



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 01:43 PM UTC

PDB ID : 1D01 / pdb_00001d01
Title : STRUCTURE OF TNF RECEPTOR ASSOCIATED FACTOR 2 IN COM-
PLEX WITH A HUMAN CD30 PEPTIDE
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Deposited on : 1999-09-07
Resolution : 2.00 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
Mogul	:	2022.3.0, CSD as543be (2022)
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

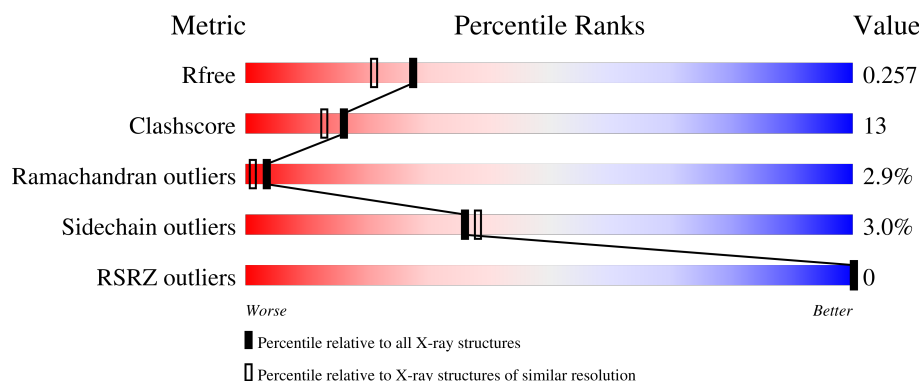
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.00 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	10052 (2.00-2.00)
Clashscore	190562	11152 (2.00-2.00)
Ramachandran outliers	187476	11031 (2.00-2.00)
Sidechain outliers	187428	11029 (2.00-2.00)
RSRZ outliers	180081	10067 (2.00-2.00)

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	168	 77% 18% 5%
1	B	168	 74% 21% 5%
1	C	168	 75% 21% 5%
1	D	168	 72% 24% 5%
1	E	168	 76% 19% 5%

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Mol	Chain	Length	Quality of chain
1	F	168	 73% 22% 5%
2	G	9	 78% 22%
2	H	9	 67% 33%
2	I	9	 67% 33%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 8705 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 TUMOR NECROSIS FACTOR RECEPTOR ASSOCIATED FACTOR 2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	168	Total	C	N	O	S	0	0	0
			1282	825	217	231	9			
1	B	168	Total	C	N	O	S	0	0	0
			1282	825	217	231	9			
1	C	168	Total	C	N	O	S	0	0	0
			1282	825	217	231	9			
1	D	168	Total	C	N	O	S	0	0	0
			1282	825	217	231	9			
1	E	168	Total	C	N	O	S	0	0	0
			1282	825	217	231	9			
1	F	168	Total	C	N	O	S	0	0	0
			1282	825	217	231	9			

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	365	ARG	LEU	conflict	UNP Q12933
B	365	ARG	LEU	conflict	UNP Q12933
C	365	ARG	LEU	conflict	UNP Q12933
D	365	ARG	LEU	conflict	UNP Q12933
E	365	ARG	LEU	conflict	UNP Q12933
F	365	ARG	LEU	conflict	UNP Q12933

- Molecule 2 is a protein called CD30 PEPTIDE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	G	9	Total	C	N	O	S	0	0	0
			62	38	8	15	1			
2	H	9	Total	C	N	O	S	0	0	0
			62	38	8	15	1			
2	I	9	Total	C	N	O	S	0	0	0
			62	38	8	15	1			

- Molecule 3 is water.

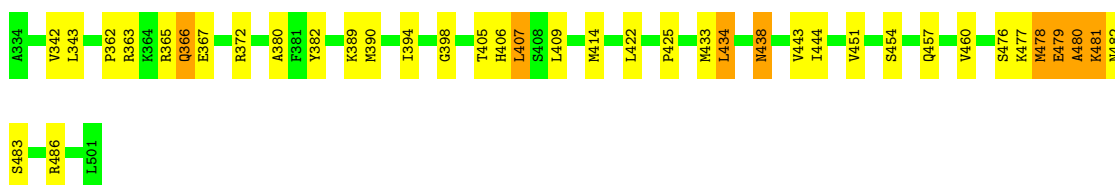
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	145	Total 145	O 145	0	0
3	B	143	Total 143	O 143	0	0
3	C	136	Total 136	O 136	0	0
3	D	116	Total 116	O 116	0	0
3	E	128	Total 128	O 128	0	0
3	F	125	Total 125	O 125	0	0
3	G	14	Total 14	O 14	0	0
3	H	9	Total 9	O 9	0	0
3	I	11	Total 11	O 11	0	0

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.

