



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 1, 2026 – 03:44 AM UTC

PDB ID : 8V52 / pdb_00008v52
Title : Crystal structure of 2A10 Fab bound to Human TGF-beta3
Authors : Yin, J.; Lupardus, P.J.
Deposited on : 2023-11-30
Resolution : 2.50 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:

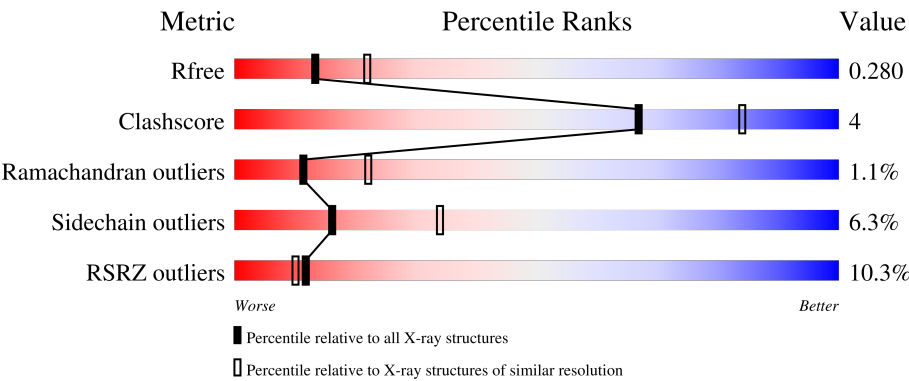
MolProbity	:	4-5-2 with Phenix2.0
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

1 Overall quality at a glance i

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))
R_{free}	180053	5829 (2.50-2.50)
Clashscore	190562	6492 (2.50-2.50)
Ramachandran outliers	187476	6378 (2.50-2.50)
Sidechain outliers	187428	6380 (2.50-2.50)
RSRZ outliers	180081	5833 (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 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	112	4% 85% 14% .
1	B	112	2% 87% 10% ..
2	C	218	2% 81% 17% ..
2	E	218	22% 62% 13% 24% .
3	D	227	3% 85% 11% .

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Mol	Chain	Length	Quality of chain
3	F	227	17% 64% 13% • 20%

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 7812 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 Transforming growth factor beta-3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	112	Total	C	N	O	S	0	0	0
			890	564	148	168	10			
1	B	112	Total	C	N	O	S	0	0	0
			884	561	145	168	10			

- Molecule 2 is a protein called 2A10 Fab Light chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	216	Total	C	N	O	S	0	0	0
			1663	1039	287	332	5			
2	E	166	Total	C	N	O	S	0	0	0
			1235	774	208	249	4			

- Molecule 3 is a protein called 2A10 Fab Heavy Chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	D	220	Total	C	N	O	S	0	0	0
			1631	1028	266	331	6			
3	F	182	Total	C	N	O	S	0	0	0
			1348	851	218	273	6			

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	15	Total	O	0	0
			15	15		
4	B	19	Total	O	0	0
			19	19		
4	C	54	Total	O	0	0
			54	54		
4	D	59	Total	O	0	0
			59	59		

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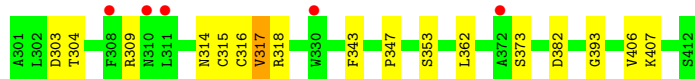
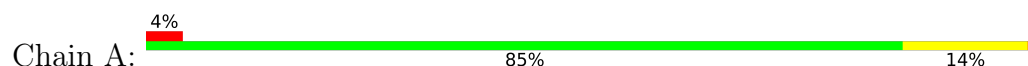
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	E	2	Total	O	0	0
			2	2		
4	F	12	Total	O	0	0
			12	12		

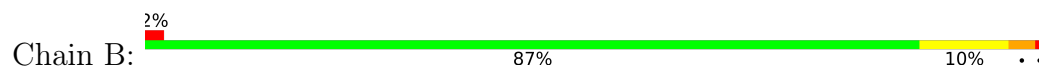
3 Residue-property plots [i](#)

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.

