



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 06:19 AM UTC

PDB ID : 6VGE / pdb_00006vge
Title : Crystal structure of the DNA binding domains of human transcription factor ERG, human Runx2 bound to core binding factor beta (Cbfb), in complex with 16mer DNA CAGAGGATGTGGCTTC
Authors : Hou, C.; Tsodikov, O.V.
Deposited on : 2020-01-07
Resolution : 4.25 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	:	4-5-2 with Phenix2.0
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

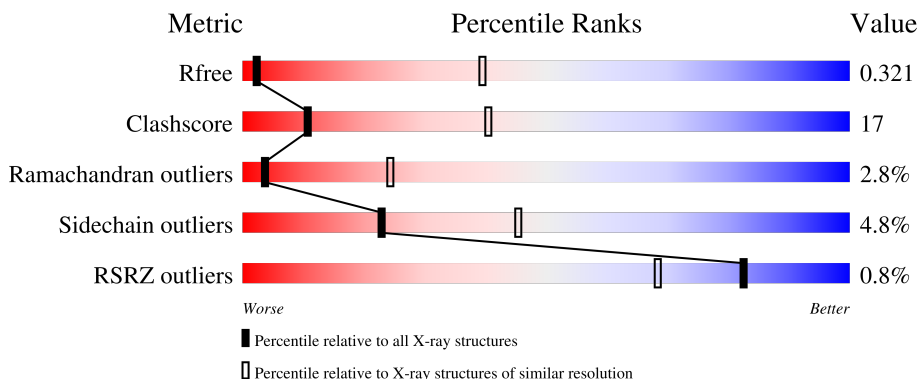
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 4.25 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}	180053	1029 (4.62-3.90)
Clashscore	190562	1074 (4.62-3.90)
Ramachandran outliers	187476	1001 (4.62-3.88)
Sidechain outliers	187428	1021 (4.66-3.86)
RSRZ outliers	180081	1026 (4.62-3.90)

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	128	2% 43% 29% 5% 23%
2	B	16	31% 69%
3	C	16	25% 75%
4	D	177	45% 19% • 34%
5	G	156	% 56% 21% • 22%

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 3361 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 Transcriptional regulator ERG.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	98	Total	C	N	O	S	0	0	0
			806	512	143	146	5			

There are 14 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	302	GLY	-	expression tag	UNP P11308
A	303	PRO	-	expression tag	UNP P11308
A	304	HIS	-	expression tag	UNP P11308
A	305	MET	-	expression tag	UNP P11308
A	420	SER	-	expression tag	UNP P11308
A	421	TYR	-	expression tag	UNP P11308
A	422	HIS	-	expression tag	UNP P11308
A	423	ALA	-	expression tag	UNP P11308
A	424	HIS	-	expression tag	UNP P11308
A	425	PRO	-	expression tag	UNP P11308
A	426	GLN	-	expression tag	UNP P11308
A	427	LYS	-	expression tag	UNP P11308
A	428	MET	-	expression tag	UNP P11308
A	429	ASN	-	expression tag	UNP P11308

- Molecule 2 is a DNA chain called DNA (5'-D(P*CP*AP*GP*AP*GP*GP*AP*TP*GP*TP*GP*GP*CP*TP*TP*C)-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	16	Total	C	N	O	P	0	0	0
			332	157	62	97	16			

- Molecule 3 is a DNA chain called DNA (5'-D(P*GP*AP*AP*GP*CP*CP*AP*CP*AP*TP*CP*CP*TP*CP*TP*G)-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	16	Total	C	N	O	P	0	0	0
			324	154	59	95	16			

- Molecule 4 is a protein called Runt-related transcription factor 2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	D	117	Total	C	N	O	S	0	0	0
			901	567	164	166	4			

- Molecule 5 is a protein called Core-binding factor subunit beta.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	G	121	Total	C	N	O	S	0	0	0
			998	622	181	189	6			

