



Full wwPDB X-ray Structure Validation Report ⓘ

Sep 16, 2023 – 10:07 PM EDT

PDB ID : 4WYM
Title : Structural basis of HIV-1 capsid recognition by CPSF6
Authors : Battacharya, A.; Taylor, A.B.; Hart, P.J.; Ivanov, D.N.
Deposited on : 2014-11-17
Resolution : 2.60 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

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Xtriage (Phenix) : 1.13
EDS : 2.35.1
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) : 2.35.1

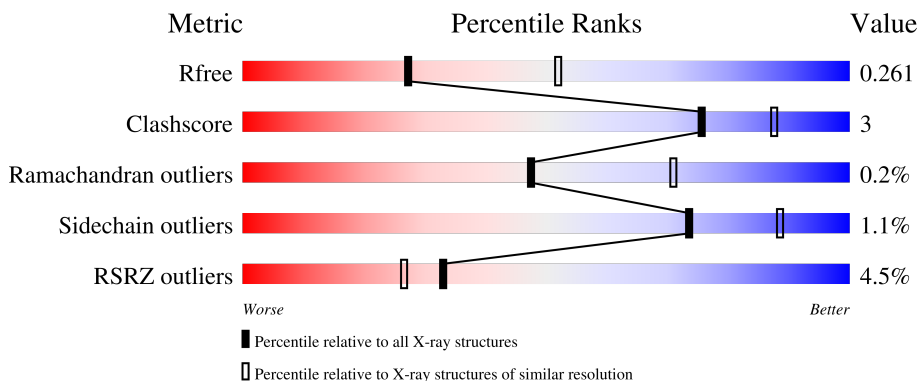
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.60 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	3163 (2.60-2.60)
Clashscore	141614	3518 (2.60-2.60)
Ramachandran outliers	138981	3455 (2.60-2.60)
Sidechain outliers	138945	3455 (2.60-2.60)
RSRZ outliers	127900	3104 (2.60-2.60)

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 of 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 $\leq 5\%$. 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	231	 3% 84% 8% 7%
1	B	231	 5% 84% 8% 8%
1	C	231	 % 88% • 8%
1	D	231	 4% 85% • 12%
1	E	231	 3% 88% 5% 7%

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Mol	Chain	Length	Quality of chain
1	F	231	
1	G	231	
1	H	231	
1	I	231	
1	J	231	
1	K	231	
1	L	231	
2	M	17	
2	N	17	
2	O	17	
2	P	17	
2	Q	17	
2	R	17	
2	S	17	
2	T	17	
2	U	17	
2	V	17	
2	W	17	

2 Entry composition [i](#)

There are 2 unique types of molecules in this entry. The entry contains 20913 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 Capsid protein p24.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	214	1659	1044	291	310	14	0	0	0
1	B	213	1658	1041	290	313	14	0	0	0
1	C	212	1654	1039	289	312	14	0	0	0
1	D	204	1597	1006	278	299	14	0	0	0
1	E	215	1671	1050	292	315	14	0	0	0
1	F	220	1704	1071	299	320	14	0	0	0
1	G	211	1642	1035	287	306	14	0	0	0
1	H	211	1642	1035	287	306	14	0	0	0
1	I	212	1647	1038	288	307	14	0	0	0
1	J	213	1661	1044	290	313	14	0	0	0
1	K	210	1638	1032	286	306	14	0	0	0
1	L	208	1630	1026	284	306	14	0	0	0

There are 48 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	14	CYS	ALA	engineered mutation	UNP P12497
A	45	CYS	GLU	engineered mutation	UNP P12497
A	184	ALA	TRP	engineered mutation	UNP P12497
A	185	ALA	MET	engineered mutation	UNP P12497
B	14	CYS	ALA	engineered mutation	UNP P12497

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Chain	Residue	Modelled	Actual	Comment	Reference
B	45	CYS	GLU	engineered mutation	UNP P12497
B	184	ALA	TRP	engineered mutation	UNP P12497
B	185	ALA	MET	engineered mutation	UNP P12497
C	14	CYS	ALA	engineered mutation	UNP P12497
C	45	CYS	GLU	engineered mutation	UNP P12497
C	184	ALA	TRP	engineered mutation	UNP P12497
C	185	ALA	MET	engineered mutation	UNP P12497
D	14	CYS	ALA	engineered mutation	UNP P12497
D	45	CYS	GLU	engineered mutation	UNP P12497
D	184	ALA	TRP	engineered mutation	UNP P12497
D	185	ALA	MET	engineered mutation	UNP P12497
E	14	CYS	ALA	engineered mutation	UNP P12497
E	45	CYS	GLU	engineered mutation	UNP P12497
E	184	ALA	TRP	engineered mutation	UNP P12497
E	185	ALA	MET	engineered mutation	UNP P12497
F	14	CYS	ALA	engineered mutation	UNP P12497
F	45	CYS	GLU	engineered mutation	UNP P12497
F	184	ALA	TRP	engineered mutation	UNP P12497
F	185	ALA	MET	engineered mutation	UNP P12497
G	14	CYS	ALA	engineered mutation	UNP P12497
G	45	CYS	GLU	engineered mutation	UNP P12497
G	184	ALA	TRP	engineered mutation	UNP P12497
G	185	ALA	MET	engineered mutation	UNP P12497
H	14	CYS	ALA	engineered mutation	UNP P12497
H	45	CYS	GLU	engineered mutation	UNP P12497
H	184	ALA	TRP	engineered mutation	UNP P12497
H	185	ALA	MET	engineered mutation	UNP P12497
I	14	CYS	ALA	engineered mutation	UNP P12497
I	45	CYS	GLU	engineered mutation	UNP P12497
I	184	ALA	TRP	engineered mutation	UNP P12497
I	185	ALA	MET	engineered mutation	UNP P12497
J	14	CYS	ALA	engineered mutation	UNP P12497
J	45	CYS	GLU	engineered mutation	UNP P12497
J	184	ALA	TRP	engineered mutation	UNP P12497
J	185	ALA	MET	engineered mutation	UNP P12497
K	14	CYS	ALA	engineered mutation	UNP P12497
K	45	CYS	GLU	engineered mutation	UNP P12497
K	184	ALA	TRP	engineered mutation	UNP P12497
K	185	ALA	MET	engineered mutation	UNP P12497
L	14	CYS	ALA	engineered mutation	UNP P12497
L	45	CYS	GLU	engineered mutation	UNP P12497
L	184	ALA	TRP	engineered mutation	UNP P12497