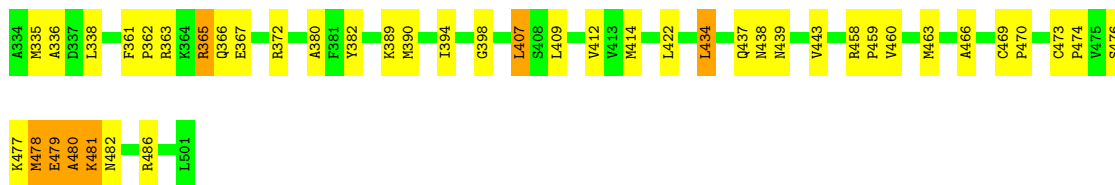
• Molecule 1: TUMOR NECROSIS FACTOR RECEPTOR ASSOCIATED FACTOR 2

Chain A: 



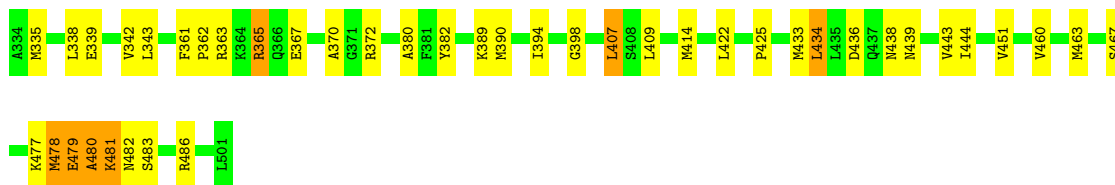
• Molecule 1: TUMOR NECROSIS FACTOR RECEPTOR ASSOCIATED FACTOR 2

Chain B: 



• Molecule 1: TUMOR NECROSIS FACTOR RECEPTOR ASSOCIATED FACTOR 2

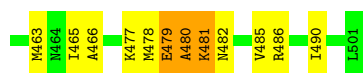
Chain C: 



• Molecule 1: TUMOR NECROSIS FACTOR RECEPTOR ASSOCIATED FACTOR 2

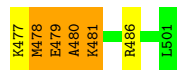
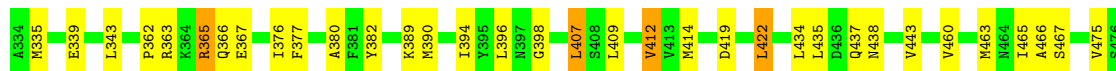
Chain D: 





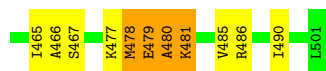
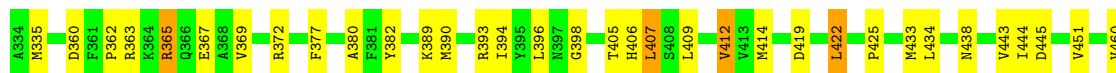
- Molecule 1: TUMOR NECROSIS FACTOR RECEPTOR ASSOCIATED FACTOR 2

Chain E: 76% 19% 5%



- Molecule 1: TUMOR NECROSIS FACTOR RECEPTOR ASSOCIATED FACTOR 2

Chain F: 73% 22% 5%



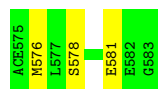
- Molecule 2: CD30 PEPTIDE

Chain G: 78% 22%



- Molecule 2: CD30 PEPTIDE

Chain H: 67% 33%



- Molecule 2: CD30 PEPTIDE

Chain I: 67% 33%



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	91.30Å 110.40Å 91.30Å 90.00° 120.00° 90.00°	Depositor
Resolution (Å)	20.00 – 2.00 20.00 – 2.00	Depositor EDS
% Data completeness (in resolution range)	(Not available) (20.00-2.00) 89.9 (20.00-2.00)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.35 (at 2.00Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.220 , 0.244 0.234 , 0.257	Depositor DCC
R_{free} test set	5709 reflections (6.00%)	wwPDB-VP
Wilson B-factor (Å ²)	18.7	Xtriage
Anisotropy	0.196	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 43.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.468 for -h-l,k,h 0.468 for l,k,-h-l 0.081 for h,-k,-h-l 0.079 for -h-l,-k,l 0.079 for l,-k,h	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	8705	wwPDB-VP
Average B, all atoms (Å ²)	22.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.25% 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: ACE