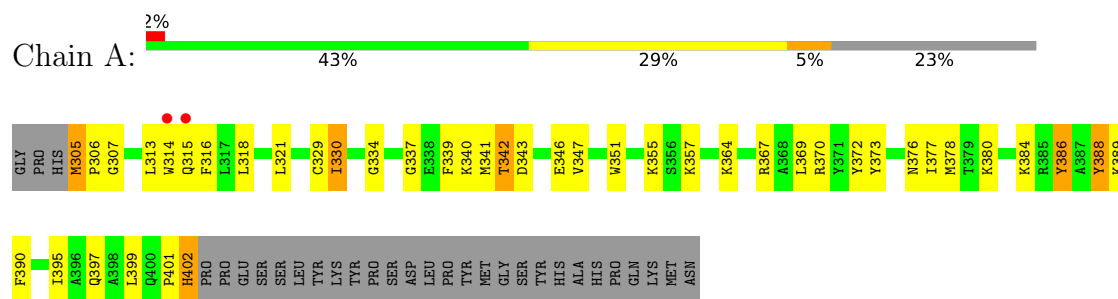
There are 14 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
G	-13	MET	-	initiating methionine	UNP Q13951
G	-12	GLY	-	expression tag	UNP Q13951
G	-11	SER	-	expression tag	UNP Q13951
G	-10	SER	-	expression tag	UNP Q13951
G	-9	HIS	-	expression tag	UNP Q13951
G	-8	HIS	-	expression tag	UNP Q13951
G	-7	HIS	-	expression tag	UNP Q13951
G	-6	HIS	-	expression tag	UNP Q13951
G	-5	HIS	-	expression tag	UNP Q13951
G	-4	HIS	-	expression tag	UNP Q13951
G	-3	SER	-	expression tag	UNP Q13951
G	-2	GLN	-	expression tag	UNP Q13951
G	-1	ASP	-	expression tag	UNP Q13951
G	0	PRO	-	expression tag	UNP Q13951

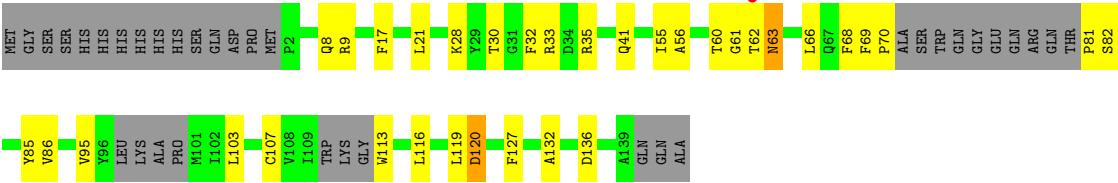
3 Residue-property plots

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: Transcriptional regulator ERG



● Molecule 5: Core-binding factor subunit beta



4 Data and refinement statistics

Property	Value	Source
Space group	P 62 2 2	Depositor
Cell constants a, b, c, α , β , γ	103.92Å 103.92Å 322.91Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	35.00 – 4.25 35.00 – 4.25	Depositor EDS
% Data completeness (in resolution range)	95.0 (35.00-4.25) 95.0 (35.00-4.25)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.70 (at 4.28Å)	Xtriage
Refinement program	REFMAC 5.8.0238	Depositor
R, R_{free}	0.312 , 0.317 0.314 , 0.321	Depositor DCC
R_{free} test set	409 reflections (5.14%)	wwPDB-VP
Wilson B-factor (Å ²)	194.8	Xtriage
Anisotropy	0.477	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 266.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.44$, $\langle L^2 \rangle = 0.27$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	3361	wwPDB-VP
Average B, all atoms (Å ²)	303.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.82% 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	0.97	0/828	1.42	2/1114 (0.2%)
2	B	0.30	0/372	0.67	0/573
3	C	0.32	0/362	0.75	0/555
4	D	1.01	0/920	1.29	2/1253 (0.2%)
5	G	0.99	0/1014	1.42	0/1355
All	All	0.89	0/3496	1.25	4/4850 (0.1%)