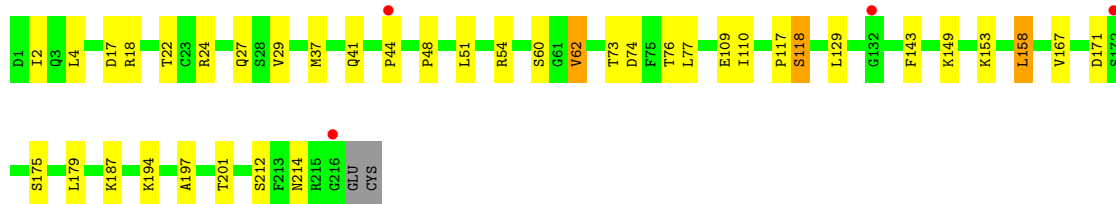
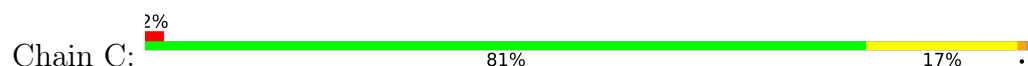
- Molecule 1: Transforming growth factor beta-3



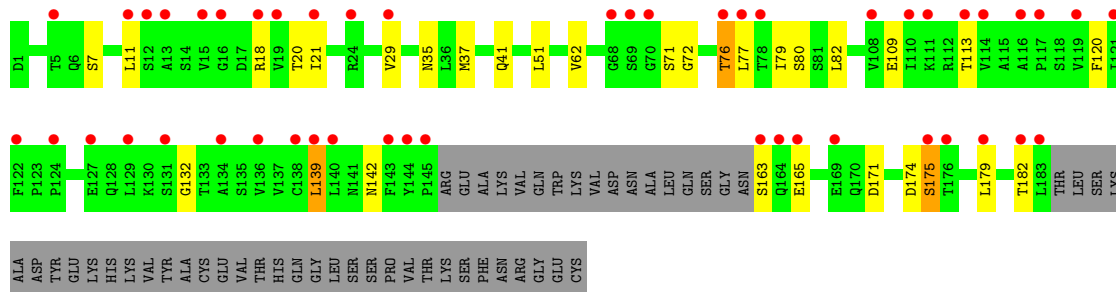
- Molecule 1: Transforming growth factor beta-3



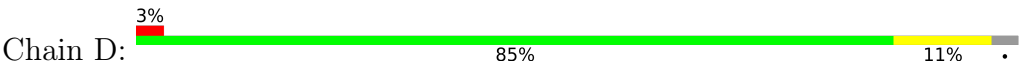
- Molecule 2: 2A10 Fab Light chain



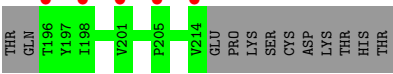
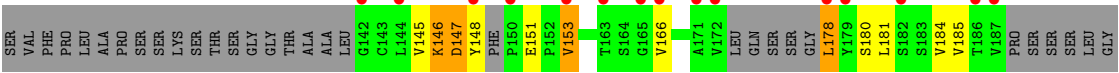
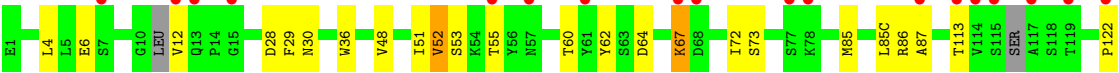
- Molecule 2: 2A10 Fab Light chain



● Molecule 3: 2A10 Fab Heavy Chain



● Molecule 3: 2A10 Fab Heavy Chain



4 Data and refinement statistics

Property	Value	Source
Space group	I 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	133.94Å 47.20Å 200.83Å 90.00° 101.68° 90.00°	Depositor
Resolution (Å)	49.17 – 2.50 49.17 – 2.50	Depositor EDS
% Data completeness (in resolution range)	99.2 (49.17-2.50) 99.1 (49.17-2.50)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.52 (at 2.51Å)	Xtriage
Refinement program	BUSTER 2.11.7	Depositor
R, R_{free}	0.221 , 0.269 0.232 , 0.280	Depositor DCC
R_{free} test set	2096 reflections (4.84%)	wwPDB-VP
Wilson B-factor (Å ²)	51.9	Xtriage
Anisotropy	0.131	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 56.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	7812	wwPDB-VP
Average B, all atoms (Å ²)	59.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.67% 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