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	0.42	0/1312	1.03	6/1781 (0.3%)
1	B	0.42	0/1312	1.04	8/1781 (0.4%)
1	C	0.42	0/1312	1.04	7/1781 (0.4%)
1	D	0.42	1/1312 (0.1%)	1.03	9/1781 (0.5%)
1	E	0.43	0/1312	1.04	8/1781 (0.4%)
1	F	0.41	0/1312	1.03	7/1781 (0.4%)
2	G	1.03	1/59 (1.7%)	0.86	0/78
2	H	1.33	1/59 (1.7%)	0.94	0/78
2	I	1.10	1/59 (1.7%)	0.89	0/78
All	All	0.45	4/8049 (0.0%)	1.03	45/10920 (0.4%)

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	H	576	MET	SD-CE	-9.29	1.56	1.79
2	I	576	MET	SD-CE	-7.29	1.61	1.79
2	G	576	MET	SD-CE	-6.58	1.63	1.79
1	D	414	MET	SD-CE	-5.30	1.66	1.79

All (45) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
1	A	460	VAL	N-CA-C	-9.12	104.51	111.90
1	E	398	GLY	N-CA-C	8.76	122.10	112.29
1	E	335	MET	N-CA-C	-8.76	101.19	112.23
1	B	460	VAL	N-CA-C	-8.27	105.20	111.90
1	B	438	ASN	N-CA-C	-8.23	102.27	113.30
1	A	438	ASN	N-CA-C	-8.16	102.88	113.17
1	C	438	ASN	N-CA-C	-8.14	102.39	113.30
1	F	438	ASN	N-CA-C	-7.96	103.59	113.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	F	398	GLY	N-CA-C	7.87	122.73	112.18
1	D	460	VAL	N-CA-C	-7.87	104.79	111.56
1	E	438	ASN	N-CA-C	-7.82	103.76	113.38
1	F	460	VAL	N-CA-C	-7.70	104.94	111.56
1	C	460	VAL	N-CA-C	-7.50	105.36	111.81
1	D	438	ASN	N-CA-C	-7.45	104.22	113.38
1	D	398	GLY	N-CA-C	7.35	121.94	112.68
1	D	335	MET	N-CA-C	-7.09	102.97	111.69
1	E	460	VAL	N-CA-C	-7.06	105.49	111.56
1	C	362	PRO	N-CA-CB	6.48	110.17	103.23
1	B	336	ALA	N-CA-C	-6.47	104.87	112.89
1	B	398	GLY	N-CA-C	6.41	120.98	112.65
1	A	398	GLY	N-CA-C	6.36	120.92	112.65
1	D	362	PRO	N-CA-CB	6.35	110.07	103.15
1	A	362	PRO	N-CA-CB	6.34	110.01	103.23
1	E	362	PRO	N-CA-CB	6.29	110.00	103.15
1	C	398	GLY	N-CA-C	6.26	120.79	112.65
1	F	407	LEU	N-CA-C	-6.22	99.06	108.96
1	B	362	PRO	N-CA-CB	6.21	110.16	103.33
1	F	362	PRO	N-CA-CB	6.19	109.89	103.15
1	A	407	LEU	N-CA-C	-6.04	99.44	109.46
1	D	407	LEU	N-CA-C	-6.02	99.38	108.96
1	B	407	LEU	N-CA-C	-5.99	99.52	109.46
1	C	407	LEU	N-CA-C	-5.90	99.58	108.96
1	C	434	LEU	N-CA-C	-5.86	97.77	108.02
1	E	407	LEU	N-CA-C	-5.85	99.66	108.96
1	B	335	MET	N-CA-C	-5.80	105.87	113.12
1	A	434	LEU	N-CA-C	-5.59	98.24	108.02
1	E	412	VAL	N-CA-C	5.42	115.93	108.12
1	B	434	LEU	N-CA-C	-5.42	98.53	108.02
1	D	465	ILE	N-CA-C	-5.38	101.27	109.78
1	E	435	LEU	N-CA-C	5.38	118.03	109.96
1	D	412	VAL	N-CA-C	5.20	115.60	108.12
1	D	435	LEU	N-CA-C	5.17	117.72	109.96
1	C	335	MET	N-CA-C	-5.12	106.55	112.89
1	F	412	VAL	N-CA-C	5.01	115.34	108.12
1	F	335	MET	N-CA-C	-5.00	105.53	111.69

There are no chirality outliers.

There are no planarity outliers.