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	D	163	ASN	CA-C-N	5.25	127.84	120.28
4	D	163	ASN	C-N-CA	5.25	127.84	120.28
1	A	334	GLY	CA-C-N	5.14	127.12	120.44
1	A	334	GLY	C-N-CA	5.14	127.12	120.44

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	806	0	777	36	0
2	B	332	0	181	14	0
3	C	324	0	180	21	0
4	D	901	0	905	22	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	G	998	0	956	29	0
All	All	3361	0	2999	103	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 17.

All (103) 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:364:LYS:HA	3:C:11:DT:H72	1.40	1.03
1:A:397:GLN:HE22	1:A:402:HIS:HB3	1.43	0.84
1:A:305:MET:HG3	1:A:306:PRO:HD2	1.65	0.79
5:G:28:LYS:HG2	5:G:120:ASP:HB2	1.69	0.74
1:A:329:CYS:HA	1:A:342:THR:HB	1.69	0.74
1:A:318:LEU:HD21	1:A:390:PHE:CZ	2.24	0.72
5:G:69:PHE:HB3	5:G:70:PRO:HD2	1.71	0.72
2:B:10:DT:H73	4:D:225:ARG:HD3	1.71	0.71
1:A:339:PHE:CZ	1:A:388:TYR:HB2	2.26	0.70
3:C:13:DC:H2''	3:C:14:DT:OP2	1.90	0.69
1:A:380:LYS:NZ	1:A:384:LYS:O	2.28	0.67
1:A:305:MET:CG	1:A:306:PRO:HD2	2.25	0.66
4:D:212:THR:HG21	5:G:17:PHE:CZ	2.30	0.66
1:A:337:GLY:O	1:A:389:LYS:HB2	1.96	0.65
4:D:212:THR:HG21	5:G:17:PHE:CE2	2.32	0.65
1:A:364:LYS:CA	3:C:11:DT:H72	2.25	0.63
5:G:21:LEU:HD21	5:G:60:THR:HG21	1.82	0.61
1:A:330:ILE:HG13	1:A:340:LYS:O	2.00	0.61
2:B:12:DG:N2	3:C:7:DC:O2	2.35	0.58
2:B:15:DT:H2''	2:B:16:DC:C6	2.38	0.58
1:A:378:MET:HB2	1:A:389:LYS:O	2.04	0.58
2:B:1:DC:H2''	2:B:2:DA:C8	2.40	0.57
1:A:318:LEU:HD21	1:A:390:PHE:CE1	2.40	0.56
5:G:132:ALA:O	5:G:136:ASP:HB2	2.06	0.56
1:A:372:TYR:HA	1:A:377:ILE:HD12	1.89	0.55
4:D:165:SER:O	5:G:33:ARG:NH1	2.40	0.55
1:A:395:ILE:O	1:A:399:LEU:HB2	2.08	0.54
5:G:69:PHE:HB3	5:G:70:PRO:CD	2.38	0.53
5:G:60:THR:HG23	5:G:62:THR:H	1.74	0.53
4:D:116:THR:OG1	4:D:121:PHE:O	2.23	0.53
3:C:14:DT:H2''	3:C:15:DC:O5'	2.09	0.52
3:C:5:DG:C4	3:C:6:DC:C6	2.97	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:16:DT:H1'	3:C:17:DG:C8	2.44	0.52
4:D:164:TYR:CE1	5:G:30:THR:HG22	2.45	0.52
1:A:376:ASN:N	1:A:376:ASN:HD22	2.08	0.51
1:A:370:ARG:HD2	2:B:4:DA:C8	2.45	0.51
5:G:8:GLN:HE21	5:G:107:CYS:H	1.60	0.50
1:A:364:LYS:HA	3:C:11:DT:C7	2.27	0.50
1:A:343:ASP:HB3	1:A:346:GLU:HB3	1.93	0.49
1:A:369:LEU:O	1:A:372:TYR:HB2	2.12	0.49
1:A:370:ARG:HA	1:A:373:TYR:CE1	2.47	0.49
5:G:69:PHE:CZ	5:G:81:PRO:N	2.80	0.49
5:G:28:LYS:HG2	5:G:120:ASP:CB	2.41	0.49
3:C:7:DC:H5	4:D:221:VAL:HG21	1.79	0.48
3:C:15:DC:H2''	3:C:16:DT:C6	2.48	0.48
3:C:4:DA:H1'	3:C:5:DG:H5''	1.95	0.48
5:G:82:SER:OG	5:G:85:TYR:HB2	2.13	0.48