5.1 Standard geometry

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	0.84	0/915	1.30	4/1248 (0.3%)
1	B	0.81	0/909	1.26	3/1241 (0.2%)
2	C	0.90	0/1700	1.22	4/2306 (0.2%)
2	E	0.87	0/1262	1.23	1/1719 (0.1%)
3	D	0.88	0/1669	1.20	3/2276 (0.1%)
3	F	0.84	1/1374 (0.1%)	1.25	9/1870 (0.5%)
All	All	0.86	1/7829 (0.0%)	1.24	24/10660 (0.2%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	F	52	VAL	CA-C	5.01	1.57	1.52

All (24) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	382	ASP	CA-CB-CG	7.60	120.20	112.60
1	A	303	ASP	CA-CB-CG	7.33	119.93	112.60
2	E	174	ASP	CA-CB-CG	7.01	119.61	112.60
3	F	29	PHE	CA-C-N	6.37	129.11	120.38
3	F	29	PHE	C-N-CA	6.37	129.11	120.38
2	C	17	ASP	CA-CB-CG	6.33	118.92	112.60
1	B	406	VAL	N-CA-CB	6.14	118.00	111.00
2	C	109	GLU	CB-CG-CD	5.96	122.73	112.60
3	F	64	ASP	CA-C-N	5.92	129.02	120.38
3	F	64	ASP	C-N-CA	5.92	129.02	120.38
2	C	118	SER	N-CA-C	-5.86	99.73	109.46
3	F	28	ASP	CA-C-N	5.68	127.82	120.44
3	F	28	ASP	C-N-CA	5.68	127.82	120.44
3	F	86	ARG	N-CA-C	5.54	116.48	107.23
3	F	146	LYS	CA-C-N	5.35	131.76	121.54
3	F	146	LYS	C-N-CA	5.35	131.76	121.54
1	A	303	ASP	CA-C-N	5.27	127.66	120.54

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	303	ASP	C-N-CA	5.27	127.66	120.54
3	D	145	LYS	CA-C-N	5.26	130.88	122.93
3	D	145	LYS	C-N-CA	5.26	130.88	122.93
1	B	306	TYR	CA-C-N	5.13	127.41	120.38
1	B	306	TYR	C-N-CA	5.13	127.41	120.38
3	D	70	PHE	CA-CB-CG	5.10	118.90	113.80
2	C	62	VAL	CB-CA-C	5.09	115.67	110.94

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	890	0	847	4	0
1	B	884	0	836	5	0
2	C	1663	0	1623	17	0
2	E	1235	0	1179	12	0
3	D	1631	0	1574	9	0
3	F	1348	0	1254	13	0
4	A	15	0	0	0	0
4	B	19	0	0	0	0
4	C	54	0	0	0	0
4	D	59	0	0	0	0
4	E	2	0	0	0	0
4	F	12	0	0	0	0
All	All	7812	0	7313	56	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 4.

