



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 28, 2026 – 08:30 PM UTC

PDB ID : 1FT1 / pdb_00001ft1
Title : CRYSTAL STRUCTURE OF PROTEIN FARNESYLTRANSFERASE AT
2.25 ANGSTROMS RESOLUTION
Authors : Beese, L.S.; Park, H.-W.
Deposited on : 1997-03-17
Resolution : 2.25 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

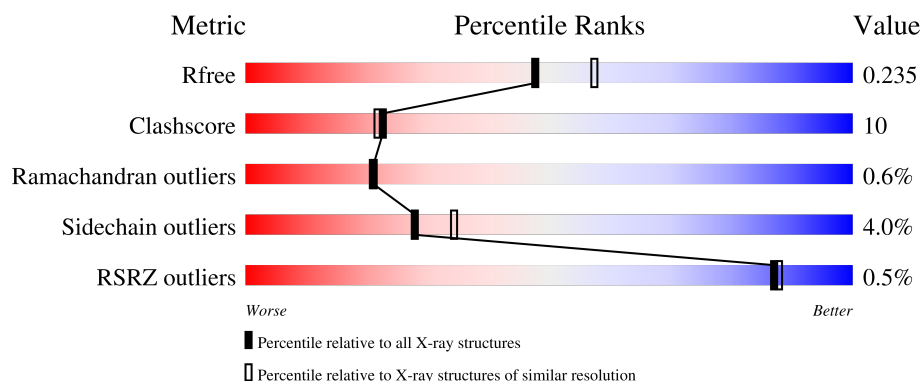
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.25 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	1898 (2.26-2.26)
Clashscore	190562	2005 (2.26-2.26)
Ramachandran outliers	187476	1965 (2.26-2.26)
Sidechain outliers	187428	1966 (2.26-2.26)
RSRZ outliers	180081	1898 (2.26-2.26)

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	377	 58% 23% 16%
2	B	437	 73% 19% 5%

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 6353 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 PROTEIN FARNESYLTRANSFERASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	315	Total	C	N	O	S	0	0	0
			2688	1712	473	498	5			

- Molecule 2 is a protein called PROTEIN FARNESYLTRANSFERASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	416	Total	C	N	O	S	0	0	0
			3262	2078	558	602	24			

- Molecule 3 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	B	1	Total	Zn	0	0
			1	1		

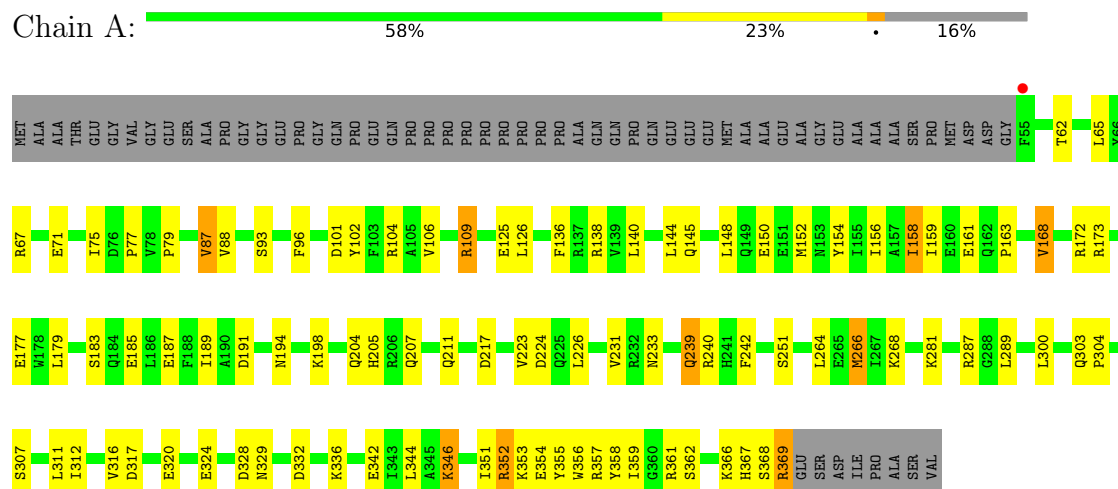
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	155	Total	O	0	0
			155	155		
4	B	247	Total	O	0	0
			247	247		