4:D:118:SER:HB3	4:D:211:ALA:HB2	1.97	0.47
5:G:68:PHE:HB3	5:G:85:TYR:HB3	1.96	0.47
1:A:367:ARG:HG2	3:C:11:DT:O4	2.15	0.47
3:C:3:DA:H4'	3:C:4:DA:OP1	2.14	0.47
1:A:341:MET:HB3	1:A:386:TYR:HB2	1.98	0.46
5:G:55:ILE:HD13	5:G:66:LEU:HD12	1.96	0.46
2:B:12:DG:H1	3:C:6:DC:H42	1.63	0.46
1:A:313:LEU:O	1:A:316:PHE:N	2.49	0.46
5:G:69:PHE:HZ	5:G:81:PRO:N	2.14	0.46
4:D:141:LYS:HG2	4:D:181:ARG:HG2	1.98	0.45
3:C:5:DG:C5	3:C:6:DC:C5	3.04	0.45
5:G:63:ASN:HD22	5:G:63:ASN:N	2.14	0.45
5:G:41:GLN:HA	5:G:119:LEU:HD21	1.99	0.45
5:G:61:GLY:O	5:G:63:ASN:ND2	2.50	0.45
4:D:131:ARG:HG3	4:D:221:VAL:O	2.16	0.45
5:G:56:ALA:CB	5:G:63:ASN:HA	2.46	0.45
4:D:133:ASN:N	4:D:187:PHE:O	2.43	0.44
1:A:377:ILE:HG23	1:A:395:ILE:HD11	1.97	0.44
2:B:14:DT:H2''	2:B:15:DT:H5'	1.99	0.44
1:A:388:TYR:N	1:A:388:TYR:CD2	2.84	0.44
1:A:370:ARG:HD2	2:B:4:DA:H8	1.82	0.44
1:A:318:LEU:HD22	1:A:321:LEU:HD22	1.99	0.44
4:D:182:PHE:O	4:D:183:ASN:C	2.61	0.44
2:B:15:DT:C2	2:B:16:DC:C2	3.05	0.44
4:D:159:GLY:CA	5:G:61:GLY:O	2.66	0.43
4:D:193:ARG:C	4:D:195:LYS:H	2.27	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:355:LYS:HE2	3:C:10:DA:OP1	2.19	0.43
4:D:116:THR:OG1	4:D:118:SER:O	2.35	0.43
4:D:132:CYS:SG	4:D:188:VAL:O	2.68	0.43
5:G:8:GLN:NE2	5:G:107:CYS:SG	2.91	0.43
5:G:32:PHE:HB3	5:G:35:ARG:CG	2.49	0.43
1:A:388:TYR:N	1:A:388:TYR:HD2	2.16	0.42
4:D:130:TRP:HE1	4:D:134:LYS:HB3	1.84	0.42
2:B:4:DA:H1'	2:B:5:DG:H5'	2.01	0.42
3:C:4:DA:C6	3:C:5:DG:C6	3.07	0.42
1:A:314:TRP:CZ3	1:A:395:ILE:HD12	2.55	0.42
1:A:364:LYS:HE2	3:C:11:DT:H2'	2.01	0.42
4:D:113:LEU:HD11	4:D:143:VAL:HG21	2.01	0.42
1:A:307:GLY:O	1:A:315:GLN:NE2	2.53	0.42
1:A:357:LYS:HE3	3:C:10:DA:H5''	2.01	0.42
2:B:11:DG:H2''	2:B:12:DG:C8	2.55	0.42
4:D:126:LEU:HD11	4:D:140:PHE:CE1	2.54	0.42
5:G:95:VAL:HG13	5:G:116:LEU:HD21	2.01	0.42
1:A:313:LEU:HD21	1:A:351:TRP:CE2	2.56	0.41
4:D:141:LYS:HD3	4:D:181:ARG:HD3	2.02	0.41
4:D:158:ALA:HB1	4:D:197:PHE:CD1	2.55	0.41
2:B:10:DT:H2''	2:B:11:DG:C8	2.56	0.41
1:A:329:CYS:CA	1:A:342:THR:HB	2.44	0.41
3:C:5:DG:C2	3:C:6:DC:C2	3.09	0.41
4:D:165:SER:CB	5:G:30:THR:HB	2.50	0.41
5:G:9:ARG:HD3	5:G:127:PHE:CE1	2.56	0.41
5:G:69:PHE:CB	5:G:70:PRO:CD	2.99	0.40
5:G:95:VAL:O	5:G:113:TRP:HA	2.22	0.40
2:B:4:DA:N6	2:B:5:DG:C6	2.89	0.40
3:C:4:DA:N1	3:C:5:DG:C6	2.89	0.40
2:B:2:DA:C6	2:B:3:DG:C6	3.09	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	96/128 (75%)	79 (82%)	12 (12%)	5 (5%)	1	16
4	D	115/177 (65%)	93 (81%)	18 (16%)	4 (4%)	3	20
5	G	113/156 (72%)	104 (92%)	9 (8%)	0	100	100
All	All	324/461 (70%)	276 (85%)	39 (12%)	9 (3%)	4	24