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Chain	Residue	Modelled	Actual	Comment	Reference
L	185	ALA	MET	engineered mutation	UNP P12497

- Molecule 2 is a protein called ISOFORM 2 OF CLEAVAGE AND POLYADENYLATION SPECIFICITY FACTOR SUBUNIT 6.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	M	13	Total	C	N	O	0	0	0
			98	68	15	15			
2	N	14	Total	C	N	O	0	0	0
			105	72	16	17			
2	O	13	Total	C	N	O	0	0	0
			98	68	15	15			
2	P	14	Total	C	N	O	0	0	0
			105	72	16	17			
2	Q	13	Total	C	N	O	0	0	0
			98	68	15	15			
2	R	14	Total	C	N	O	0	0	0
			105	72	16	17			
2	S	15	Total	C	N	O	0	0	0
			109	74	17	18			
2	T	13	Total	C	N	O	0	0	0
			98	68	15	15			
2	U	13	Total	C	N	O	0	0	0
			98	68	15	15			
2	V	13	Total	C	N	O	0	0	0
			98	68	15	15			
2	W	13	Total	C	N	O	0	0	0
			98	68	15	15			

There are 22 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
M	311	GLY	-	expression tag	UNP Q16630
M	312	THR	-	expression tag	UNP Q16630
N	311	GLY	-	expression tag	UNP Q16630
N	312	THR	-	expression tag	UNP Q16630
O	311	GLY	-	expression tag	UNP Q16630
O	312	THR	-	expression tag	UNP Q16630
P	311	GLY	-	expression tag	UNP Q16630
P	312	THR	-	expression tag	UNP Q16630
Q	311	GLY	-	expression tag	UNP Q16630
Q	312	THR	-	expression tag	UNP Q16630
R	311	GLY	-	expression tag	UNP Q16630

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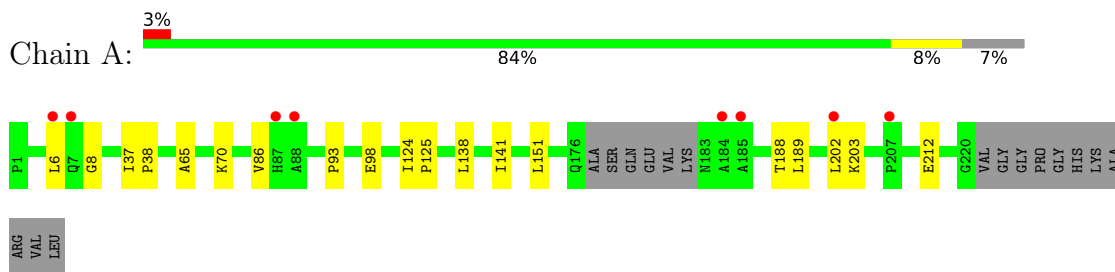
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Chain	Residue	Modelled	Actual	Comment	Reference
R	312	THR	-	expression tag	UNP Q16630
S	311	GLY	-	expression tag	UNP Q16630
S	312	THR	-	expression tag	UNP Q16630
T	311	GLY	-	expression tag	UNP Q16630
T	312	THR	-	expression tag	UNP Q16630
U	311	GLY	-	expression tag	UNP Q16630
U	312	THR	-	expression tag	UNP Q16630
V	311	GLY	-	expression tag	UNP Q16630
V	312	THR	-	expression tag	UNP Q16630
W	311	GLY	-	expression tag	UNP Q16630
W	312	THR	-	expression tag	UNP Q16630

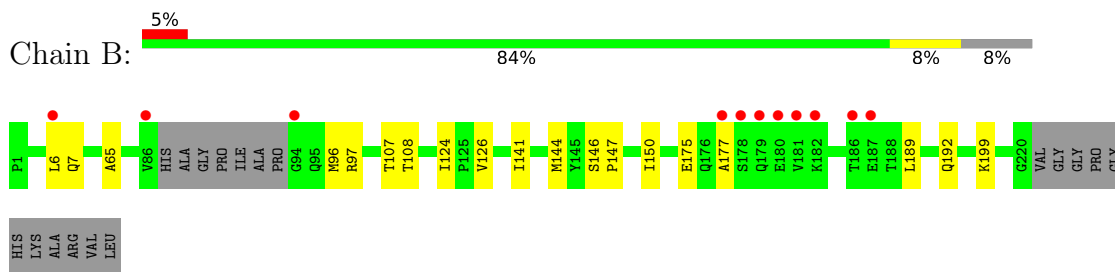
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide 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.

