wwPDB X-ray Structure Validation Summary Report (i)

Feb 1, 2016 – 12:25 AM GMT

PDB ID	:	2ACL
Title	:	Liver X-Receptor alpha Ligand Binding Domain with SB313987
Authors	:	Jaye, M.C.; Krawiec, J.A.; Campobasso, N.; Smallwood, A.; Qiu, C.; Lu, Q.; Kerrigan, J.J.
Deposited on	:	2005-07-19
Resolution	:	2.80 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
http://wwpdb.org/validation/2016/XrayValidationReportHelp
with specific help available everywhere you see the (i) symbol.

The following versions of software and data (see references (1)) were used in the production of this report:

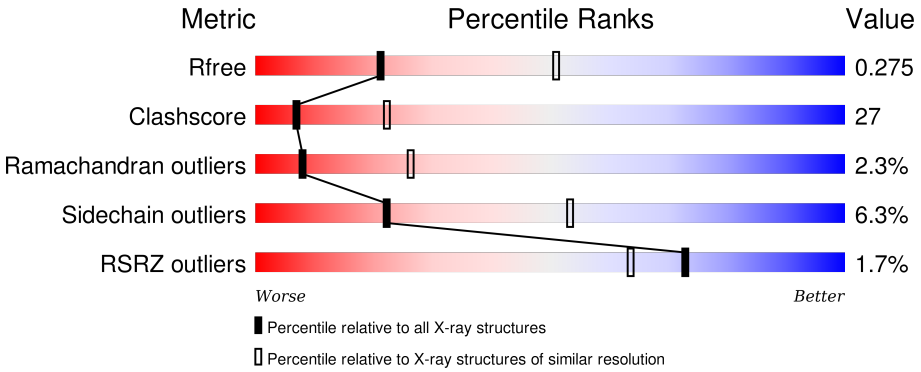
MolProbity	:	4.02b-467
Mogul	:	1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix)	:	1.9-1692
EDS	:	rb-20026688
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac	:	5.8.0135
CCP4	:	6.5.0
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	trunk26865

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 2.80 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}	91344	2393 (2.80-2.80)
Clashscore	102246	2827 (2.80-2.80)
Ramachandran outliers	100387	2782 (2.80-2.80)
Sidechain outliers	100360	2784 (2.80-2.80)
RSRZ outliers	91569	2404 (2.80-2.80)

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 <=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	238	50% 35% 5% 10%
1	C	238	56% 32% • 10%
1	E	238	55% 31% 5% 10%
1	G	238	47% 39% • 10%
2	B	244	52% 42% 5% ••

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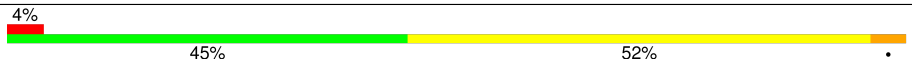
Mol	Chain	Length	Quality of chain
2	D	244	
2	F	244	
2	H	244	

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 14858 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 Retinoic acid receptor RXR-alpha.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	214	Total	C	N	O	S	0	0	0
			1682	1078	289	305	10			
1	C	215	Total	C	N	O	S	0	0	0
			1689	1083	290	306	10			
1	E	214	Total	C	N	O	S	0	0	0
			1682	1078	289	305	10			
1	G	214	Total	C	N	O	S	0	0	0
			1682	1078	289	305	10			

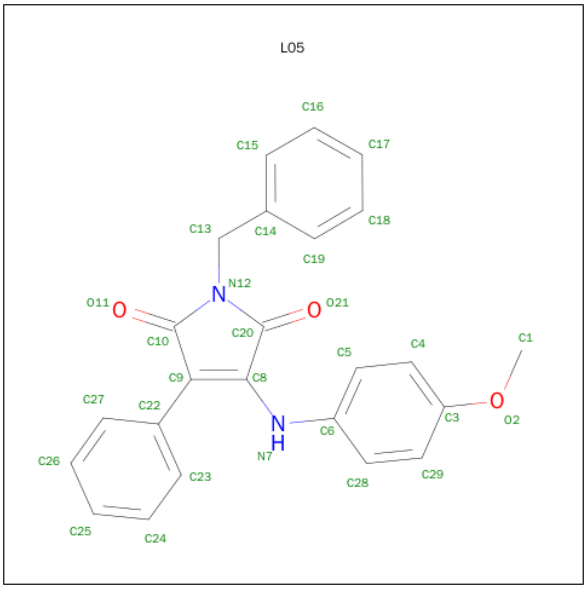
- Molecule 2 is a protein called Oxysterols receptor LXR-alpha.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	242	Total	C	N	O	S	0	0	0
			1966	1255	343	361	7			
2	D	242	Total	C	N	O	S	0	0	0
			1966	1255	343	361	7			
2	F	242	Total	C	N	O	S	0	0	0
			1966	1255	343	361	7			
2	H	244	Total	C	N	O	S	0	0	0
			1985	1266	347	365	7			