All (9) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	342	THR
1	A	386	TYR
4	D	163	ASN
4	D	135	THR
4	D	150	ASP
4	D	224	PRO
1	A	347	VAL
1	A	330	ILE
1	A	401	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	85/113 (75%)	82 (96%)	3 (4%)	32	53
4	D	100/156 (64%)	93 (93%)	7 (7%)	14	36
5	G	106/135 (78%)	102 (96%)	4 (4%)	29	51
All	All	291/404 (72%)	277 (95%)	14 (5%)	23	45

All (14) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	305	MET

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Mol	Chain	Res	Type
1	A	388	TYR
1	A	402	HIS
4	D	134	LYS
4	D	141	LYS
4	D	152	THR
4	D	190	ARG
4	D	200	THR
4	D	221	VAL
4	D	222	ASP
5	G	63	ASN
5	G	86	VAL
5	G	103	LEU
5	G	120	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (8) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	315	GLN
1	A	376	ASN
1	A	397	GLN
4	D	160	ASN
5	G	8	GLN
5	G	63	ASN
5	G	67	GLN
5	G	134	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 ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry

There are no ligands in this entry.

5.7 Other polymers

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	98/128 (76%)	-0.16	2 (2%) 65 50	213, 252, 281, 296	0
2	B	16/16 (100%)	-0.17	0 100 100	251, 272, 299, 304	0
3	C	16/16 (100%)	-0.12	0 100 100	239, 278, 331, 335	0
4	D	117/177 (66%)	-0.54	0 100 100	234, 274, 305, 322	0
5	G	121/156 (77%)	-0.51	1 (0%) 82 68	354, 382, 421, 432	0
All	All	368/493 (74%)	-0.39	3 (0%) 82 68	213, 280, 412, 432	0

All (3) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	315	GLN	3.2
5	G	62	THR	2.9
1	A	314	TRP	2.6

6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

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

6.3 Carbohydrates [i](#)

There are no oligosaccharides 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.