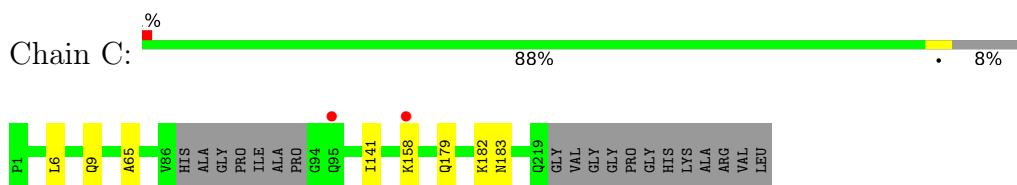
- Molecule 1: Capsid protein p24



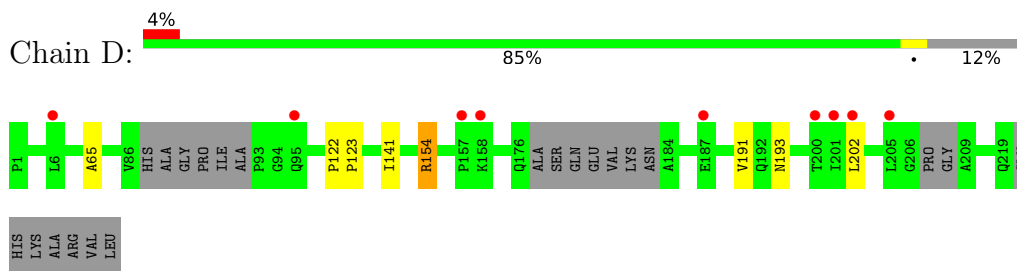
- Molecule 1: Capsid protein p24



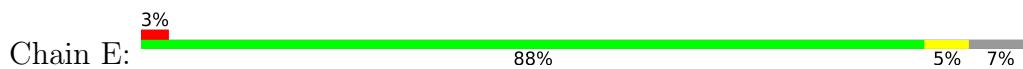
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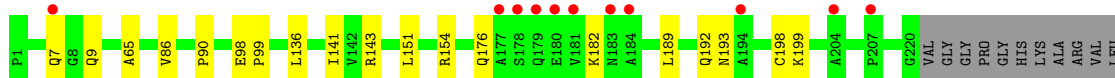
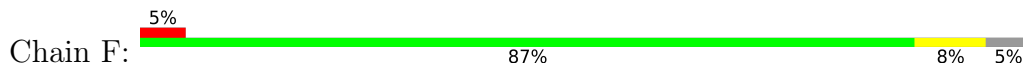
- Molecule 1: Capsid protein p24



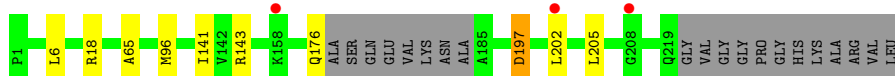
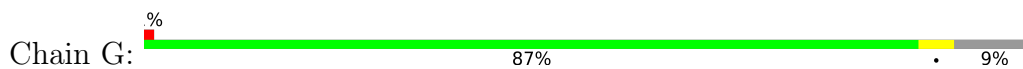
- Molecule 1: Capsid protein p24



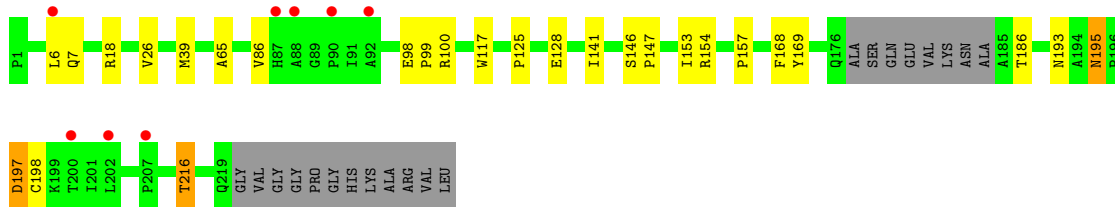
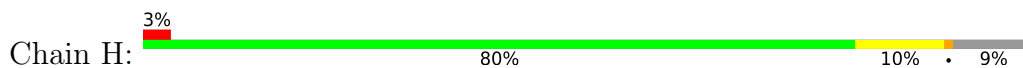
- Molecule 1: Capsid protein p24



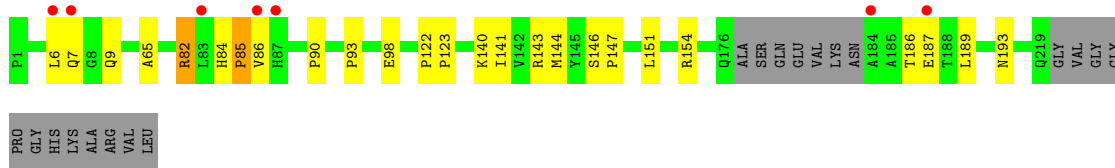
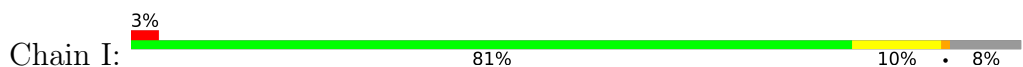
- Molecule 1: Capsid protein p24



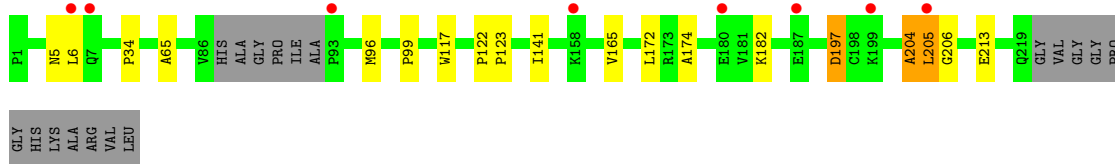
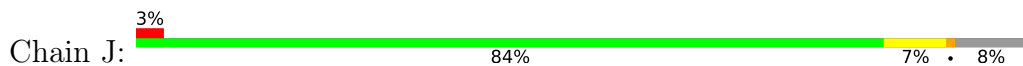
- Molecule 1: Capsid protein p24



