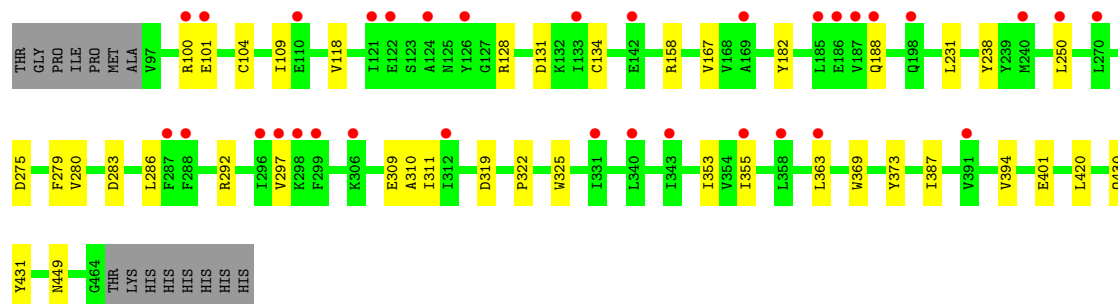
• Molecule 3: ADHESION G PROTEIN-COUPLLED RECEPTOR L3



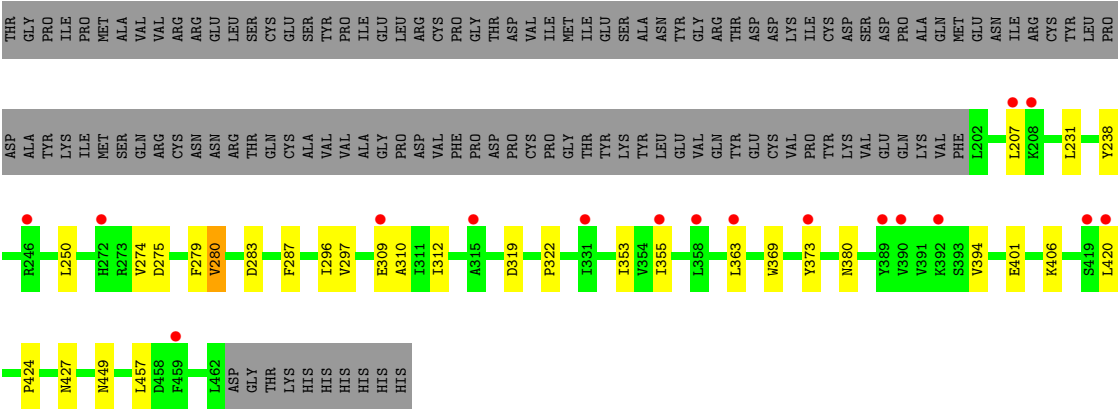
• Molecule 3: ADHESION G PROTEIN-COUPLLED RECEPTOR L3



• Molecule 3: ADHESION G PROTEIN-COUPLLED RECEPTOR L3



• Molecule 3: ADHESION G PROTEIN-COUPLLED RECEPTOR L3



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	231.96Å 141.49Å 151.49Å 90.00° 117.94° 90.00°	Depositor
Resolution (Å)	133.83 – 3.40 116.43 – 3.40	Depositor EDS
% Data completeness (in resolution range)	98.5 (133.83-3.40) 98.5 (116.43-3.40)	Depositor EDS
R_{merge}	0.15	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.23 (at 3.41Å)	Xtriage
Refinement program	BUSTER 2.10.2	Depositor
R, R_{free}	0.225 , 0.245 0.249 , 0.276	Depositor DCC
R_{free} test set	2832 reflections (4.83%)	wwPDB-VP
Wilson B-factor (Å ²)	121.2	Xtriage
Anisotropy	0.167	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.26 , 115.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.45$, $\langle L^2 \rangle = 0.27$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	19610	wwPDB-VP
Average B, all atoms (Å ²)	185.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.65% 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: NA, CA, NAG