There are 8 discrepancies between the modelled and reference sequences:

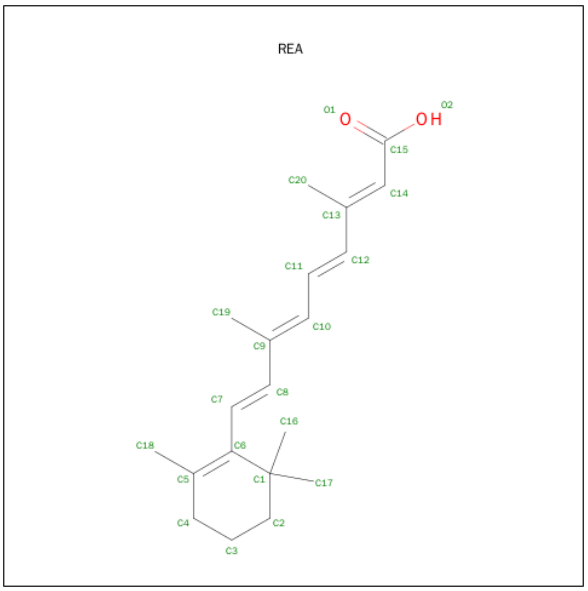
Chain	Residue	Modelled	Actual	Comment	Reference
B	202	VAL	-	CLONING ARTIFACT	UNP Q9Z0Y9
B	399	PRO	ARG	VARIANT	UNP Q9Z0Y9
D	202	VAL	-	CLONING ARTIFACT	UNP Q9Z0Y9
D	399	PRO	ARG	VARIANT	UNP Q9Z0Y9
F	202	VAL	-	CLONING ARTIFACT	UNP Q9Z0Y9
F	399	PRO	ARG	VARIANT	UNP Q9Z0Y9
H	202	VAL	-	CLONING ARTIFACT	UNP Q9Z0Y9
H	399	PRO	ARG	VARIANT	UNP Q9Z0Y9

- Molecule 3 is 1-BENZYL-3-(4-METHOXYPHENYLAMINO)-4-PHENYLPYRROLE-2,5-DIONE (three-letter code: L05) (formula: $C_{24}H_{20}N_2O_3$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	B	1	Total	C	N	O	0	0
			29	24	2	3		
3	D	1	Total	C	N	O	0	0
			29	24	2	3		
3	F	1	Total	C	N	O	0	0
			29	24	2	3		
3	H	1	Total	C	N	O	0	0
			29	24	2	3		

- Molecule 4 is RETINOIC ACID (three-letter code: REA) (formula: $C_{20}H_{28}O_2$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	G	1	Total C O 22 20 2	0	0
4	A	1	Total C O 22 20 2	0	0
4	C	1	Total C O 22 20 2	0	0
4	E	1	Total C O 22 20 2	0	0

- Molecule 5 is water.

