wwPDB X-ray Structure Validation Summary Report (i)

May 15, 2020 – 07:42 am BST

PDB ID	:	2J0F
Title	:	Structural basis for non-competitive product inhibition in human thymidine phosphorylase: implication for drug design
Authors	:	El Omari, K.; Bronckaers, A.; Liekens, S.; Perez-Perez, M.J.; Balzarini, J.; Stammers, D.K.
Deposited on	:	2006-08-02
Resolution	:	2.31 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 (i) symbol.

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

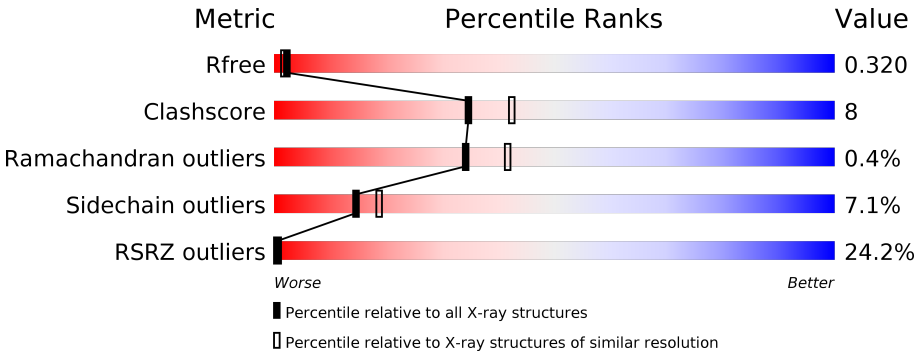
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.11
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.11

1 Overall quality at a glance (i)

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

The reported resolution of this entry is 2.31 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	5974 (2.34-2.30)
Clashscore	141614	6604 (2.34-2.30)
Ramachandran outliers	138981	6523 (2.34-2.30)
Sidechain outliers	138945	6523 (2.34-2.30)
RSRZ outliers	127900	5855 (2.34-2.30)

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 respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions <=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	482	9% 76% 14% • 7%
1	B	482	13% 74% 16% • • 7%
1	C	482	13% 77% 14% • 7%
1	D	482	55% 77% 13% • 7%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 13513 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.

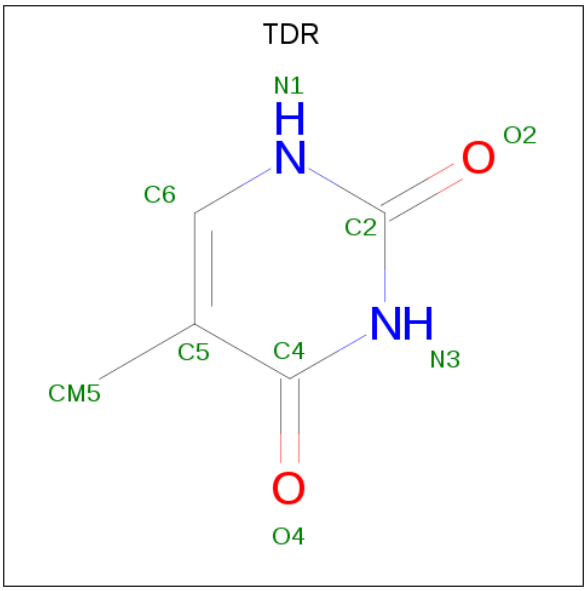
- Molecule 1 is a protein called THYMIDINE PHOSPHORYLASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	446	Total	C	N	O	S	0	0	0
			3259	2038	597	608	16			
1	B	446	Total	C	N	O	S	0	0	0
			3259	2038	597	608	16			
1	C	446	Total	C	N	O	S	0	0	0
			3259	2038	597	608	16			
1	D	446	Total	C	N	O	S	0	0	0
			3259	2038	597	608	16			

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	238	ALA	GLY	conflict	UNP P19971
A	239	GLY	ALA	conflict	UNP P19971
A	471	LEU	SER	conflict	UNP P19971
B	238	ALA	GLY	conflict	UNP P19971
B	239	GLY	ALA	conflict	UNP P19971
B	471	LEU	SER	conflict	UNP P19971
C	238	ALA	GLY	conflict	UNP P19971
C	239	GLY	ALA	conflict	UNP P19971
C	471	LEU	SER	conflict	UNP P19971
D	238	ALA	GLY	conflict	UNP P19971
D	239	GLY	ALA	conflict	UNP P19971
D	471	LEU	SER	conflict	UNP P19971

- Molecule 2 is THYMINE (three-letter code: TDR) (formula: $C_5H_6N_2O_2$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total C N O 9 5 2 2	0	0
2	B	1	Total C N O 9 5 2 2	0	0
2	C	1	Total C N O 9 5 2 2	0	0

- Molecule 3 is water.