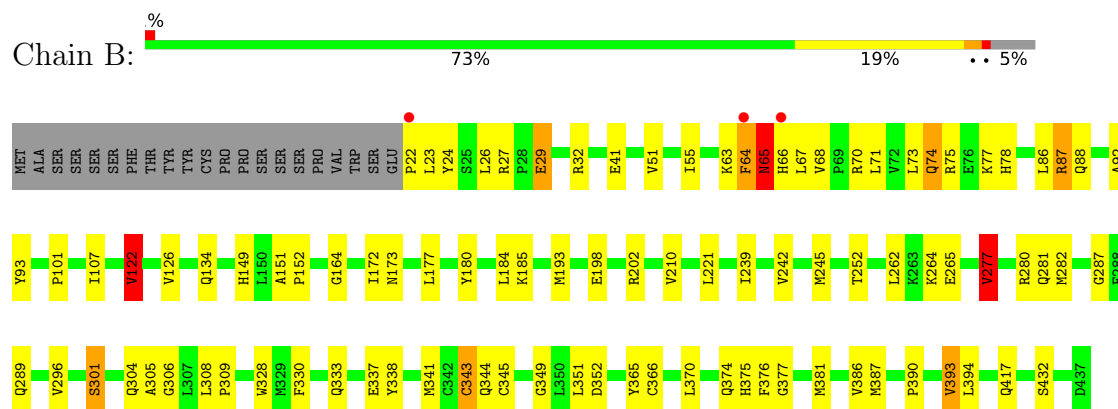
3 Residue-property plots [i](#)

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: PROTEIN FARNESYLTRANSFERASE



• Molecule 2: PROTEIN FARNESYLTRANSFERASE



4 Data and refinement statistics

Property	Value	Source
Space group	P 65	Depositor
Cell constants a, b, c, α , β , γ	167.06Å 167.06Å 97.90Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	6.00 – 2.25 6.00 – 2.25	Depositor EDS
% Data completeness (in resolution range)	89.6 (6.00-2.25) 84.7 (6.00-2.25)	Depositor EDS
R_{merge}	0.05	Depositor
R_{sym}	0.05	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.71 (at 2.10Å)	Xtriage
Refinement program	X-PLOR	Depositor
R, R_{free}	0.210 , 0.260 0.194 , 0.235	Depositor DCC
R_{free} test set	3846 reflections (5.06%)	wwPDB-VP
Wilson B-factor (Å ²)	25.3	Xtriage
Anisotropy	0.352	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.49 , 97.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.035 for h,-h-k,-l	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	6353	wwPDB-VP
Average B, all atoms (Å ²)	31.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.81% 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

Bond lengths and bond angles in the following residue types are not validated in this section: ZN

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	0.59	0/2754	0.94	6/3738 (0.2%)
2	B	0.65	0/3349	1.08	20/4549 (0.4%)
All	All	0.62	0/6103	1.02	26/8287 (0.3%)

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
2	B	0	1

There are no bond length outliers.

All (26) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	352	ASP	N-CA-C	-8.80	99.89	111.24
2	B	351	LEU	N-CA-C	8.73	121.57	109.18
2	B	301	SER	N-CA-C	-8.68	101.72	111.71
2	B	277	VAL	CB-CA-C	-8.17	101.52	111.97
2	B	65	ASN	N-CA-C	7.99	122.26	109.24
1	A	185	GLU	N-CA-C	7.13	123.06	111.37
2	B	417	GLN	N-CA-C	-6.65	104.65	112.89
1	A	183	SER	N-CA-C	6.56	118.44	111.28
2	B	63	LYS	N-CA-C	-6.52	103.45	111.40
2	B	365	TYR	N-CA-C	6.22	119.03	111.82
2	B	164	GLY	N-CA-C	6.10	123.70	114.61
2	B	92	ALA	N-CA-C	-5.83	105.43	112.54
2	B	70	ARG	N-CA-C	5.82	120.54	113.38
2	B	366	CYS	N-CA-C	-5.59	105.27	111.36

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	87	VAL	N-CA-C	-5.57	99.77	108.95
1	A	150	GLU	N-CA-C	-5.30	105.42	111.14
2	B	242	VAL	N-CA-C	-5.23	104.91	109.19
2	B	172	ILE	N-CA-C	5.20	115.71	108.84
2	B	345	CYS	CA-C-N	5.19	124.82	119.05
2	B	345	CYS	C-N-CA	5.19	124.82	119.05
2	B	343	CYS	N-CA-C	5.15	118.88	112.59
1	A	93	SER	N-CA-C	-5.13	104.10	110.41
1	A	217	ASP	N-CA-C	5.11	119.80	111.37
2	B	126	VAL	N-CA-C	-5.04	105.80	110.53
2	B	122	VAL	CB-CA-C	-5.03	105.28	112.22
2	B	193	MET	N-CA-C	-5.00	105.91	111.36

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	B	93	TYR	Sidechain

5.2 Too-close contacts ⓘ

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	2688	0	2614	65	0
2	B	3262	0	3173	63	0
3	B	1	0	0	0	0
4	A	155	0	0	2	0
4	B	247	0	0	8	0
All	All	6353	0	5787	123	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 10.