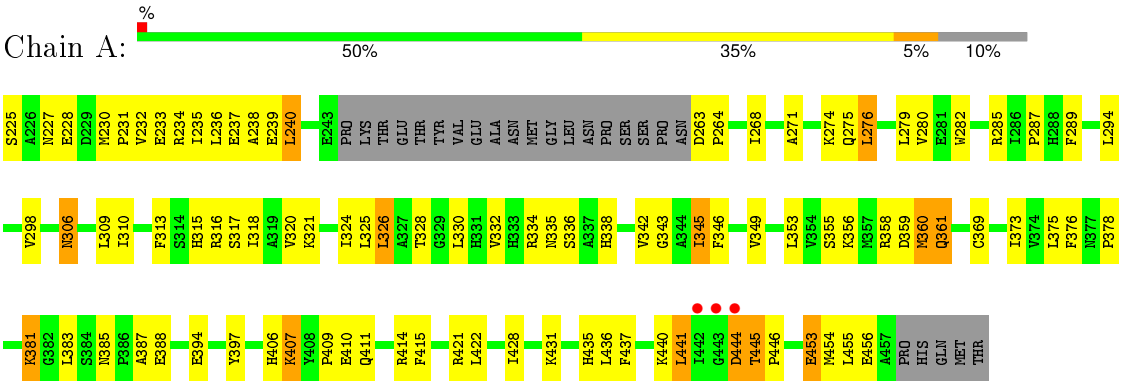
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	5	Total O 5 5	0	0
5	B	4	Total O 4 4	0	0
5	C	3	Total O 3 3	0	0
5	D	7	Total O 7 7	0	0
5	E	4	Total O 4 4	0	0
5	F	6	Total O 6 6	0	0
5	G	5	Total O 5 5	0	0
5	H	2	Total O 2 2	0	0

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 errors 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.

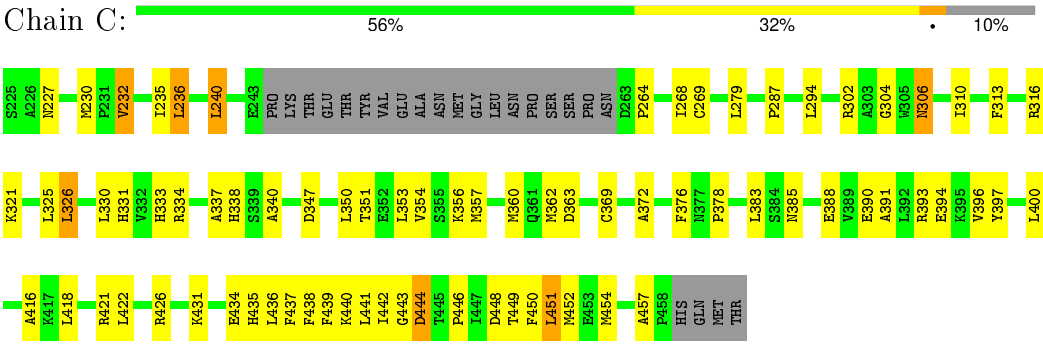
- Molecule 1: Retinoic acid receptor RXR-alpha

Chain A:



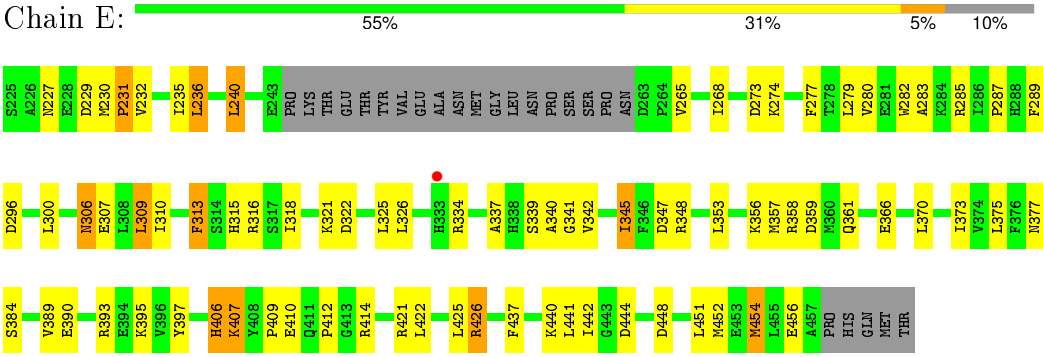
- Molecule 1: Retinoic acid receptor RXR-alpha

Chain C:



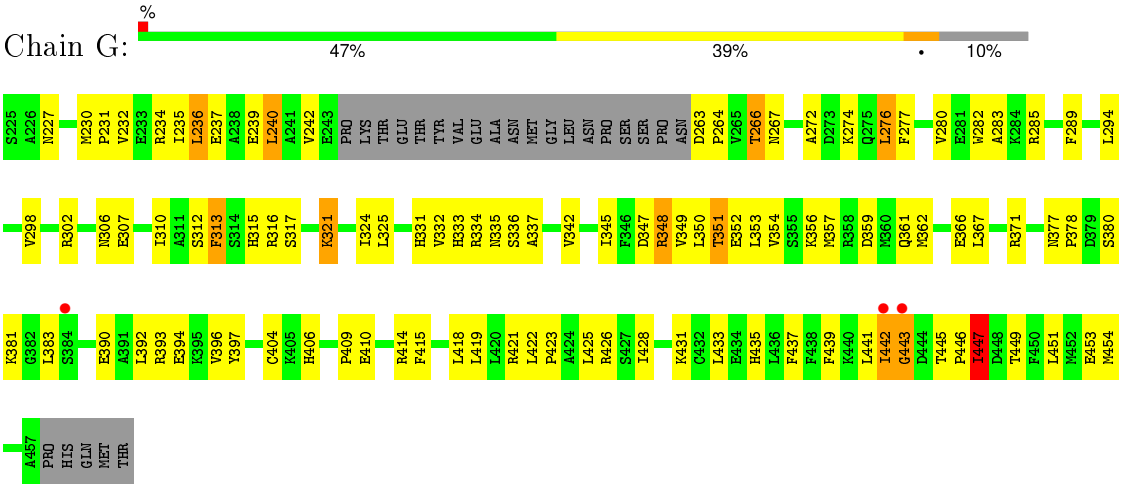
- Molecule 1: Retinoic acid receptor RXR-alpha

Chain E:



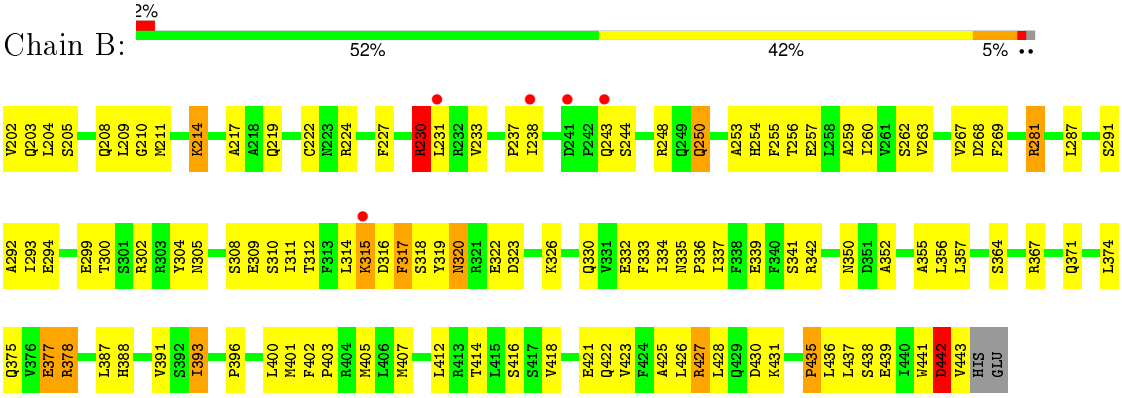
- Molecule 1: Retinoic acid receptor RXR-alpha

Chain G:



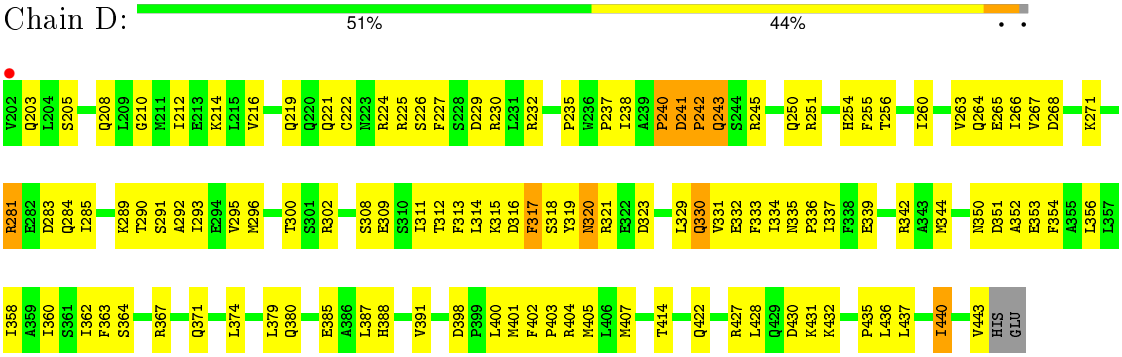
- Molecule 2: Oxysterols receptor LXR-alpha