All (56) 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)
3:F:85:MET:HE2	3:F:85(C):LEU:HD21	1.69	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:335:GLU:HG3	2:C:54:ARG:NH2	2.09	0.68
2:C:29:VAL:HG21	2:C:37:MET:HE2	1.83	0.60
2:E:171:ASP:HB3	2:E:175:SER:H	1.66	0.60
3:F:122:PRO:HB3	3:F:148:TYR:HB3	1.83	0.60
3:F:36:TRP:HD1	3:F:72:ILE:HD12	1.66	0.60
2:C:167:VAL:HG22	2:C:179:LEU:HD12	1.85	0.59
2:C:51:LEU:HA	2:C:62:VAL:HG21	1.85	0.58
2:C:153:LYS:HG2	2:C:158:LEU:HD12	1.86	0.58
3:D:4:LEU:HD11	3:D:97:VAL:HG23	1.85	0.57
1:A:314:ASN:HA	1:A:347:PRO:HD2	1.87	0.56
2:E:79:ILE:HG21	2:E:82:LEU:HD12	1.86	0.56
3:F:12:VAL:HG11	3:F:85(C):LEU:HD13	1.88	0.54
2:E:163:SER:HA	2:E:182:THR:O	2.07	0.54
3:F:166:VAL:HG13	3:F:185:VAL:HG22	1.90	0.54
2:E:139:LEU:HD11	3:F:184:VAL:HG21	1.91	0.53
1:A:393:GLY:HA2	3:F:52:VAL:HG11	1.91	0.53
2:E:120:PHE:HB2	2:E:139:LEU:HB3	1.91	0.52
2:C:194:LYS:HE3	2:C:214:ASN:HB3	1.92	0.52
2:E:20:THR:HG23	2:E:76:THR:HG23	1.92	0.51
3:F:52:VAL:HG12	3:F:53:SER:N	2.26	0.51
2:E:21:ILE:HG13	2:E:77:LEU:HB3	1.92	0.50
2:C:149:LYS:HB3	2:C:201:THR:HB	1.95	0.48
2:E:41:GLN:HB2	2:E:51:LEU:HD11	1.95	0.48
3:D:34:MET:HB3	3:D:81:LEU:HD22	1.95	0.48
2:E:29:VAL:HG21	2:E:37:MET:HE2	1.96	0.48
1:A:317:VAL:HG13	1:A:406:VAL:HG12	1.95	0.48
2:C:41:GLN:HB2	2:C:51:LEU:HD11	1.97	0.47
2:C:129:LEU:O	2:C:187:LYS:HD2	2.15	0.47
3:F:147:ASP:HB3	3:F:178:LEU:HD23	1.95	0.47
3:D:144:VAL:HG11	3:D:152:VAL:HG11	1.96	0.46
3:F:146:LYS:HA	3:F:180:SER:OG	2.15	0.46
2:C:2:ILE:HG12	2:C:27:GLN:HB2	1.98	0.45
3:F:145:VAL:HG11	3:F:153:VAL:HG11	1.99	0.44
3:F:62:TYR:HB2	3:F:67:LYS:HG3	1.99	0.44
2:C:48:PRO:HD2	3:D:105:TRP:CE3	2.53	0.44
1:A:318:ARG:HB2	1:A:343:PHE:CE1	2.53	0.44
2:C:171:ASP:O	2:C:175:SER:HA	2.18	0.43
1:B:358:HIS:O	1:B:362:LEU:HB2	2.17	0.43
2:E:35:ASN:OD1	2:E:71:SER:HA	2.19	0.43
2:E:51:LEU:HA	2:E:62:VAL:HG21	2.00	0.43
2:C:24:ARG:HD3	2:C:74:ASP:OD1	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:D:62:TYR:HB2	3:D:67:LYS:HG3	2.01	0.42
2:C:117:PRO:HB3	2:C:143:PHE:HB3	2.02	0.42
3:F:51:ILE:HG13	3:F:60:THR:HG22	2.02	0.42
1:B:364:LEU:HD23	1:B:368:LEU:HD13	2.02	0.42
3:D:12:VAL:HG11	3:D:85(C):LEU:HD13	2.02	0.41
2:C:197:ALA:HB2	2:C:212:SER:HB3	2.03	0.41
2:C:4:LEU:HD22	2:C:37:MET:HE1	2.03	0.41
3:D:35:SER:HB3	3:D:47:LEU:CD1	2.51	0.41
2:E:18:ARG:HG3	2:E:80:SER:HA	2.03	0.40
1:B:318:ARG:HG3	1:B:345:SER:HB3	2.03	0.40
1:B:362:LEU:HD23	1:B:362:LEU:HA	1.86	0.40
3:D:150:GLU:HG3	3:D:151:PRO:HA	2.02	0.40
3:D:22:CYS:HB3	3:D:81:LEU:HB3	2.04	0.40
2:C:24:ARG:HA	2:C:73:THR:O	2.20	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	110/112 (98%)	98 (89%)	9 (8%)	3 (3%)	4	6
1	B	110/112 (98%)	102 (93%)	7 (6%)	1 (1%)	14	27
2	C	214/218 (98%)	205 (96%)	8 (4%)	1 (0%)	24	43
2	E	162/218 (74%)	144 (89%)	14 (9%)	4 (2%)	4	7
3	D	218/227 (96%)	208 (95%)	10 (5%)	0	100	100
3	F	168/227 (74%)	156 (93%)	10 (6%)	2 (1%)	10	20
All	All	982/1114 (88%)	913 (93%)	58 (6%)	11 (1%)	11	22

