



wwPDB X-ray Structure Validation Summary Report ⓘ

Jan 31, 2016 – 08:25 PM GMT

PDB ID : 1K7L
Title : The 2.5 Angstrom resolution crystal structure of the human PPARalpha ligand binding domain bound with GW409544 and a co-activator peptide.
Authors : Xu, H.E.; Lambert, M.H.; Montana, V.G.; Moore, L.B.; Collins, J.L.; Oplinger, J.A.; Kliewer, S.A.; Gampe Jr., R.T.; McKee, D.D.; Moore, J.T.; Willson, T.M.
Deposited on : 2001-10-19
Resolution : 2.50 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 ⓘ 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 (RC4), CSD as536be (2015)
Xtriage (Phenix) : **NOT EXECUTED**
EDS : **NOT EXECUTED**
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

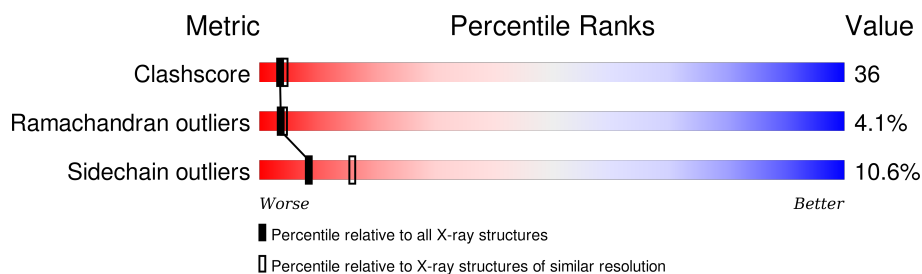
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.50 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
Clashscore	102246	4242 (2.50-2.50)
Ramachandran outliers	100387	4156 (2.50-2.50)
Sidechain outliers	100360	4158 (2.50-2.50)


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.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	288	
1	C	288	
1	E	288	
1	G	288	
2	B	21	
2	D	21	
2	F	21	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
2	H	21	 A horizontal bar chart showing the quality of chain H. The bar is divided into four segments: 14% (green), 43% (yellow), 5% (orange), and 38% (grey). The segments are labeled with their respective percentages: 14%, 43%, 5%, and 38%.

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
4	544	A	469	X	-	-	-
4	544	C	470	X	-	-	-
4	544	E	501	X	-	-	-
4	544	G	601	X	-	-	-

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 9308 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 Peroxisome proliferator activated receptor alpha.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	267	Total	C	N	O	S	0	0	0
			2118	1359	355	386	18			
1	C	267	Total	C	N	O	S	0	0	0
			2118	1359	355	386	18			
1	E	267	Total	C	N	O	S	0	0	0
			2118	1359	355	386	18			
1	G	267	Total	C	N	O	S	0	0	0
			2118	1359	355	386	18			

There are 44 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	181	MET	-	EXPRESSION TAG	UNP Q07869
A	182	LYS	-	EXPRESSION TAG	UNP Q07869
A	183	LYS	-	EXPRESSION TAG	UNP Q07869
A	184	GLY	-	EXPRESSION TAG	UNP Q07869
A	185	HIS	-	EXPRESSION TAG	UNP Q07869
A	186	HIS	-	EXPRESSION TAG	UNP Q07869
A	187	HIS	-	EXPRESSION TAG	UNP Q07869
A	188	HIS	-	EXPRESSION TAG	UNP Q07869
A	189	HIS	-	EXPRESSION TAG	UNP Q07869
A	190	HIS	-	EXPRESSION TAG	UNP Q07869
A	191	GLY	-	EXPRESSION TAG	UNP Q07869
C	181	MET	-	EXPRESSION TAG	UNP Q07869
C	182	LYS	-	EXPRESSION TAG	UNP Q07869
C	183	LYS	-	EXPRESSION TAG	UNP Q07869
C	184	GLY	-	EXPRESSION TAG	UNP Q07869
C	185	HIS	-	EXPRESSION TAG	UNP Q07869
C	186	HIS	-	EXPRESSION TAG	UNP Q07869
C	187	HIS	-	EXPRESSION TAG	UNP Q07869
C	188	HIS	-	EXPRESSION TAG	UNP Q07869
C	189	HIS	-	EXPRESSION TAG	UNP Q07869
C	190	HIS	-	EXPRESSION TAG	UNP Q07869