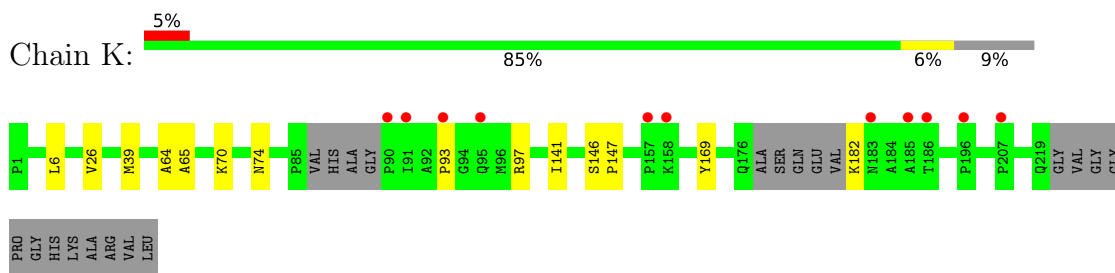
- Molecule 1: Capsid protein p24



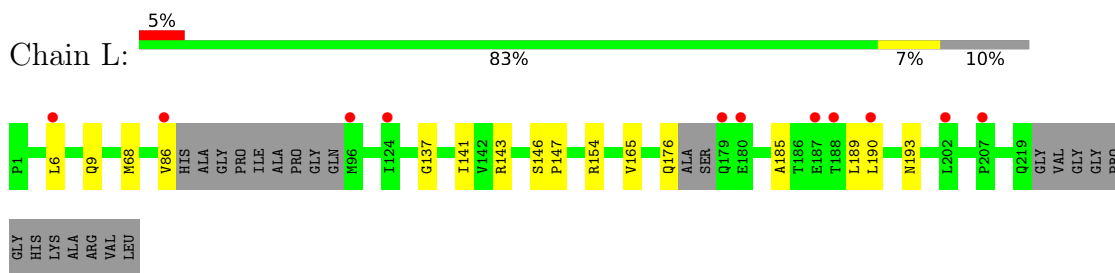
- Molecule 1: Capsid protein p24



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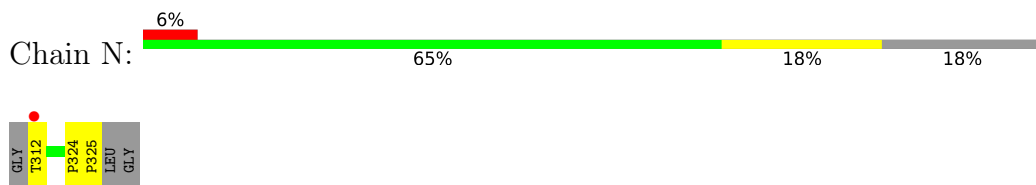
- Molecule 1: Capsid protein p24



- Molecule 2: ISOFORM 2 OF CLEAVAGE AND POLYADENYLATION SPECIFICITY FACTOR SUBUNIT 6



- Molecule 2: ISOFORM 2 OF CLEAVAGE AND POLYADENYLATION SPECIFICITY FACTOR SUBUNIT 6

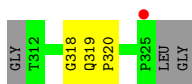


- Molecule 2: ISOFORM 2 OF CLEAVAGE AND POLYADENYLATION SPECIFICITY FACTOR SUBUNIT 6



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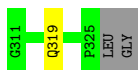
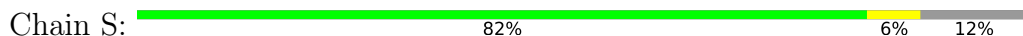
- Molecule 2: ISOFORM 2 OF CLEAVAGE AND POLYADENYLATION SPECIFICITY FACTOR SUBUNIT 6



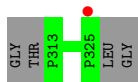
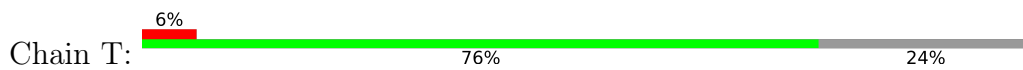
- Molecule 2: ISOFORM 2 OF CLEAVAGE AND POLYADENYLATION SPECIFICITY FACTOR SUBUNIT 6



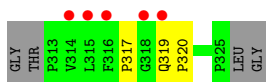
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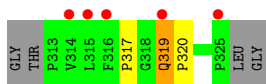


- Molecule 2: ISOFORM 2 OF CLEAVAGE AND POLYADENYLATION SPECIFICITY FACTOR SUBUNIT 6





- Molecule 2: ISOFORM 2 OF CLEAVAGE AND POLYADENYLATION SPECIFICITY FACTOR SUBUNIT 6



4 Data and refinement statistics i

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	134.79Å 136.03Å 207.26Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	48.47 – 2.60 48.47 – 2.60	Depositor EDS
% Data completeness (in resolution range)	100.0 (48.47-2.60) 99.9 (48.47-2.60)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.07	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.15 (at 2.61Å)	Xtrriage
Refinement program	PHENIX (phenix.refine: 1.9_1692)	Depositor
R, R_{free}	0.219 , 0.259 0.223 , 0.261	Depositor DCC
R_{free} test set	2005 reflections (1.71%)	wwPDB-VP
Wilson B-factor (Å ²)	62.7	Xtrriage
Anisotropy	0.229	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 46.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtrriage
Estimated twinning fraction	0.027 for k,h,-l	Xtrriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	20913	wwPDB-VP
Average B, all atoms (Å ²)	73.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.86% 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

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	0.21	0/1695	0.38	0/2303
1	B	0.21	0/1691	0.37	0/2294
1	C	0.22	0/1687	0.36	0/2289
1	D	0.20	0/1628	0.37	0/2206
1	E	0.21	0/1705	0.37	0/2314
1	F	0.21	0/1741	0.36	0/2366
1	G	0.20	0/1678	0.37	0/2280
1	H	0.21	0/1678	0.37	0/2280
1	I	0.27	1/1683 (0.1%)	0.40	1/2287 (0.0%)
1	J	0.21	0/1695	0.39	0/2300
1	K	0.21	0/1672	0.36	0/2268
1	L	0.22	0/1662	0.36	0/2254
2	M	0.21	0/104	0.39	0/143
2	N	0.25	0/111	0.51	0/154
2	O	0.22	0/104	0.39	0/143
2	P	0.26	0/111	0.52	0/154
2	Q	0.22	0/104	0.37	0/143
2	R	0.23	0/111	0.48	0/154
2	S	0.23	0/115	0.43	0/159
2	T	0.23	0/104	0.41	0/143
2	U	0.22	0/104	0.39	0/143
2	V	0.21	0/104	0.39	0/143
2	W	0.22	0/104	0.35	0/143
All	All	0.22	1/21391 (0.0%)	0.37	1/29063 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	I	85	PRO	N-CD	5.61	1.55	1.47