All (123) 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:159:ILE:HG12	1:A:168:VAL:HG13	1.41	1.02
2:B:77:LYS:HA	2:B:77:LYS:HE2	1.56	0.87
2:B:333:GLN:HG3	2:B:387:MET:HE2	1.56	0.84
1:A:266:MET:HE3	1:A:266:MET:HA	1.63	0.81
1:A:96:PHE:HA	1:A:126:LEU:HD13	1.67	0.77
2:B:74:GLN:H	2:B:344:GLN:HE22	1.35	0.74
2:B:134:GLN:HE22	2:B:173:ASN:H	1.33	0.74
1:A:289:LEU:HD12	1:A:317:ASP:HB3	1.72	0.72
1:A:75:ILE:HD11	1:A:109:ARG:HD3	1.73	0.70
2:B:281:GLN:HG3	4:B:1391:HOH:O	1.92	0.70
2:B:74:GLN:H	2:B:344:GLN:NE2	1.91	0.69
1:A:159:ILE:HG12	1:A:168:VAL:CG1	2.21	0.68
2:B:51:VAL:O	2:B:55:ILE:HG12	1.96	0.66
2:B:338:TYR:CE2	2:B:343:CYS:SG	2.90	0.65
2:B:386:VAL:HG21	2:B:393:VAL:HG13	1.78	0.64
2:B:24:TYR:HE2	4:B:1250:HOH:O	1.80	0.64
2:B:301:SER:O	2:B:305:ALA:HB3	1.97	0.63
1:A:352:ARG:NH2	2:B:281:GLN:O	2.32	0.63
2:B:78:HIS:HD1	2:B:349:GLY:H	1.45	0.63
1:A:156:ILE:HD11	1:A:172:ARG:HH22	1.64	0.62
1:A:148:LEU:HB2	1:A:179:LEU:HD21	1.82	0.62
2:B:277:VAL:O	2:B:280:ARG:HB2	1.99	0.62
1:A:357:ARG:O	1:A:361:ARG:HB2	2.01	0.61
2:B:185:LYS:HE3	2:B:221:LEU:O	2.01	0.60
1:A:281:LYS:NZ	1:A:289:LEU:HD11	2.16	0.60
2:B:24:TYR:HA	2:B:27:ARG:HE	1.65	0.59
1:A:189:ILE:HD11	1:A:205:HIS:HD2	1.67	0.58
1:A:138:ARG:NH2	4:A:1056:HOH:O	2.35	0.58
2:B:239:ILE:HB	2:B:252:THR:HA	1.85	0.58
2:B:390:PRO:O	2:B:393:VAL:HG22	2.04	0.58
1:A:204:GLN:HB2	2:B:245:MET:HE2	1.86	0.57
2:B:73:LEU:HA	2:B:344:GLN:HE22	1.69	0.56
1:A:239:GLN:HE21	1:A:239:GLN:HA	1.71	0.56
1:A:303:GLN:O	1:A:307:SER:HB2	2.06	0.56
1:A:368:SER:C	1:A:369:ARG:HG3	2.31	0.55
1:A:173:ARG:HD2	2:B:198:GLU:OE2	2.07	0.55
1:A:307:SER:HA	1:A:311:LEU:HD13	1.87	0.55
2:B:32:ARG:HG3	2:B:32:ARG:HH11	1.71	0.55
2:B:280:ARG:NH2	4:B:1009:HOH:O	2.40	0.55
2:B:337:GLU:HB3	2:B:341:MET:HE3	1.90	0.54
1:A:101:ASP:HA	1:A:104:ARG:NH1	2.23	0.54
2:B:71:LEU:HD21	2:B:341:MET:HG3	1.90	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:280:ARG:HG3	2:B:304:GLN:NE2	2.23	0.53
2:B:177:LEU:HD21	2:B:210:VAL:CG1	2.39	0.53
2:B:386:VAL:CG2	2:B:393:VAL:HG13	2.38	0.53
2:B:333:GLN:HG3	2:B:387:MET:CE	2.32	0.53
2:B:32:ARG:HG3	2:B:32:ARG:NH1	2.23	0.52
2:B:370:LEU:O	2:B:374:GLN:HG3	2.08	0.52
2:B:29:GLU:H	2:B:29:GLU:CD	2.17	0.52
1:A:366:LYS:HG3	1:A:367:HIS:CE1	2.44	0.52
1:A:156:ILE:CD1	1:A:172:ARG:HH12	2.23	0.52
1:A:354:GLU:HG2	2:B:328:TRP:O	2.10	0.52
1:A:223:VAL:HG11	1:A:240:ARG:HB2	1.92	0.52
2:B:86:LEU:HB2	2:B:107:ILE:HG21	1.91	0.51
1:A:191:ASP:O	1:A:194:ASN:HB2	2.11	0.51
1:A:266:MET:HA	1:A:266:MET:CE	2.34	0.51
2:B:68:VAL:HG22	4:B:1351:HOH:O	2.11	0.51
2:B:87:ARG:NH1	2:B:122:VAL:HG13	2.25	0.51
1:A:154:TYR:CZ	1:A:158:ILE:HD11	2.46	0.50
1:A:161:GLU:C	1:A:163:PRO:HD3	2.36	0.50
1:A:342:GLU:OE1	1:A:346:LYS:HG3	2.12	0.49