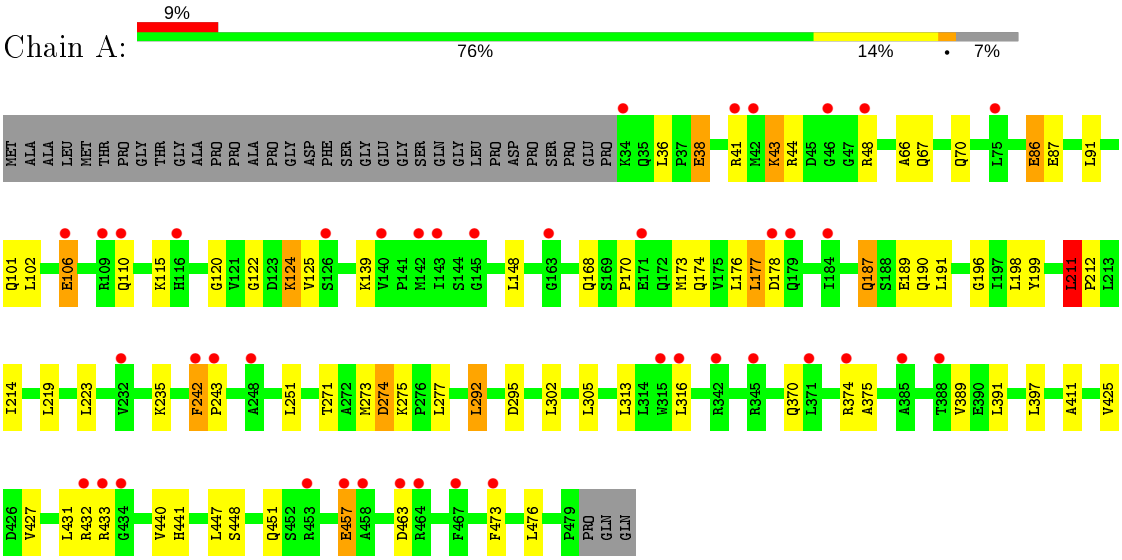
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	119	Total O 119 119	0	0
3	B	95	Total O 95 95	0	0
3	C	169	Total O 169 169	0	0
3	D	67	Total O 67 67	0	0

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.