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	I	84	HIS	C-N-CD	5.41	139.75	128.40

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	1659	0	1659	13	0
1	B	1658	0	1660	13	0
1	C	1654	0	1657	6	0
1	D	1597	0	1601	4	0
1	E	1671	0	1674	9	0
1	F	1704	0	1704	11	0
1	G	1642	0	1643	6	0
1	H	1642	0	1643	19	0
1	I	1647	0	1650	20	0
1	J	1661	0	1665	20	0
1	K	1638	0	1645	9	0
1	L	1630	0	1633	10	0
2	M	98	0	95	3	0
2	N	105	0	101	1	0
2	O	98	0	95	2	0
2	P	105	0	101	3	0
2	Q	98	0	95	0	0
2	R	105	0	101	2	0
2	S	109	0	104	0	0
2	T	98	0	95	0	0
2	U	98	0	95	2	0
2	V	98	0	95	1	0
2	W	98	0	95	2	0
All	All	20913	0	20906	129	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 (129) 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:L:154:ARG:HG2	1:L:193:ASN:HB3	1.67	0.77
1:C:179:GLN:O	1:C:179:GLN:NE2	2.25	0.69
1:H:6:LEU:HD13	1:I:6:LEU:HD12	1.74	0.69
1:E:91:ILE:HG22	1:E:92:ALA:N	2.09	0.68
1:H:154:ARG:HG2	1:H:193:ASN:HB3	1.77	0.66
1:L:165:VAL:HG22	1:L:190:LEU:HD11	1.78	0.66
1:F:65:ALA:HB1	1:F:141:ILE:HD13	1.80	0.63
1:H:65:ALA:HB1	1:H:141:ILE:HD13	1.81	0.62
2:P:319:GLN:HA	2:P:319:GLN:OE1	1.99	0.62
1:E:65:ALA:HB1	1:E:141:ILE:HD13	1.80	0.62
1:D:65:ALA:HB1	1:D:141:ILE:HD13	1.81	0.62
1:A:37:ILE:HD12	1:A:138:LEU:HB3	1.82	0.61
1:B:7:GLN:HA	1:B:7:GLN:OE1	2.00	0.61
2:P:319:GLN:OE1	2:P:320:PRO:HD3	2.01	0.61
1:K:65:ALA:HB1	1:K:141:ILE:HD13	1.83	0.60
1:A:70:LYS:HG2	2:M:315:LEU:HD13	1.84	0.60
1:A:203:LYS:O	1:A:203:LYS:HG2	2.01	0.59
1:K:70:LYS:O	1:K:74:ASN:ND2	2.35	0.59
1:C:65:ALA:HB1	1:C:141:ILE:HD13	1.85	0.59
1:L:143:ARG:NH1	1:L:176:GLN:OE1	2.36	0.59
1:I:6:LEU:CD1	1:J:6:LEU:HD12	2.33	0.58
1:B:65:ALA:HB1	1:B:141:ILE:HD13	1.87	0.57
1:J:172:LEU:HG	1:J:182:LYS:HG2	1.87	0.57
1:K:26:VAL:HG21	1:K:39:MET:HG2	1.85	0.56
1:D:191:VAL:HG12	1:D:202:LEU:HD11	1.86	0.56
1:J:197:ASP:N	1:J:197:ASP:OD1	2.39	0.56
1:I:65:ALA:HB1	1:I:141:ILE:HD13	1.87	0.56
1:G:65:ALA:HB1	1:G:141:ILE:HD13	1.87	0.56
1:H:86:VAL:HG13	1:H:98:GLU:HB2	1.88	0.55
1:H:26:VAL:HG21	1:H:39:MET:HG2	1.88	0.55
1:J:205:LEU:HD11	1:J:213:GLU:OE1	2.06	0.55
1:A:8:GLY:HA3	1:I:9:GLN:HE21	1.73	0.54
1:E:91:ILE:HG22	1:E:92:ALA:H	1.73	0.54
1:E:172:LEU:HD21	1:E:182:LYS:HB3	1.90	0.54
1:D:154:ARG:HG3	1:D:193:ASN:HB3	1.89	0.54
1:J:172:LEU:CD2	1:J:182:LYS:HG2	2.38	0.54
1:J:65:ALA:HB1	1:J:141:ILE:HD13	1.90	0.53
1:F:143:ARG:HD3	1:F:176:GLN:HB2	1.91	0.53
1:C:179:GLN:NE2	1:C:183:ASN:OD1	2.42	0.53
1:I:82:ARG:O	1:I:85:PRO:HD3	2.09	0.52
1:A:151:LEU:HD23	1:A:189:LEU:HD21	1.90	0.52
1:I:186:THR:OG1	1:I:187:GLU:N	2.41	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:91:ILE:CG2	1:E:92:ALA:N	2.72	0.52
1:E:6:LEU:HD22	1:F:7:GLN:HG2	1.93	0.50
1:F:151:LEU:HD23	1:F:189:LEU:HD11	1.93	0.50
1:A:212:GLU:HG3	1:B:144:MET:HE1	1.92	0.50
1:I:140:LYS:HG2	1:I:143:ARG:HH22	1.77	0.50
1:L:154:ARG:HG2	1:L:193:ASN:CB	2.40	0.50
1:A:93:PRO:HB3	1:J:96:MET:HE2	1.93	0.50
1:E:129:ILE:HG12	1:E:132:ARG:NH2	2.27	0.50
1:G:18:ARG:NH2	1:H:18:ARG:HH21	2.10	0.50
1:H:99:PRO:HG3	1:H:117:TRP:CE2	2.46	0.50
1:I:151:LEU:HD23	1:I:189:LEU:HD11	1.94	0.49
1:I:6:LEU:HD13	1:J:6:LEU:HD12	1.94	0.49
1:A:65:ALA:HB1	1:A:141:ILE:HD13	1.94	0.49
1:F:182:LYS:HD3	2:M:318:GLY:HA3	1.95	0.49
1:K:169:TYR:HE1	2:W:317:PRO:HB3	1.78	0.48
1:H:86:VAL:HG21	1:H:100:ARG:HG2	1.95	0.48
1:C:182:LYS:HD3	2:P:318:GLY:HA3	1.95	0.47
1:C:158:LYS:HG2	1:C:158:LYS:O	2.14	0.47
1:G:197:ASP:OD2	1:G:197:ASP:N	2.45	0.47
1:H:169:TYR:HE1	2:U:317:PRO:HB3	1.80	0.47
1:L:137:GLY:O	1:L:141:ILE:HG12	2.14	0.47
1:J:205:LEU:HD11	1:J:213:GLU:HB3	1.96	0.47
1:J:99:PRO:HG3	1:J:117:TRP:CE2	2.50	0.47
1:B:6:LEU:HB3	1:C:6:LEU:HG	1.96	0.47
1:J:204:ALA:O	1:J:206:GLY:N	2.47	0.47
1:B:107:THR:HG22	1:B:108:THR:HG23	1.98	0.46
1:E:91:ILE:CG2	1:E:92:ALA:H	2.27	0.46