Chain B:



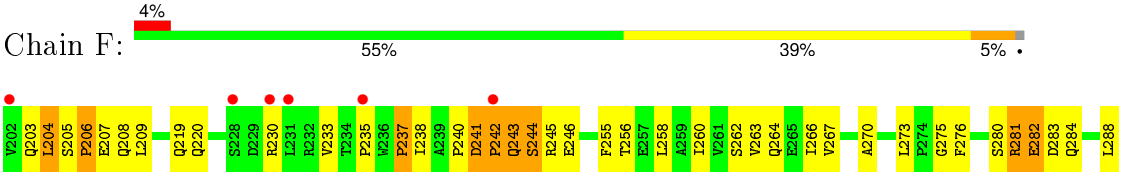
- Molecule 2: Oxysterols receptor LXR-alpha

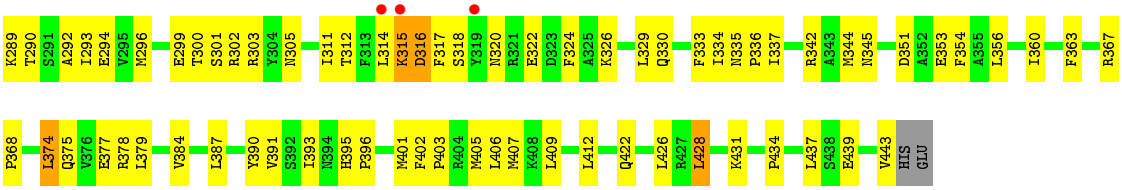
Chain D:



- Molecule 2: Oxysterols receptor LXR-alpha

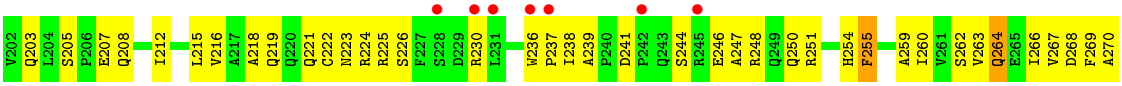
Chain F:

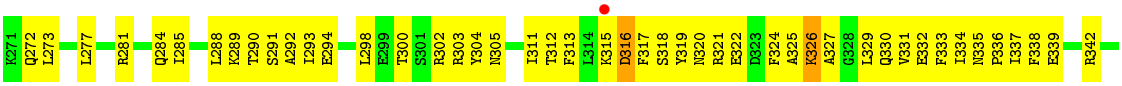


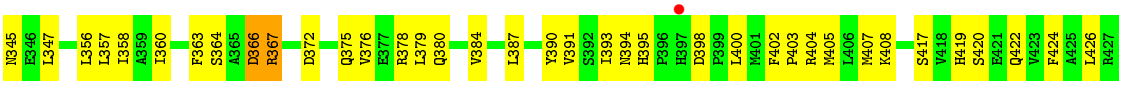


- Molecule 2: Oxysterols receptor LXR-alpha

Chain H:







4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α, β, γ	60.77Å 81.95Å 111.44Å 88.98° 75.20° 78.27°	Depositor
Resolution (Å)	30.00 – 2.80 45.58 – 2.74	Depositor EDS
% Data completeness (in resolution range)	95.0 (30.00-2.80) 89.9 (45.58-2.74)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.81 (at 2.73Å)	Xtriage
Refinement program	CNX	Depositor
R, R_{free}	0.210 , 0.280 0.205 , 0.275	Depositor DCC
R_{free} test set	2412 reflections (5.48%)	DCC
Wilson B-factor (Å^2)	39.6	Xtriage
Anisotropy	0.371	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.31 , 48.3	EDS
Estimated twinning fraction	0.008 for -h,-k,-h+l	Xtriage
L-test for twinning[2]	$< \|L\| > = 0.49$, $< L^2 > = 0.32$	Xtriage
Outliers	0 of 50018 reflections	Xtriage
F_o,F_c correlation	0.92	EDS
Total number of atoms	14858	wwPDB-VP
Average B, all atoms (Å^2)	39.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.81% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ for acentric reflections are 0.5, 0.375 respectively for untwinned datasets, and 0.333, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: L05, REA