All (11) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	E	175	SER
3	F	147	ASP
2	E	72	GLY
3	F	87	ALA
1	A	309	ARG
1	A	353	SER
2	E	132	GLY
1	A	315	CYS
2	C	44	PRO
2	E	142	ASN
1	B	368	LEU

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	102/102 (100%)	96 (94%)	6 (6%)	18	37
1	B	101/102 (99%)	91 (90%)	10 (10%)	7	16
2	C	190/192 (99%)	182 (96%)	8 (4%)	26	52
2	E	139/192 (72%)	131 (94%)	8 (6%)	18	38
3	D	183/193 (95%)	173 (94%)	10 (6%)	19	40
3	F	146/193 (76%)	134 (92%)	12 (8%)	10	23
All	All	861/974 (88%)	807 (94%)	54 (6%)	16	34

All (54) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	304	THR
1	A	316	CYS
1	A	317	VAL
1	A	362	LEU
1	A	373	SER
1	A	407	LYS
1	B	316	CYS
1	B	317	VAL

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Mol	Chain	Res	Type
1	B	335	GLU
1	B	344	CYS
1	B	351	LEU
1	B	357	THR
1	B	362	LEU
1	B	368	LEU
1	B	400	GLN
1	B	406	VAL
2	C	18	ARG
2	C	22	THR
2	C	60	SER
2	C	76	THR
2	C	77	LEU
2	C	110	ILE
2	C	118	SER
2	C	158	LEU
3	D	5	LEU
3	D	6	GLU
3	D	48	VAL
3	D	67	LYS
3	D	130	SER
3	D	132	SER
3	D	133	THR
3	D	134	SER
3	D	140	LEU
3	D	197	ILE
2	E	7	SER
2	E	11	LEU
2	E	76	THR
2	E	109	GLU
2	E	113	THR
2	E	139	LEU
2	E	165	GLU
2	E	179	LEU
3	F	4	LEU
3	F	6	GLU
3	F	30	ASN
3	F	48	VAL
3	F	55	THR
3	F	67	LYS
3	F	73	SER
3	F	113	THR

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Mol	Chain	Res	Type
3	F	151	GLU
3	F	153	VAL
3	F	178	LEU
3	F	181	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (15) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	334	HIS
1	A	366	ASN
1	A	403	ASN
2	C	57	ASN
2	C	141	ASN
2	C	151	GLN
2	C	164	GLN
3	D	30	ASN
3	D	84	GLN
3	D	85(A)	ASN
3	D	107	GLN
2	E	3	GLN
2	E	128	GLN
2	E	142	ASN
3	F	84	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

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, 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	112/112 (100%)	0.38	5 (4%)	38	33	39, 52, 75, 84	0
1	B	112/112 (100%)	0.38	2 (1%)	67	64	41, 54, 77, 83	0
2	C	216/218 (99%)	0.07	4 (1%)	66	62	29, 45, 68, 80	0
2	E	166/218 (76%)	1.54	48 (28%)	1	1	39, 79, 113, 121	0
3	D	220/227 (96%)	0.09	7 (3%)	50	46	30, 45, 70, 87	0
3	F	182/227 (80%)	1.32	38 (20%)	2	2	38, 75, 98, 108	0
All	All	1008/1114 (90%)	0.61	104 (10%)	12	10	29, 55, 98, 121	0