1:I:154:ARG:NH1	1:I:193:ASN:OD1	2.49	0.46
1:H:98:GLU:HA	1:H:99:PRO:HD3	1.82	0.46
1:J:6:LEU:HD13	1:K:6:LEU:HG	1.97	0.46
1:J:172:LEU:CG	1:J:182:LYS:HG2	2.46	0.45
1:A:86:VAL:HG22	1:A:98:GLU:HB2	1.99	0.45
1:B:7:GLN:O	1:H:7:GLN:NE2	2.49	0.45
1:B:97:ARG:HB2	1:I:90:PRO:HB2	1.98	0.45
1:J:205:LEU:HD11	1:J:213:GLU:CB	2.46	0.45
2:M:316:PHE:O	2:M:319:GLN:HG2	2.16	0.45
1:G:143:ARG:NE	1:G:176:GLN:OE1	2.43	0.45
1:L:146:SER:HA	1:L:147:PRO:HD3	1.78	0.45
1:A:6:LEU:HD11	1:B:6:LEU:HD12	1.98	0.45
1:H:6:LEU:O	1:I:7:GLN:HG2	2.17	0.44
1:G:202:LEU:HA	1:G:205:LEU:HD12	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:172:LEU:HD21	1:J:182:LYS:HG2	1.99	0.44
2:V:324:PRO:HA	2:V:325:PRO:HD3	1.87	0.44
1:I:6:LEU:HD13	1:J:6:LEU:HB2	2.00	0.44
2:U:319:GLN:HA	2:U:320:PRO:HD3	1.86	0.44
1:H:6:LEU:HD13	1:I:6:LEU:CD1	2.46	0.43
1:L:68:MET:HE2	1:L:141:ILE:CD1	2.47	0.43
1:F:154:ARG:HA	1:F:193:ASN:HB3	2.01	0.43
1:B:192:GLN:HA	1:B:199:LYS:HE3	2.01	0.43
1:I:6:LEU:HD22	1:J:5:ASN:HB2	2.00	0.43
2:O:324:PRO:HA	2:O:325:PRO:HD3	1.91	0.43
1:I:146:SER:HA	1:I:147:PRO:HD3	1.86	0.43
1:B:96:MET:HE2	1:I:93:PRO:HA	2.01	0.42
1:F:90:PRO:HB2	1:K:97:ARG:HB2	2.01	0.42
2:O:319:GLN:NE2	2:O:323:GLN:OE1	2.53	0.42
1:F:98:GLU:HA	1:F:99:PRO:HD3	1.78	0.42
2:R:324:PRO:HA	2:R:325:PRO:HD3	1.92	0.42
1:H:153:ILE:HG21	1:H:168:PHE:HA	2.02	0.42
1:A:124:ILE:HA	1:A:125:PRO:HD3	1.89	0.42
1:F:154:ARG:HG2	1:F:193:ASN:HB3	2.01	0.42
1:K:182:LYS:HE2	1:K:182:LYS:HB3	1.86	0.42
1:E:44:SER:OG	1:E:131:LYS:HE2	2.19	0.41
1:A:37:ILE:HB	1:A:38:PRO:HD3	2.02	0.41
1:H:146:SER:HA	1:H:147:PRO:HD3	1.88	0.41
1:J:165:VAL:HG12	1:K:64:ALA:HB2	2.02	0.41
1:A:202:LEU:HD23	1:A:202:LEU:HA	1.91	0.41
1:I:122:PRO:HA	1:I:123:PRO:HD3	1.81	0.41
1:L:68:MET:CE	1:L:141:ILE:HD13	2.50	0.41
1:H:125:PRO:HB2	1:H:128:GLU:HB2	2.03	0.41
1:H:197:ASP:OD2	1:H:197:ASP:N	2.53	0.41
1:B:124:ILE:O	1:B:126:VAL:N	2.52	0.41
1:B:150:ILE:N	1:B:175:GLU:OE2	2.52	0.41
1:H:216:THR:HG23	1:I:144:MET:SD	2.61	0.41
1:J:34:PRO:HG3	1:J:174:ALA:HA	2.03	0.41
1:B:146:SER:HA	1:B:147:PRO:HD3	1.84	0.41
2:R:320:PRO:HD2	2:R:323:GLN:OE1	2.21	0.41
1:D:122:PRO:HA	1:D:123:PRO:HD3	1.85	0.40
1:F:86:VAL:HG13	1:F:98:GLU:HG3	2.02	0.40
1:I:86:VAL:HG13	1:I:98:GLU:HB2	2.03	0.40
1:K:146:SER:HA	1:K:147:PRO:HD3	1.90	0.40
1:H:157:PRO:HA	1:H:195:ASN:HD21	1.87	0.40
1:L:185:ALA:O	1:L:189:LEU:HB2	2.20	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:N:324:PRO:HA	2:N:325:PRO:HD3	1.91	0.40
1:F:192:GLN:HA	1:F:199:LYS:HE3	2.04	0.40
1:G:6:LEU:HG	1:L:6:LEU:HB3	2.02	0.40
1:J:122:PRO:HA	1:J:123:PRO:HD3	1.88	0.40
2:W:319:GLN:HA	2:W:320:PRO:HD3	1.90	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	210/231 (91%)	204 (97%)	6 (3%)	0	100	100
1	B	209/231 (90%)	203 (97%)	5 (2%)	1 (0%)	29	52
1	C	208/231 (90%)	204 (98%)	4 (2%)	0	100	100
1	D	196/231 (85%)	192 (98%)	4 (2%)	0	100	100
1	E	211/231 (91%)	206 (98%)	5 (2%)	0	100	100
1	F	218/231 (94%)	213 (98%)	5 (2%)	0	100	100
1	G	207/231 (90%)	204 (99%)	3 (1%)	0	100	100
1	H	207/231 (90%)	204 (99%)	3 (1%)	0	100	100
1	I	208/231 (90%)	206 (99%)	2 (1%)	0	100	100
1	J	209/231 (90%)	194 (93%)	13 (6%)	2 (1%)	15	32
1	K	204/231 (88%)	197 (97%)	6 (3%)	1 (0%)	29	52
1	L	202/231 (87%)	198 (98%)	4 (2%)	0	100	100
2	M	11/17 (65%)	11 (100%)	0	0	100	100
2	N	12/17 (71%)	12 (100%)	0	0	100	100
2	O	11/17 (65%)	11 (100%)	0	0	100	100
2	P	12/17 (71%)	12 (100%)	0	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	Q	11/17 (65%)	11 (100%)	0	0	100	100
2	R	12/17 (71%)	12 (100%)	0	0	100	100
2	S	13/17 (76%)	13 (100%)	0	0	100	100
2	T	11/17 (65%)	11 (100%)	0	0	100	100
2	U	11/17 (65%)	11 (100%)	0	0	100	100
2	V	11/17 (65%)	11 (100%)	0	0	100	100
2	W	11/17 (65%)	11 (100%)	0	0	100	100
All	All	2615/2959 (88%)	2551 (98%)	60 (2%)	4 (0%)	47	71