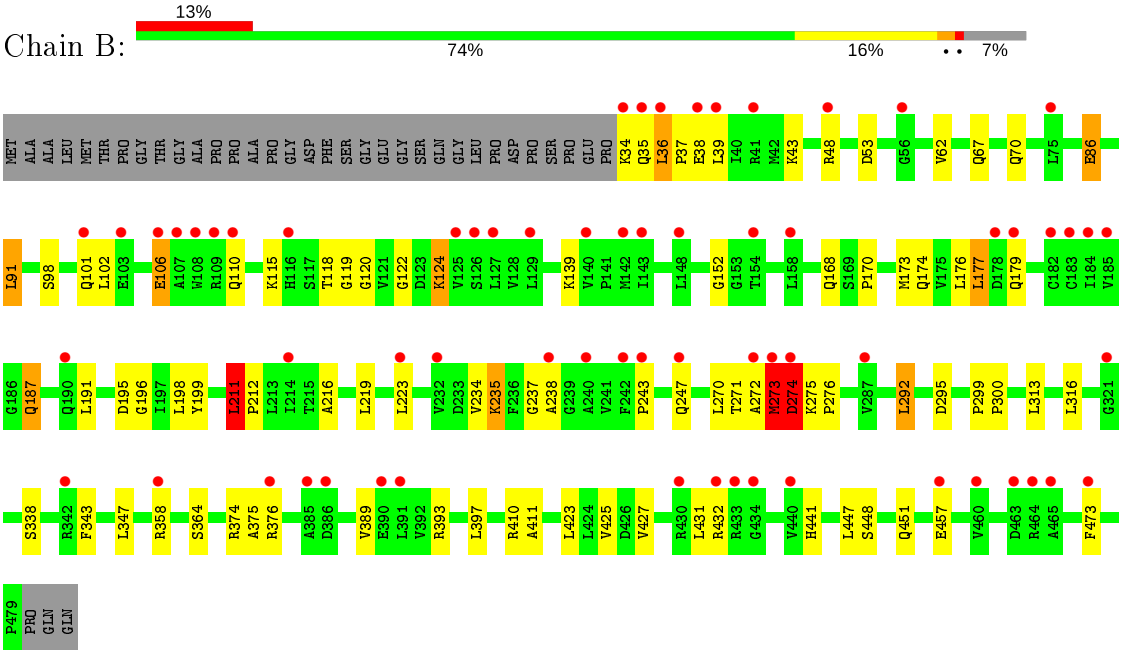
- Molecule 1: THYMIDINE PHOSPHORYLASE

Chain A:



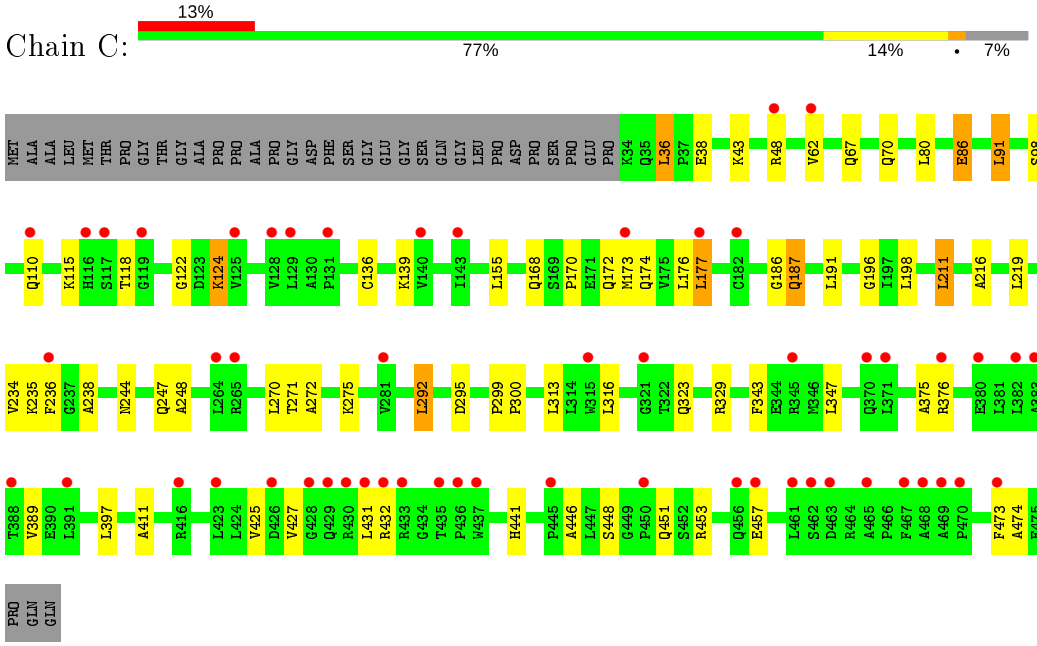
- Molecule 1: THYMIDINE PHOSPHORYLASE

Chain B:



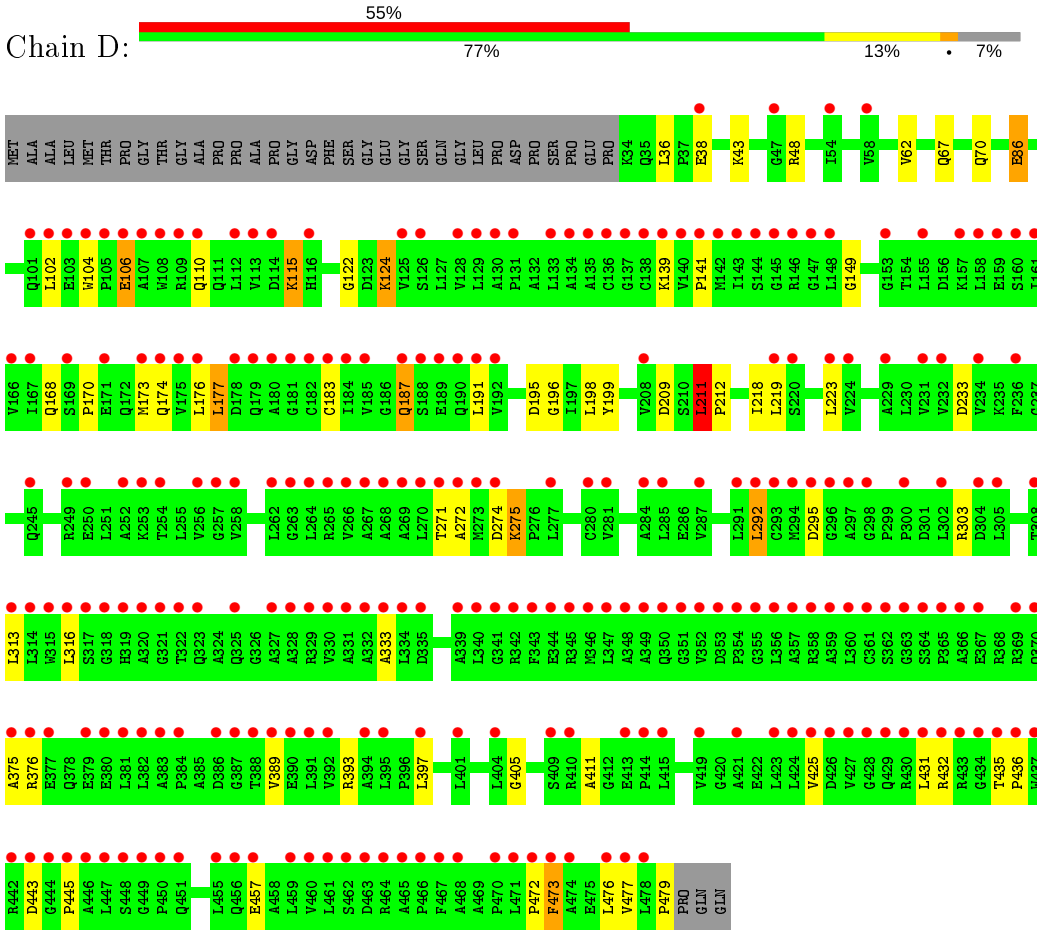
• Molecule 1: THYMIDINE PHOSPHORYLASE

Chain C:



• Molecule 1: THYMIDINE PHOSPHORYLASE

Chain D:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	103.08Å 76.09Å 99.58Å 90.00° 98.61° 90.00°	Depositor
Resolution (Å)	102.06 – 2.31 29.96 – 2.31	Depositor EDS
% Data completeness (in resolution range)	99.3 (102.06-2.31) 99.4 (29.96-2.31)	Depositor EDS
R_{merge}	0.12	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	3.01 (at 2.31Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.246 , 0.287 0.289 , 0.320	Depositor DCC
R_{free} test set	3368 reflections (5.07%)	wwPDB-VP
Wilson B-factor (Å^2)	32.0	Xtriage
Anisotropy	0.538	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.39 , 32.9	EDS
L-test for twinning[2]	$< \|L\| > = 0.50$, $< L^2 > = 0.34$	Xtriage
Estimated twinning fraction	0.000 for l,-k,h	Xtriage
F_o,F_c correlation	0.91	EDS
Total number of atoms	13513	wwPDB-VP
Average B, all atoms (Å^2)	12.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 45.03 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 1.4005e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

[1] Intensities estimated from amplitudes.

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

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	0.48	0/3305	0.66	1/4483 (0.0%)
1	B	0.46	0/3305	0.65	1/4483 (0.0%)
1	C	0.46	0/3305	0.64	1/4483 (0.0%)
1	D	0.35	0/3305	0.59	1/4483 (0.0%)
All	All	0.44	0/13220	0.63	4/17932 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand.A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	B	0	2

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	C	211	LEU	CA-CB-CG	6.53	130.32	115.30
1	A	211	LEU	CA-CB-CG	5.55	128.07	115.30
1	B	211	LEU	CA-CB-CG	5.25	127.36	115.30
1	D	211	LEU	CA-CB-CG	5.05	126.91	115.30

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	272	ALA	Peptide
1	B	273	MET	Peptide

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	3259	0	3361	69	1
1	B	3259	0	3361	60	2
1	C	3259	0	3361	53	0
1	D	3259	0	3361	53	1
2	A	9	0	6	1	0
2	B	9	0	6	1	0
2	C	9	0	6	1	0
3	A	119	0	0	14	0
3	B	95	0	0	6	0
3	C	169	0	0	9	0
3	D	67	0	0	15	0
All	All	13513	0	13462	220	2

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 8.