1:A:353:LYS:O	1:A:357:ARG:HG2	2.12	0.49
2:B:377:GLY:HA2	2:B:381:MET:O	2.12	0.49
1:A:289:LEU:CD1	1:A:317:ASP:HB3	2.42	0.49
2:B:202:ARG:HD2	4:B:1374:HOH:O	2.12	0.49
1:A:158:ILE:HG22	1:A:168:VAL:HG21	1.94	0.48
2:B:306:GLY:O	2:B:309:PRO:HD2	2.13	0.48
2:B:23:LEU:HB2	2:B:26:LEU:HD12	1.95	0.48
2:B:280:ARG:HH11	2:B:289:GLN:NE2	2.11	0.48
2:B:328:TRP:CZ2	2:B:376:PHE:HA	2.48	0.48
1:A:211:GLN:HG3	1:A:242:PHE:HZ	1.78	0.48
1:A:328:ASP:O	1:A:329:ASN:HB2	2.15	0.47
1:A:312:ILE:O	1:A:316:VAL:HG23	2.14	0.47
2:B:64:PHE:HD1	2:B:65:ASN:HB2	1.78	0.47
1:A:207:GLN:HE21	1:A:239:GLN:NE2	2.12	0.47
2:B:41:GLU:HG2	4:B:1189:HOH:O	2.15	0.47
2:B:74:GLN:N	2:B:344:GLN:HE22	2.08	0.47
1:A:189:ILE:HD11	1:A:205:HIS:CD2	2.48	0.47
1:A:346:LYS:HG3	1:A:357:ARG:HH21	1.78	0.47
2:B:282:MET:HG3	2:B:296:VAL:HB	1.96	0.47
1:A:355:TYR:O	1:A:358:TYR:HB3	2.15	0.46
2:B:177:LEU:HD21	2:B:210:VAL:HG13	1.97	0.46
2:B:75:ARG:HD3	4:B:1216:HOH:O	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:375:HIS:CE1	2:B:394:LEU:O	2.69	0.46
1:A:79:PRO:HA	1:A:101:ASP:OD1	2.16	0.46
1:A:65:LEU:HD13	1:A:67:ARG:CZ	2.45	0.45
2:B:151:ALA:HB3	2:B:152:PRO:CD	2.47	0.45
2:B:308:LEU:HD13	2:B:330:PHE:HB3	1.99	0.45
1:A:144:LEU:O	1:A:145:GLN:C	2.60	0.44
1:A:152:MET:O	1:A:156:ILE:HG12	2.17	0.44
1:A:187:GLU:HG3	4:A:1301:HOH:O	2.16	0.44
1:A:332:ASP:O	1:A:336:LYS:HG3	2.18	0.44
2:B:180:TYR:CZ	2:B:184:LEU:HD11	2.53	0.44
2:B:149:HIS:HB3	2:B:152:PRO:CG	2.47	0.44
1:A:342:GLU:OE1	1:A:342:GLU:HA	2.16	0.43
1:A:351:ILE:HG12	2:B:281:GLN:HG2	2.00	0.43
1:A:231:VAL:HG22	1:A:231:VAL:O	2.19	0.43
1:A:357:ARG:HA	1:A:357:ARG:HD3	1.85	0.43
1:A:77:PRO:HB3	1:A:102:TYR:CE1	2.53	0.43
1:A:224:ASP:OD1	1:A:240:ARG:NH2	2.51	0.43
1:A:251:SER:HA	1:A:287:ARG:HH12	1.84	0.43
1:A:77:PRO:HB2	1:A:101:ASP:HB3	2.00	0.43
2:B:280:ARG:HD3	2:B:280:ARG:HA	1.76	0.43
1:A:320:GLU:O	1:A:324:GLU:HG2	2.18	0.43
2:B:375:HIS:HE1	2:B:394:LEU:O	2.01	0.43
2:B:282:MET:HG2	2:B:287:GLY:O	2.19	0.42
1:A:136:PHE:CE2	1:A:140:LEU:HD11	2.54	0.42
1:A:264:LEU:O	1:A:268:LYS:HG3	2.19	0.42
1:A:300:LEU:O	1:A:303:GLN:HB2	2.20	0.42
2:B:149:HIS:HB3	2:B:152:PRO:HG2	2.02	0.42
2:B:22:PRO:HG2	2:B:27:ARG:HG2	2.02	0.41
1:A:87:VAL:O	1:A:88:VAL:C	2.63	0.41
1:A:198:LYS:HE2	1:A:233:ASN:HA	2.02	0.41
2:B:24:TYR:H	2:B:333:GLN:NE2	2.18	0.41
1:A:156:ILE:CD1	1:A:172:ARG:HH22	2.32	0.41
2:B:71:LEU:CD2	2:B:341:MET:HG3	2.49	0.41
2:B:287:GLY:C	4:B:1391:HOH:O	2.64	0.41
1:A:156:ILE:HD13	1:A:172:ARG:HH12	1.84	0.41
2:B:262:LEU:O	2:B:264:LYS:HG2	2.19	0.41
1:A:154:TYR:CE1	1:A:158:ILE:HD11	2.55	0.41
1:A:329:ASN:HB3	1:A:332:ASP:HB3	2.02	0.41
1:A:355:TYR:CE1	1:A:359:ILE:HD11	2.56	0.41
1:A:344:LEU:HD13	1:A:356:TRP:CZ2	2.55	0.40