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
C	191	GLY	-	EXPRESSION TAG	UNP Q07869
E	181	MET	-	EXPRESSION TAG	UNP Q07869
E	182	LYS	-	EXPRESSION TAG	UNP Q07869
E	183	LYS	-	EXPRESSION TAG	UNP Q07869
E	184	GLY	-	EXPRESSION TAG	UNP Q07869
E	185	HIS	-	EXPRESSION TAG	UNP Q07869
E	186	HIS	-	EXPRESSION TAG	UNP Q07869
E	187	HIS	-	EXPRESSION TAG	UNP Q07869
E	188	HIS	-	EXPRESSION TAG	UNP Q07869
E	189	HIS	-	EXPRESSION TAG	UNP Q07869
E	190	HIS	-	EXPRESSION TAG	UNP Q07869
E	191	GLY	-	EXPRESSION TAG	UNP Q07869
G	181	MET	-	EXPRESSION TAG	UNP Q07869
G	182	LYS	-	EXPRESSION TAG	UNP Q07869
G	183	LYS	-	EXPRESSION TAG	UNP Q07869
G	184	GLY	-	EXPRESSION TAG	UNP Q07869
G	185	HIS	-	EXPRESSION TAG	UNP Q07869
G	186	HIS	-	EXPRESSION TAG	UNP Q07869
G	187	HIS	-	EXPRESSION TAG	UNP Q07869
G	188	HIS	-	EXPRESSION TAG	UNP Q07869
G	189	HIS	-	EXPRESSION TAG	UNP Q07869
G	190	HIS	-	EXPRESSION TAG	UNP Q07869
G	191	GLY	-	EXPRESSION TAG	UNP Q07869

- Molecule 2 is a protein called steroid receptor coactivator.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf	Trace
2	B	13	Total C N O 110 68 24 18	0	0	0
2	D	13	Total C N O 110 68 24 18	0	0	0
2	F	13	Total C N O 110 68 24 18	0	0	0
2	H	13	Total C N O 110 68 24 18	0	0	0

- Molecule 3 is YTTRIUM (III) ION (three-letter code: YT3) (formula: Y).

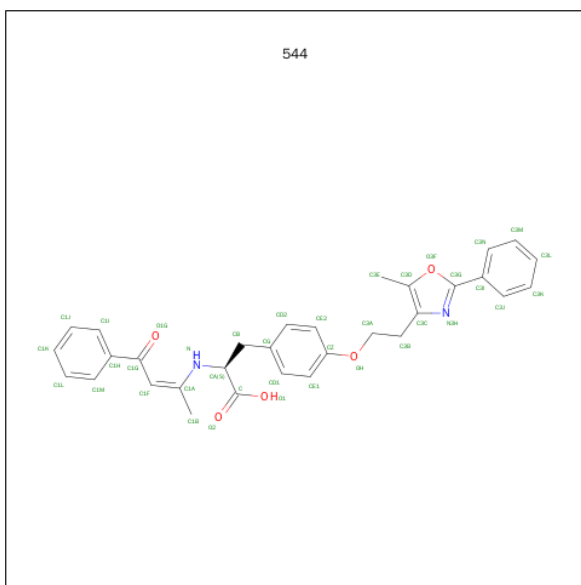
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	C	1	Total Y 1 1	0	0

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	E	1	Total Y 1 1	0	0

- Molecule 4 is 2-(1-METHYL-3-OXO-3-PHENYL-PROPYLAMINO)-3-{4-[2-(5-METHYL-2-PHENYL-OXAZOL-4-YL)-ETHOXY]-PHENYL}-PROPIONIC ACID (three-letter code: 544) (formula: C₃₁H₃₀N₂O₅).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total C N O 38 31 2 5	0	0
4	C	1	Total C N O 38 31 2 5	0	0
4	E	1	Total C N O 38 31 2 5	0	0
4	G	1	Total C N O 38 31 2 5	0	0

- Molecule 5 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	46	Total O 46 46	0	0
5	C	76	Total O 76 76	0	0
5	D	7	Total O 7 7	0	0

Continued on next page...

Continued from previous page...