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	J	204	ALA
1	B	177	ALA
1	J	205	LEU
1	K	93	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	181/193 (94%)	180 (99%)	1 (1%)	86	95
1	B	182/193 (94%)	181 (100%)	1 (0%)	88	96
1	C	182/193 (94%)	181 (100%)	1 (0%)	88	96
1	D	176/193 (91%)	175 (99%)	1 (1%)	86	95
1	E	183/193 (95%)	183 (100%)	0	100	100
1	F	186/193 (96%)	183 (98%)	3 (2%)	62	82
1	G	180/193 (93%)	178 (99%)	2 (1%)	73	88
1	H	180/193 (93%)	175 (97%)	5 (3%)	43	69
1	I	180/193 (93%)	179 (99%)	1 (1%)	86	95

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	J	183/193 (95%)	182 (100%)	1 (0%)	88	96
1	K	180/193 (93%)	180 (100%)	0	100	100
1	L	180/193 (93%)	178 (99%)	2 (1%)	73	88
2	M	11/13 (85%)	11 (100%)	0	100	100
2	N	12/13 (92%)	11 (92%)	1 (8%)	11	22
2	O	11/13 (85%)	10 (91%)	1 (9%)	9	18
2	P	12/13 (92%)	12 (100%)	0	100	100
2	Q	11/13 (85%)	10 (91%)	1 (9%)	9	18
2	R	12/13 (92%)	11 (92%)	1 (8%)	11	22
2	S	12/13 (92%)	11 (92%)	1 (8%)	11	22
2	T	11/13 (85%)	11 (100%)	0	100	100
2	U	11/13 (85%)	11 (100%)	0	100	100
2	V	11/13 (85%)	10 (91%)	1 (9%)	9	18
2	W	11/13 (85%)	10 (91%)	1 (9%)	9	18
All	All	2298/2459 (94%)	2273 (99%)	25 (1%)	73	88

All (25) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	188	THR
1	B	189	LEU
1	C	9	GLN
1	D	154	ARG
1	F	9	GLN
1	F	136	LEU
1	F	198	CYS
1	G	96	MET
1	G	197	ASP
1	H	186	THR
1	H	195	ASN
1	H	197	ASP
1	H	198	CYS
1	H	216	THR
1	I	82	ARG
1	J	197	ASP
1	L	9	GLN
1	L	86	VAL

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Mol	Chain	Res	Type
2	N	312	THR
2	O	319	GLN
2	Q	319	GLN
2	R	312	THR
2	S	319	GLN
2	V	319	GLN
2	W	319	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	7	GLN
1	C	112	GLN
1	F	7	GLN
1	G	50	GLN
1	I	9	GLN
2	S	319	GLN
2	U	319	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 monosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