All (104) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	E	144	TYR	5.6
3	F	117	ALA	4.7
3	D	132	SER	4.5
2	E	145	PRO	4.4
3	F	196	THR	4.2
2	E	183	LEU	4.2
3	F	172	VAL	4.2
2	E	16	GLY	4.1
3	F	187	VAL	4.1
3	F	12	VAL	3.9
3	F	57	ASN	3.8
3	F	198	ILE	3.8
2	E	140	LEU	3.7
2	E	119	VAL	3.6
3	D	133	THR	3.6
2	E	117	PRO	3.6
2	E	68	GLY	3.6
2	E	121	ILE	3.6
3	F	214	VAL	3.5

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Mol	Chain	Res	Type	RSRZ
2	E	21	ILE	3.5
3	F	166	VAL	3.4
3	F	179	TYR	3.4
2	E	129	LEU	3.4
3	F	178	LEU	3.3
2	E	127	GLU	3.3
2	E	136	VAL	3.2
1	B	367	THR	3.2
2	C	216	GLY	3.2
3	D	131	LYS	3.1
2	E	139	LEU	3.0
3	F	115	SER	3.0
2	E	164	GLN	3.0
2	E	78	THR	3.0
3	F	163	THR	3.0
1	A	372	ALA	3.0
3	F	142	GLY	3.0
2	E	19	VAL	2.9
2	E	182	THR	2.9
3	F	148	TYR	2.9
2	E	114	VAL	2.9
2	E	176	THR	2.9
3	F	165	GLY	2.9
2	E	131	SER	2.8
2	E	175	SER	2.8
3	F	119	THR	2.8
2	E	15	VAL	2.8
3	F	150	PRO	2.7
2	E	143	PHE	2.7
2	E	77	LEU	2.7
1	A	308	PHE	2.7
2	E	24	ARG	2.6
2	E	11	LEU	2.6
3	F	186	THR	2.6
3	F	144	LEU	2.6
1	A	310	ASN	2.6
3	F	153	VAL	2.6
2	E	110	ILE	2.5
3	F	114	VAL	2.5
2	E	111	LYS	2.5
3	F	122	PRO	2.5
3	F	7	SER	2.5

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Mol	Chain	Res	Type	RSRZ
3	F	205	PRO	2.4
3	F	68	ASP	2.4
3	F	61	TYR	2.4
2	E	13	ALA	2.4
3	F	171	ALA	2.4
2	E	5	THR	2.4
2	E	169	GLU	2.4
2	C	172	SER	2.3
2	E	12	SER	2.3
2	E	69	SER	2.3
2	E	124	PRO	2.3
2	E	134	ALA	2.3
2	E	113	THR	2.3
3	F	15	GLY	2.3
2	E	165	GLU	2.3
3	F	87	ALA	2.3
3	D	134	SER	2.3
1	B	344	CYS	2.3
2	E	70	GLY	2.2
2	E	163	SER	2.2
2	C	44	PRO	2.2
2	C	132	GLY	2.2
2	E	179	LEU	2.1
2	E	138	CYS	2.1
2	E	18	ARG	2.1
3	D	129	SER	2.1
3	F	182	SER	2.1
3	D	78	LYS	2.1
2	E	29	VAL	2.1
3	F	67	LYS	2.1
2	E	122	PHE	2.1
3	F	78	LYS	2.1
3	D	95	CYS	2.1
3	F	13	GLN	2.0
1	A	330	TRP	2.0
3	F	113	THR	2.0
3	F	77	SER	2.0
2	E	108	VAL	2.0
3	F	201	VAL	2.0
1	A	311	LEU	2.0
2	E	116	ALA	2.0
2	E	76	THR	2.0

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Mol	Chain	Res	Type	RSRZ
3	F	55	THR	2.0

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.