The worst 5 of 220 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:242:PHE:HZ	1:A:251:LEU:CD2	1.57	1.16
1:D:183:CYS:SG	3:D:2019:HOH:O	1.96	1.14
1:C:476:LEU:O	1:D:376:ARG:NH1	1.80	1.13
1:A:242:PHE:CZ	1:A:251:LEU:CD2	2.34	1.08
1:A:242:PHE:CZ	1:A:251:LEU:HD22	1.89	1.06

All (2) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:178:ASP:OD2	1:B:393:ARG:NH2[1_556]	2.11	0.09
1:B:364:SER:OG	1:D:97:GLN:O[2_544]	2.18	0.02

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	444/482 (92%)	435 (98%)	8 (2%)	1 (0%)	47	58
1	B	444/482 (92%)	434 (98%)	8 (2%)	2 (0%)	29	35
1	C	444/482 (92%)	433 (98%)	10 (2%)	1 (0%)	47	58
1	D	444/482 (92%)	434 (98%)	7 (2%)	3 (1%)	22	26
All	All	1776/1928 (92%)	1736 (98%)	33 (2%)	7 (0%)	34	41

5 of 7 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	275	LYS
1	B	274	ASP
1	A	243	PRO
1	B	238	ALA
1	C	446	ALA

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	333/359 (93%)	310 (93%)	23 (7%)	15	20
1	B	333/359 (93%)	308 (92%)	25 (8%)	13	16
1	C	333/359 (93%)	311 (93%)	22 (7%)	16	22
1	D	333/359 (93%)	309 (93%)	24 (7%)	14	18
All	All	1332/1436 (93%)	1238 (93%)	94 (7%)	14	19

5 of 94 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	274	ASP
1	C	91	LEU
1	D	292	LEU
1	B	292	LEU
1	B	457	GLU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 34 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	325	GLN
1	C	101	GLN
1	D	190	GLN
1	C	70	GLN
1	A	244	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)

3 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	$\#\|Z\|>2$
2	TDR	A	1480	-	8,9,9	1.97	1 (12%)	6,12,12	5.29	4 (66%)
2	TDR	C	1480	-	8,9,9	1.70	1 (12%)	6,12,12	5.34	4 (66%)
2	TDR	B	1480	-	8,9,9	1.78	1 (12%)	6,12,12	5.57	4 (66%)

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	TDR	A	1480	-	-	-	0/1/1/1
2	TDR	C	1480	-	-	-	0/1/1/1
2	TDR	B	1480	-	-	-	0/1/1/1

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	1480	TDR	O4-C4	4.54	1.36	1.24
2	B	1480	TDR	O4-C4	3.92	1.34	1.24
2	C	1480	TDR	O4-C4	3.73	1.33	1.24

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

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	B	1480	TDR	N1-C2-N3	-10.31	120.23	128.43
2	C	1480	TDR	N1-C2-N3	-9.76	120.67	128.43
2	A	1480	TDR	N1-C2-N3	-9.04	121.24	128.43
2	A	1480	TDR	C4-N3-C2	6.15	120.33	115.14
2	A	1480	TDR	C5-C6-N1	-5.94	119.11	125.16

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

3 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	1480	TDR	1	0
2	C	1480	TDR	1	0
2	B	1480	TDR	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	446/482 (92%)	0.88	42 (9%)	8 11	3, 9, 28, 46	2 (0%)
1	B	446/482 (92%)	1.14	65 (14%)	2 3	4, 10, 28, 46	2 (0%)
1	C	446/482 (92%)	1.08	62 (13%)	2 4	4, 9, 27, 46	2 (0%)
1	D	446/482 (92%)	2.55	263 (58%)	0 0	4, 10, 30, 51	2 (0%)
All	All	1784/1928 (92%)	1.41	432 (24%)	0 1	3, 10, 28, 51	8 (0%)

The worst 5 of 432 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	107	ALA	10.5
1	D	445	PRO	9.2
1	D	446	ALA	8.0
1	C	383	ALA	8.0
1	D	465	ALA	7.8

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. 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	B-factors(Å^2)	Q<0.9
2	TDR	C	1480	9/9	0.94	0.22	2,2,2,2	0
2	TDR	B	1480	9/9	0.94	0.23	2,3,3,4	0
2	TDR	A	1480	9/9	0.95	0.21	2,2,2,2	0

6.5 Other polymers (i)

There are no such residues in this entry.