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	0.35	0/2109	0.54	0/2863
1	E	0.34	0/2090	0.54	0/2836
2	B	0.38	0/2637	0.58	0/3583
2	F	0.38	0/2694	0.60	0/3661
3	C	0.38	0/3021	0.60	0/4115
3	D	0.37	0/2189	0.56	0/2982
3	G	0.38	0/3046	0.57	0/4149
3	H	0.37	0/2178	0.58	0/2969
All	All	0.37	0/19964	0.57	0/27158

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	2060	0	1970	12	0
1	E	2041	0	1955	16	0
2	B	2587	0	2593	22	0
2	F	2641	0	2648	25	0
3	C	2943	0	2786	21	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	D	2131	0	2015	14	0
3	G	2968	0	2817	20	0
3	H	2119	0	2009	15	0
4	A	28	0	26	0	0
4	B	14	0	13	0	0
4	C	14	0	13	0	0
4	E	28	0	26	0	0
4	F	14	0	13	0	0
4	G	14	0	13	0	0
5	C	1	0	0	0	0
5	D	1	0	0	0	0
5	G	1	0	0	0	0
5	H	1	0	0	0	0
6	C	1	0	0	0	0
6	D	1	0	0	0	0
6	G	1	0	0	0	0
6	H	1	0	0	0	0
All	All	19610	0	18897	134	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 134 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)
3:C:393:SER:HA	3:C:405:ASN:H	1.49	0.77
3:G:310:ALA:HB2	3:G:363:LEU:HB3	1.77	0.66
2:B:200:PHE:HB3	2:B:229:LEU:HD11	1.79	0.64
3:D:310:ALA:HB2	3:D:363:LEU:HB3	1.78	0.64
2:F:200:PHE:HB3	2:F:229:LEU:HD11	1.79	0.64

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	260/285 (91%)	247 (95%)	10 (4%)	3 (1%)	14	51
1	E	257/285 (90%)	246 (96%)	10 (4%)	1 (0%)	36	73
2	B	322/339 (95%)	280 (87%)	40 (12%)	2 (1%)	27	66
2	F	330/339 (97%)	291 (88%)	37 (11%)	2 (1%)	27	66
3	C	363/383 (95%)	332 (92%)	31 (8%)	0	100	100
3	D	259/383 (68%)	234 (90%)	25 (10%)	0	100	100
3	G	366/383 (96%)	333 (91%)	33 (9%)	0	100	100
3	H	259/383 (68%)	236 (91%)	23 (9%)	0	100	100
All	All	2416/2780 (87%)	2199 (91%)	209 (9%)	8 (0%)	43	77

5 of 8 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	304	PRO
2	B	223	GLU
1	A	130	TYR
1	A	219	ALA
1	E	130	TYR

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	225/244 (92%)	217 (96%)	8 (4%)	38	71
1	E	223/244 (91%)	216 (97%)	7 (3%)	43	75
2	B	297/308 (96%)	287 (97%)	10 (3%)	40	72
2	F	303/308 (98%)	294 (97%)	9 (3%)	44	75
3	C	324/340 (95%)	312 (96%)	12 (4%)	37	70
3	D	231/340 (68%)	227 (98%)	4 (2%)	63	84

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
3	G	327/340 (96%)	320 (98%)	7 (2%)	56 82
3	H	230/340 (68%)	224 (97%)	6 (3%)	49 78
All	All	2160/2464 (88%)	2097 (97%)	63 (3%)	45 76

5 of 63 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	C	428	SER
1	E	63	ILE
3	H	280	VAL
3	C	429	TYR
3	D	280	VAL

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

Mol	Chain	Res	Type
3	D	415	GLN
3	H	415	GLN
3	G	188	GLN
3	D	212	GLN
3	G	415	GLN

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 16 ligands modelled in this entry, 8 are monoatomic - leaving 8 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	$\# Z > 2$
4	NAG	A	1308	1	14,14,15	0.54	0	17,19,21	1.09	2 (11%)
4	NAG	A	1309	1	14,14,15	0.53	0	17,19,21	1.17	2 (11%)
4	NAG	B	1362	2	14,14,15	0.45	0	17,19,21	1.15	2 (11%)
4	NAG	C	1465	3	14,14,15	0.57	0	17,19,21	1.03	1 (5%)
4	NAG	E	1304	1	14,14,15	0.53	0	17,19,21	1.09	2 (11%)
4	NAG	E	1305	1	14,14,15	0.51	0	17,19,21	1.18	2 (11%)
4	NAG	F	1368	2	14,14,15	0.45	0	17,19,21	1.15	2 (11%)
4	NAG	G	1465	3	14,14,15	0.59	0	17,19,21	0.88	1 (5%)