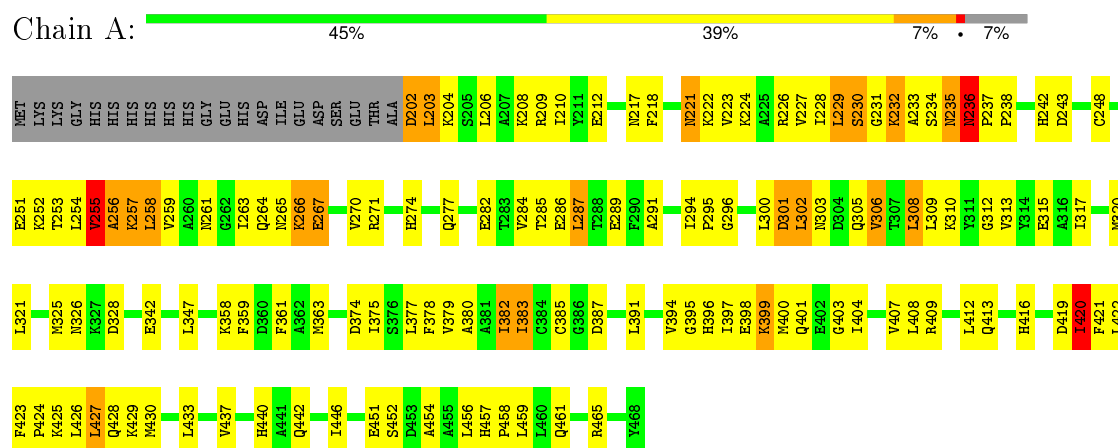
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	E	51	Total 51	O 51	0	0
5	F	1	Total 1	O 1	0	0
5	G	57	Total 57	O 57	0	0
5	H	4	Total 4	O 4	0	0

3 Residue-property plots

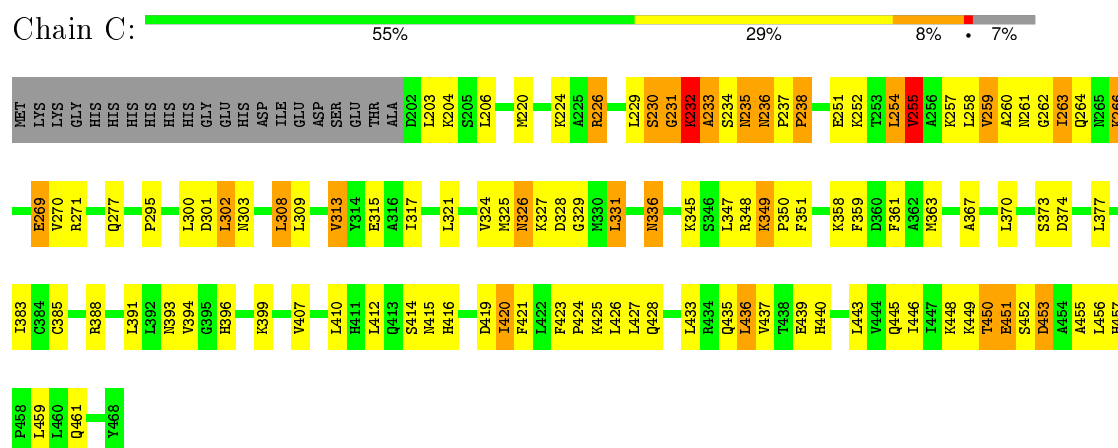
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according 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.

Note EDS was not executed.

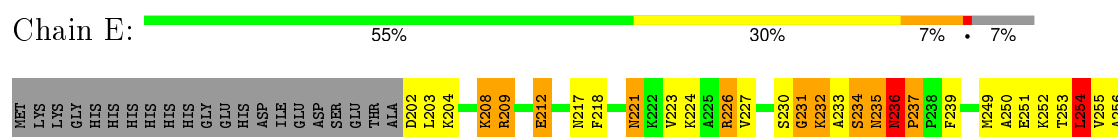
- Molecule 1: Peroxisome proliferator activated receptor alpha