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 [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	214/231 (92%)	0.15	8 (3%) 41 34	39, 63, 113, 131	0
1	B	213/231 (92%)	0.06	11 (5%) 27 21	42, 66, 109, 141	0
1	C	212/231 (91%)	0.02	2 (0%) 84 82	44, 63, 96, 112	0
1	D	204/231 (88%)	0.23	9 (4%) 34 27	40, 66, 118, 133	0
1	E	215/231 (93%)	0.18	8 (3%) 41 34	41, 66, 102, 139	0
1	F	220/231 (95%)	0.27	11 (5%) 28 23	42, 66, 115, 159	0
1	G	211/231 (91%)	0.14	3 (1%) 75 71	47, 71, 109, 119	0
1	H	211/231 (91%)	0.29	8 (3%) 40 33	48, 79, 117, 135	0
1	I	212/231 (91%)	0.11	7 (3%) 46 39	47, 72, 106, 125	0
1	J	213/231 (92%)	0.20	8 (3%) 40 33	45, 64, 113, 130	0
1	K	210/231 (90%)	0.23	11 (5%) 27 21	43, 73, 115, 128	0
1	L	208/231 (90%)	0.27	11 (5%) 26 20	45, 70, 111, 143	0
2	M	13/17 (76%)	0.70	1 (7%) 13 10	60, 84, 99, 100	0
2	N	14/17 (82%)	0.60	1 (7%) 16 11	56, 88, 102, 117	0
2	O	13/17 (76%)	1.10	2 (15%) 2 1	55, 85, 101, 102	0
2	P	14/17 (82%)	0.60	1 (7%) 16 11	54, 92, 99, 99	0
2	Q	13/17 (76%)	1.55	4 (30%) 0 0	70, 100, 109, 115	0
2	R	14/17 (82%)	0.19	1 (7%) 16 11	62, 82, 98, 108	0
2	S	15/17 (88%)	0.45	0 100 100	63, 91, 112, 115	0
2	T	13/17 (76%)	0.85	1 (7%) 13 10	72, 93, 110, 116	0
2	U	13/17 (76%)	1.67	5 (38%) 0 0	72, 100, 111, 113	0
2	V	13/17 (76%)	1.10	2 (15%) 2 1	64, 92, 103, 104	0
2	W	13/17 (76%)	2.48	5 (38%) 0 0	69, 101, 117, 125	0
All	All	2691/2959 (90%)	0.22	120 (4%) 33 26	39, 70, 113, 159	0

All (120) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	F	180	GLU	9.6
2	W	316	PHE	8.4
1	B	178	SER	8.1
1	J	6	LEU	7.3
1	D	6	LEU	6.8
1	H	207	PRO	6.2
2	W	315	LEU	5.4
1	F	177	ALA	5.4
1	L	179	GLN	5.2
2	W	325	PRO	5.1
1	J	205	LEU	5.0
1	H	6	LEU	4.9
1	B	6	LEU	4.9
1	L	202	LEU	4.7
1	B	187	GLU	4.7
2	T	325	PRO	4.6
2	W	319	GLN	4.6
1	B	182	LYS	4.4
1	D	202	LEU	4.4
1	J	7	GLN	4.3
1	E	91	ILE	4.3
2	V	325	PRO	4.3
1	B	179	GLN	4.2
1	E	178	SER	4.0
1	L	180	GLU	4.0
1	D	187	GLU	3.9
1	B	186	THR	3.9
1	A	7	GLN	3.9
1	K	93	PRO	3.8
1	B	177	ALA	3.8
2	O	325	PRO	3.7
1	D	95	GLN	3.7
2	Q	325	PRO	3.6
1	J	158	LYS	3.6
2	O	316	PHE	3.6
1	D	201	ILE	3.6
1	A	202	LEU	3.5
1	E	180	GLU	3.4
1	G	202	LEU	3.4
1	A	6	LEU	3.3
1	D	158	LYS	3.3
1	H	88	ALA	3.3

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Mol	Chain	Res	Type	RSRZ
1	K	196	PRO	3.3
1	L	207	PRO	3.3
1	F	181	VAL	3.3
1	K	207	PRO	3.2
1	B	181	VAL	3.2
1	B	180	GLU	3.1
2	U	314	VAL	3.1
1	A	87	HIS	3.1
1	E	92	ALA	3.1
1	H	202	LEU	3.1
1	I	83	LEU	3.1
1	H	87	HIS	3.1
2	N	312	THR	2.9
1	K	183	ASN	2.9
1	F	194	ALA	2.9
1	F	178	SER	2.8
1	C	95	GLN	2.8
1	B	86	VAL	2.8
2	R	312	THR	2.8
1	A	88	ALA	2.8
1	B	94	GLY	2.8
1	G	158	LYS	2.8
2	U	316	PHE	2.7
1	J	93	PRO	2.7
2	U	315	LEU	2.7
2	P	325	PRO	2.7
1	A	207	PRO	2.6
1	F	183	ASN	2.6
1	K	90	PRO	2.6
1	D	157	PRO	2.6
1	D	205	LEU	2.6
2	V	316	PHE	2.6
1	F	7	GLN	2.5
1	C	158	LYS	2.5
1	I	7	GLN	2.5
1	E	177	ALA	2.5
1	J	180	GLU	2.4
1	K	158	LYS	2.4
2	Q	319	GLN	2.4
2	U	318	GLY	2.4
1	F	184	ALA	2.4
1	I	87	HIS	2.4

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Mol	Chain	Res	Type	RSRZ
1	L	187	GLU	2.4
1	E	94	GLY	2.3
2	M	314	VAL	2.3
1	K	186	THR	2.3
1	K	95	GLN	2.3
2	Q	316	PHE	2.3
1	F	207	PRO	2.3
1	K	185	ALA	2.3
1	I	187	GLU	2.3
1	K	157	PRO	2.2
2	Q	313	PRO	2.2
1	L	96	MET	2.2
1	G	208	GLY	2.2
1	L	188	THR	2.2
1	I	184	ALA	2.2
2	U	319	GLN	2.2
1	H	92	ALA	2.2
1	J	187	GLU	2.2
1	A	184	ALA	2.2
1	I	6	LEU	2.1
1	L	6	LEU	2.1
1	F	204	ALA	2.1
1	L	124	ILE	2.1
1	D	200	THR	2.1
1	I	86	VAL	2.1
1	L	190	LEU	2.1
1	F	179	GLN	2.1
1	K	91	ILE	2.1
2	W	314	VAL	2.1
1	A	185	ALA	2.1
1	E	6	LEU	2.0
1	E	93	PRO	2.0
1	L	86	VAL	2.0
1	H	200	THR	2.0
1	J	199	LYS	2.0
1	H	90	PRO	2.0

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 [i](#)

There are no monosaccharides in this entry.

6.4 Ligands [i](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.