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	NAG	A	1308	1	-	0/6/23/26	0/1/1/1
4	NAG	A	1309	1	-	0/6/23/26	0/1/1/1
4	NAG	B	1362	2	-	0/6/23/26	0/1/1/1
4	NAG	C	1465	3	-	0/6/23/26	0/1/1/1
4	NAG	E	1304	1	-	0/6/23/26	0/1/1/1
4	NAG	E	1305	1	-	0/6/23/26	0/1/1/1
4	NAG	F	1368	2	-	0/6/23/26	0/1/1/1
4	NAG	G	1465	3	-	0/6/23/26	0/1/1/1

There are no bond length outliers.

The worst 5 of 14 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	E	1305	NAG	C4-C3-C2	-2.47	107.40	111.02
4	A	1309	NAG	C4-C3-C2	-2.36	107.56	111.02
4	B	1362	NAG	C4-C3-C2	-2.32	107.62	111.02
4	F	1368	NAG	C4-C3-C2	-2.32	107.62	111.02

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	E	1304	NAG	C4-C3-C2	-2.26	107.70	111.02

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](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
2	B	1
3	D	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	B	307:ALA	C	308:ARG	N	3.10
1	D	295:ASN	C	296:ILE	N	3.01

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	262/285 (91%)	0.08	10 (3%) 40 38	162, 190, 241, 269	0
1	E	259/285 (90%)	0.11	15 (5%) 23 23	155, 185, 236, 251	0
2	B	326/339 (96%)	0.61	41 (12%) 3 4	127, 162, 226, 250	0
2	F	332/339 (97%)	0.55	44 (13%) 3 4	120, 159, 208, 237	0
3	C	365/383 (95%)	0.37	32 (8%) 10 11	112, 152, 257, 274	0
3	D	263/383 (68%)	-0.22	5 (1%) 66 65	187, 227, 271, 278	0
3	G	368/383 (96%)	0.32	33 (8%) 9 11	121, 173, 262, 277	0
3	H	261/383 (68%)	0.17	17 (6%) 19 20	153, 190, 239, 255	0
All	All	2436/2780 (87%)	0.28	197 (8%) 12 13	112, 181, 254, 278	0

The worst 5 of 197 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	C	166	ALA	9.9
3	C	110	GLU	8.3
1	E	303	CYS	7.3
1	E	302	LEU	6.8
3	D	296	ILE	6.1

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

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	NAG	E	1304	14/15	0.80	0.29	223,227,230,231	0
4	NAG	C	1465	14/15	-	-	256,264,272,272	14
4	NAG	F	1368	14/15	-	-	209,210,212,213	14
4	NAG	B	1362	14/15	-	-	188,192,199,203	14
6	CA	C	1467	1/1	0.98	0.30	138,138,138,138	0
4	NAG	G	1465	14/15	-	-	262,269,274,275	14
4	NAG	A	1308	14/15	0.69	0.28	227,230,233,234	0
4	NAG	A	1309	14/15	0.75	0.36	212,216,218,220	0
6	CA	H	1464	1/1	0.86	0.17	196,196,196,196	0
4	NAG	E	1305	14/15	0.90	0.20	205,209,211,211	0
6	CA	D	1466	1/1	0.90	0.10	221,221,221,221	0
6	CA	G	1467	1/1	0.93	0.24	146,146,146,146	0
5	NA	C	1466	1/1	0.93	0.14	136,136,136,136	0
5	NA	D	1465	1/1	0.94	0.06	221,221,221,221	0
5	NA	G	1466	1/1	0.97	0.08	130,130,130,130	0
5	NA	H	1463	1/1	0.98	0.10	195,195,195,195	0

6.5 Other polymers

There are no such residues in this entry.