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	0/1714	0.64	0/2317
1	C	0.42	0/1722	0.63	0/2329
1	E	0.37	0/1714	0.62	0/2317
1	G	0.40	0/1714	0.61	0/2317
2	B	0.40	0/2008	0.60	0/2721
2	D	0.42	0/2008	0.59	0/2721
2	F	0.38	0/2008	0.54	0/2721
2	H	0.39	0/2028	0.56	0/2748
All	All	0.39	0/14916	0.60	0/20191

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

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	1682	0	1713	101	0
1	C	1689	0	1720	82	0
1	E	1682	0	1713	80	0
1	G	1682	0	1713	115	0
2	B	1966	0	1973	108	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	D	1966	0	1973	129	0
2	F	1966	0	1973	94	0
2	H	1985	0	1986	154	0
3	B	29	0	20	0	0
3	D	29	0	20	2	0
3	F	29	0	20	1	0
3	H	29	0	20	1	0
4	A	22	0	27	0	0
4	C	22	0	27	0	0
4	E	22	0	27	0	0
4	G	22	0	27	0	0
5	A	5	0	0	0	0
5	B	4	0	0	1	0
5	C	3	0	0	1	0
5	D	7	0	0	0	0
5	E	4	0	0	0	0
5	F	6	0	0	2	0
5	G	5	0	0	0	0
5	H	2	0	0	2	0
All	All	14858	0	14952	793	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 27.

The worst 5 of 793 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:A:385:ASN:HD22	1:A:388:GLU:HG3	1.31	0.95
2:H:387:LEU:O	2:H:391:VAL:HG22	1.69	0.91
1:E:454:MET:HE2	2:F:263:VAL:HG12	1.52	0.91
2:F:299:GLU:HG3	2:F:303:ARG:HH12	1.33	0.91
1:C:302:ARG:HH12	2:H:330:GLN:HE22	1.22	0.88

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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	210/238 (88%)	181 (86%)	23 (11%)	6 (3%)	6 19
1	C	211/238 (89%)	191 (90%)	19 (9%)	1 (0%)	34 69
1	E	210/238 (88%)	189 (90%)	18 (9%)	3 (1%)	14 42
1	G	210/238 (88%)	185 (88%)	21 (10%)	4 (2%)	10 32
2	B	240/244 (98%)	206 (86%)	24 (10%)	10 (4%)	3 11
2	D	240/244 (98%)	220 (92%)	16 (7%)	4 (2%)	11 36
2	F	240/244 (98%)	209 (87%)	23 (10%)	8 (3%)	5 16
2	H	242/244 (99%)	206 (85%)	31 (13%)	5 (2%)	9 29
All	All	1803/1928 (94%)	1587 (88%)	175 (10%)	41 (2%)	8 26

5 of 41 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	441	LEU
1	A	454	MET
2	B	314	LEU
2	D	203	GLN
2	D	240	PRO

5.3.2 Protein sidechains

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	182/205 (89%)	171 (94%)	11 (6%)	24 56

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	C	183/205 (89%)	172 (94%)	11 (6%)	24 56
1	E	182/205 (89%)	167 (92%)	15 (8%)	14 38
1	G	182/205 (89%)	170 (93%)	12 (7%)	21 51
2	B	219/221 (99%)	201 (92%)	18 (8%)	14 38
2	D	219/221 (99%)	204 (93%)	15 (7%)	20 49
2	F	219/221 (99%)	208 (95%)	11 (5%)	30 64
2	H	221/221 (100%)	213 (96%)	8 (4%)	42 76
All	All	1607/1704 (94%)	1506 (94%)	101 (6%)	22 53

5 of 101 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	D	293	ILE
1	E	236	LEU
2	H	255	PHE
2	D	317	PHE
2	D	385	GLU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 62 such sidechains are listed below:

Mol	Chain	Res	Type
2	D	320	ASN
1	E	275	GLN
2	H	320	ASN
2	D	380	GLN
1	E	335	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)