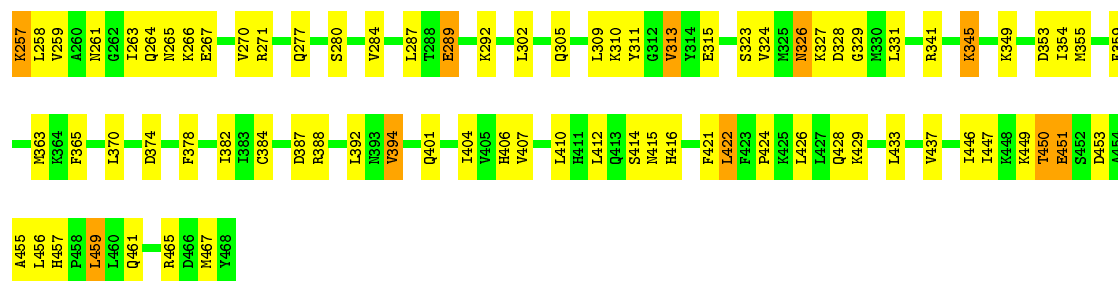


- Molecule 1: Peroxisome proliferator activated receptor alpha



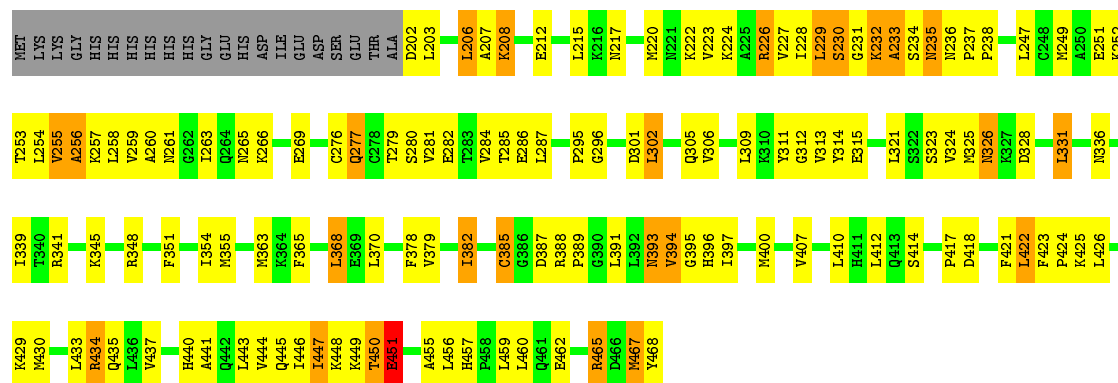
- Molecule 1: Peroxisome proliferator activated receptor alpha





- Molecule 1: Peroxisome proliferator activated receptor alpha

Chain G: 46% 38% 9% 7%



- Molecule 2: steroid receptor coactivator

Chain B: 24% 33% 5% 38%



- Molecule 2: steroid receptor coactivator

Chain D: 24% 24% 14% 38%



- Molecule 2: steroid receptor coactivator

Chain F: 19% 38% 5% 38%



- Molecule 2: steroid receptor coactivator

Chain H: 14% 43% 5% 38%

HIS	SER	SER	LEU	THR	E685	E686	H687	E688	L689	L690	H691	E692	L693	L694	Q695	E696	E697	SER	PRO	SER
-----	-----	-----	-----	-----	------	------	------	------	------	------	------	------	------	------	------	------	------	-----	-----	-----

4 Data and refinement statistics

Xtriage (Phenix) and EDS were not executed - this section will therefore be incomplete.

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	95.56 Å 121.60 Å 121.99 Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	19.99 – 2.50	Depositor
% Data completeness (in resolution range)	98.3 (19.99-2.50)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	0.05	Depositor
Refinement program	CNX 2000.1	Depositor
R, R_{free}	0.247 , 0.284	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	9308	wwPDB-VP
Average B, all atoms (Å ²)	58.0	wwPDB-VP

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: YT3, 544

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	0.40	0/2156	0.63	3/2906 (0.1%)
1	C	0.44	0/2156	0.68	1/2906 (0.0%)
1	E	0.42	0/2156	0.65	0/2906
1	G	0.42	0/2156	0.65	1/2906 (0.0%)
2	B	0.30	0/111	0.48	0/147
2	D	0.37	0/111	0.67	0/147
2	F	0.40	0/111	0.53	0/147
2	H	0.30	0/111	0.41	0/147
All	All	0.42	0/9068	0.65	5/12212 (0.0%)

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	256	ALA	N-CA-C	-5.90	95.07	111.00
1	G	256	ALA	N-CA-C	-5.74	95.50	111.00
1	A	266	LYS	N-CA-C	-5.57	95.96	111.00
1	C	266	LYS	N-CA-C	-5.17	97.04	111.00
1	A	258	LEU	CA-CB-CG	5.13	127.09	115.30

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	2118	0	2161	179	0
1	C	2118	0	2161	179	0
1	E	2118	0	2161	122	0
1	G	2118	0	2161	167	0
2	B	110	0	108	14	0
2	D	110	0	108	11	0
2	F	110	0	108	12	0
2	H	110	0	108	16	0
3	C	1	0	0	0	0
3	E	1	0	0	0	0
4	A	38	0	28	1	0
4	C	38	0	28	2	0
4	E	38	0	29	0	0
4	G	38	0	29	0	0
5	A	46	0	0	0	0
5	C	76	0	0	10	0
5	D	7	0	0	1	0
5	E	51	0	0	2	0
5	F	1	0	0	0	0
5	G	57	0	0	3	0
5	H	4	0	0	1	0
All	All	9308	0	9190	660	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 36.