There are no symmetry-related clashes.

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	313/377 (83%)	282 (90%)	30 (10%)	1 (0%)	36	40
2	B	414/437 (95%)	396 (96%)	15 (4%)	3 (1%)	18	17
All	All	727/814 (89%)	678 (93%)	45 (6%)	4 (1%)	21	21

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	304	PRO
2	B	432	SER
2	B	74	GLN
2	B	64	PHE

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	294/338 (87%)	279 (95%)	15 (5%)	21	23
2	B	351/371 (95%)	340 (97%)	11 (3%)	35	44
All	All	645/709 (91%)	619 (96%)	26 (4%)	28	34

All (26) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	62	THR
1	A	71	GLU

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Mol	Chain	Res	Type
1	A	106	VAL
1	A	109	ARG
1	A	125	GLU
1	A	158	ILE
1	A	168	VAL
1	A	177	GLU
1	A	226	LEU
1	A	239	GLN
1	A	266	MET
1	A	346	LYS
1	A	352	ARG
1	A	362	SER
1	A	369	ARG
2	B	29	GLU
2	B	65	ASN
2	B	66	HIS
2	B	67	LEU
2	B	87	ARG
2	B	88	GLN
2	B	101	PRO
2	B	122	VAL
2	B	265	GLU
2	B	277	VAL
2	B	393	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (17) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	135	HIS
1	A	149	GLN
1	A	234	ASN
1	A	239	GLN
1	A	246	ASN
1	A	294	ASN
1	A	306	HIS
1	A	367	HIS
2	B	80	HIS
2	B	134	GLN
2	B	275	GLN
2	B	289	GLN
2	B	332	GLN
2	B	333	GLN

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Mol	Chain	Res	Type
2	B	344	GLN
2	B	375	HIS
2	B	410	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 ⓘ

Of 1 ligands modelled in this entry, 1 is monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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	315/377 (83%)	-0.60	1 (0%) 90 90	20, 34, 51, 68	0
2	B	416/437 (95%)	-0.76	3 (0%) 84 85	13, 26, 45, 65	0
All	All	731/814 (89%)	-0.70	4 (0%) 87 88	13, 30, 48, 68	0

All (4) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	55	PHE	2.4
2	B	64	PHE	2.4
2	B	66	HIS	2.2
2	B	22	PRO	2.2

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](#)

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, 95th 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
3	ZN	B	1001	1/1	0.99	0.03	27,27,27,27	0

6.5 Other polymers [i](#)

There are no such residues in this entry.