8 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
4	REA	A	502	-	19,22,22	2.01	4 (21%)	26,30,30	1.25	1 (3%)
3	L05	B	101	-	32,32,32	1.74	10 (31%)	40,44,44	0.81	1 (2%)
4	REA	C	503	-	19,22,22	1.74	3 (15%)	26,30,30	1.45	3 (11%)
3	L05	D	102	-	32,32,32	1.61	9 (28%)	40,44,44	0.81	1 (2%)
4	REA	E	504	-	19,22,22	1.65	3 (15%)	26,30,30	1.22	2 (7%)
3	L05	F	103	-	32,32,32	1.79	12 (37%)	40,44,44	0.85	2 (5%)
4	REA	G	501	-	19,22,22	1.60	3 (15%)	26,30,30	1.26	3 (11%)
3	L05	H	104	-	32,32,32	1.67	11 (34%)	40,44,44	0.83	2 (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	REA	A	502	-	-	0/13/32/32	0/1/1/1
3	L05	B	101	-	-	0/14/34/34	0/4/4/4
4	REA	C	503	-	-	0/13/32/32	0/1/1/1
3	L05	D	102	-	-	0/14/34/34	0/4/4/4
4	REA	E	504	-	-	0/13/32/32	0/1/1/1
3	L05	F	103	-	-	0/14/34/34	0/4/4/4
4	REA	G	501	-	-	0/13/32/32	0/1/1/1
3	L05	H	104	-	-	0/14/34/34	0/4/4/4

The worst 5 of 55 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	101	L05	C28-C6	2.00	1.42	1.39
3	H	104	L05	C5-C4	2.01	1.42	1.38
3	D	102	L05	C16-C15	2.02	1.43	1.38
3	F	103	L05	C4-C3	2.02	1.42	1.38
4	E	504	REA	C20-C13	2.03	1.55	1.50

The worst 5 of 15 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
4	G	501	REA	C18-C5-C4	-2.55	108.58	113.43
4	E	504	REA	C18-C5-C4	-2.44	108.81	113.43
4	C	503	REA	C18-C5-C4	-2.34	108.98	113.43
3	D	102	L05	O11-C10-C9	-2.25	124.64	128.97
3	F	103	L05	O11-C10-C9	-2.19	124.74	128.97

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

3 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	D	102	L05	2	0
3	F	103	L05	1	0
3	H	104	L05	1	0

5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

6 Fit of model and data

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, 95^{th} 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	214/238 (89%)	-0.38	3 (1%) 78 69	12, 33, 58, 84	0
1	C	215/238 (90%)	-0.61	0 100 100	9, 28, 48, 54	0
1	E	214/238 (89%)	-0.48	1 (0%) 91 88	16, 36, 54, 64	0
1	G	214/238 (89%)	-0.32	3 (1%) 78 69	15, 37, 61, 82	0
2	B	242/244 (99%)	-0.30	5 (2%) 67 56	13, 36, 76, 99	0
2	D	242/244 (99%)	-0.44	1 (0%) 93 90	9, 30, 64, 90	0
2	F	242/244 (99%)	-0.13	9 (3%) 45 33	16, 40, 100, 110	0
2	H	244/244 (100%)	-0.14	9 (3%) 45 33	21, 43, 94, 104	0
All	All	1827/1928 (94%)	-0.34	31 (1%) 73 63	9, 36, 76, 110	0

The worst 5 of 31 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	F	202	VAL	6.4
1	A	442	ILE	5.0
2	H	231	LEU	4.8
2	D	202	VAL	4.6
1	A	443	GLY	4.6

6.2 Non-standard residues in protein, DNA, RNA chains

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates

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. 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, 95^{th} 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
4	REA	C	503	22/22	0.96	0.17	1.54	6,19,20,21	0
3	L05	F	103	29/29	0.92	0.21	0.84	37,42,49,52	0
4	REA	A	502	22/22	0.93	0.19	0.74	23,28,31,32	0
4	REA	E	504	22/22	0.95	0.18	0.41	11,16,23,25	0
3	L05	H	104	29/29	0.94	0.17	0.39	30,35,43,49	0
3	L05	D	102	29/29	0.96	0.16	0.37	8,14,21,24	0
4	REA	G	501	22/22	0.95	0.17	0.26	11,20,25,26	0
3	L05	B	101	29/29	0.97	0.14	-0.12	22,25,31,32	0

6.5 Other polymers

There are no such residues in this entry.