The worst 5 of 660 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:E:253:THR:HG23	1:E:254:LEU:H	1.09	1.09
1:A:252:LYS:HG3	1:A:259:VAL:HG21	1.39	1.04
1:E:251:GLU:HA	1:E:255:VAL:HB	1.41	1.02
1:C:420:ILE:HG13	1:C:421:PHE:H	1.23	1.00
1:E:202:ASP:O	1:E:204:LYS:N	1.93	1.00

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	265/288 (92%)	233 (88%)	23 (9%)	9 (3%)	5	6
1	C	265/288 (92%)	233 (88%)	18 (7%)	14 (5%)	2	2
1	E	265/288 (92%)	240 (91%)	16 (6%)	9 (3%)	5	6
1	G	265/288 (92%)	236 (89%)	18 (7%)	11 (4%)	3	4
2	B	11/21 (52%)	8 (73%)	3 (27%)	0	100	100
2	D	11/21 (52%)	8 (73%)	3 (27%)	0	100	100
2	F	11/21 (52%)	9 (82%)	2 (18%)	0	100	100
2	H	11/21 (52%)	9 (82%)	0	2 (18%)	0	0
All	All	1104/1236 (89%)	976 (88%)	83 (8%)	45 (4%)	3	4

5 of 45 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	230	SER
1	A	232	LYS
1	A	236	ASN
1	A	420	ILE
1	C	232	LYS

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	234/252 (93%)	207 (88%)	27 (12%)	7	13

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	C	234/252 (93%)	214 (92%)	20 (8%)	13	25
1	E	234/252 (93%)	209 (89%)	25 (11%)	8	15
1	G	234/252 (93%)	209 (89%)	25 (11%)	8	15
2	B	11/20 (55%)	9 (82%)	2 (18%)	2	3
2	D	11/20 (55%)	8 (73%)	3 (27%)	0	0
2	F	11/20 (55%)	9 (82%)	2 (18%)	2	3
2	H	11/20 (55%)	11 (100%)	0	100	100
All	All	980/1088 (90%)	876 (89%)	104 (11%)	8	16

5 of 104 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	451	GLU
1	E	234	SER
1	G	385	CYS
1	C	453	ASP
1	E	208	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 50 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	416	HIS
2	D	695	GLN
1	G	326	ASN
1	C	440	HIS
1	C	461	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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 6 ligands modelled in this entry, 2 are monoatomic - leaving 4 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	544	A	469	-	34,41,41	2.56	15 (44%)	42,55,55	1.45	3 (7%)
4	544	C	470	-	34,41,41	2.63	13 (38%)	42,55,55	1.46	4 (9%)
4	544	E	501	-	34,41,41	2.55	16 (47%)	42,55,55	1.36	2 (4%)
4	544	G	601	-	34,41,41	2.63	15 (44%)	42,55,55	1.46	3 (7%)

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	544	A	469	-	1/1/4/6	0/23/30/30	0/3/4/4
4	544	C	470	-	1/1/4/6	0/23/30/30	0/3/4/4
4	544	E	501	-	1/1/4/6	0/23/30/30	0/3/4/4
4	544	G	601	-	1/1/4/6	0/23/30/30	0/3/4/4

The worst 5 of 59 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	469	544	C1H-C1G	-2.96	1.44	1.49
4	G	601	544	C1H-C1G	-2.41	1.45	1.49
4	C	470	544	C1H-C1G	-2.31	1.45	1.49
4	E	501	544	C1H-C1G	-2.27	1.45	1.49
4	G	601	544	C1B-C1A	2.01	1.54	1.50

The worst 5 of 12 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
4	A	469	544	C1F-C1A-N	-5.64	116.74	121.31
4	E	501	544	C1F-C1A-N	-5.53	116.83	121.31
4	G	601	544	C1F-C1A-N	-5.47	116.88	121.31
4	C	470	544	C1F-C1A-N	-4.27	117.84	121.31
4	G	601	544	CB-CA-C	2.12	116.10	111.55

All (4) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
4	A	469	544	C1A
4	G	601	544	C1A
4	C	470	544	C1A
4	E	501	544	C1A

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	469	544	1	0
4	C	470	544	2	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 ⓘ

EDS was not executed - this section will therefore be empty.

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

EDS was not executed - this section will therefore be empty.

6.3 Carbohydrates ⓘ

EDS was not executed - this section will therefore be empty.

6.4 Ligands ⓘ

EDS was not executed - this section will therefore be empty.

6.5 Other polymers ⓘ

EDS was not executed - this section will therefore be empty.