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	1282	0	1238	32	0
1	B	1282	0	1238	31	0
1	C	1282	0	1238	36	0
1	D	1282	0	1238	36	0
1	E	1282	0	1238	34	0
1	F	1282	0	1238	37	0
2	G	62	0	58	2	0
2	H	62	0	58	2	0
2	I	62	0	58	3	0
3	A	145	0	0	5	0
3	B	143	0	0	4	0
3	C	136	0	0	6	0
3	D	116	0	0	2	0
3	E	128	0	0	4	0
3	F	125	0	0	4	0
3	G	14	0	0	0	0
3	H	9	0	0	0	0
3	I	11	0	0	0	0
All	All	8705	0	7602	203	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 13.

All (203) 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:E:389:LYS:HG2	1:E:414:MET:HE3	1.29	1.08
1:A:389:LYS:HG2	1:A:414:MET:HE3	1.34	1.07
1:D:389:LYS:HG2	1:D:414:MET:HE3	1.33	1.07
1:F:389:LYS:HG2	1:F:414:MET:HE3	1.31	1.06
1:C:389:LYS:HG2	1:C:414:MET:HE3	1.36	1.06
1:B:389:LYS:HG2	1:B:414:MET:HE3	1.33	1.05
1:F:425:PRO:HG3	1:F:451:VAL:HG13	1.51	0.91
1:E:389:LYS:HG2	1:E:414:MET:CE	2.04	0.88
1:D:380:ALA:CB	1:D:414:MET:HE1	2.06	0.86

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:380:ALA:CB	1:A:414:MET:HE1	2.07	0.84
1:C:425:PRO:HG3	1:C:451:VAL:HG13	1.59	0.84
1:A:425:PRO:HG3	1:A:451:VAL:HG13	1.58	0.84
1:F:380:ALA:CB	1:F:414:MET:HE1	2.07	0.83
1:F:389:LYS:HG2	1:F:414:MET:CE	2.08	0.83
1:D:389:LYS:HG2	1:D:414:MET:CE	2.09	0.81
1:D:380:ALA:HB1	1:D:414:MET:HE1	1.63	0.80
1:B:380:ALA:CB	1:B:414:MET:HE1	2.11	0.80
1:C:380:ALA:CB	1:C:414:MET:HE1	2.12	0.80
1:E:380:ALA:CB	1:E:414:MET:HE1	2.11	0.80
1:E:380:ALA:HB1	1:E:414:MET:HE1	1.64	0.79
1:E:394:ILE:HD11	1:E:407:LEU:HD11	1.63	0.79
1:D:394:ILE:HD11	1:D:407:LEU:HD11	1.64	0.79
1:A:394:ILE:HD11	1:A:407:LEU:HD11	1.66	0.78
1:F:380:ALA:HB1	1:F:414:MET:HE1	1.64	0.77
1:A:380:ALA:HB2	1:A:414:MET:HE1	1.66	0.75
1:B:394:ILE:HD11	1:B:407:LEU:HD11	1.69	0.74
1:B:380:ALA:HB2	1:B:414:MET:HE1	1.69	0.73
1:C:380:ALA:HB2	1:C:414:MET:HE1	1.69	0.71
1:F:465:ILE:HG13	3:F:9235:HOH:O	1.90	0.71
1:A:389:LYS:HG2	1:A:414:MET:CE	2.19	0.70
1:F:393:ARG:NH1	2:I:581:GLU:OE1	2.25	0.70
1:C:390:MET:C	1:C:414:MET:HE2	2.16	0.70
1:C:394:ILE:HD11	1:C:407:LEU:HD11	1.74	0.70
1:A:363:ARG:O	1:A:367:GLU:HG3	1.92	0.70
1:F:394:ILE:HD11	1:F:407:LEU:HD11	1.74	0.70
1:B:363:ARG:O	1:B:367:GLU:HG3	1.92	0.69
1:D:393:ARG:NH1	2:G:581:GLU:OE1	2.24	0.69
1:B:389:LYS:HG2	1:B:414:MET:CE	2.18	0.68
1:A:390:MET:C	1:A:414:MET:HE2	2.19	0.68
1:D:425:PRO:HG3	1:D:451:VAL:HG13	1.75	0.68
1:E:465:ILE:HG13	3:E:9329:HOH:O	1.94	0.67
1:B:478:MET:SD	1:B:479:GLU:N	2.67	0.67
1:B:390:MET:C	1:B:414:MET:HE2	2.19	0.67
1:C:370:ALA:HB1	1:D:377:PHE:CZ	2.30	0.66
1:C:389:LYS:HG2	1:C:414:MET:CE	2.20	0.66
1:C:467:SER:HB3	3:C:9242:HOH:O	1.95	0.66
1:D:451:VAL:HG21	3:D:9815:HOH:O	1.96	0.66
1:F:444:ILE:HG23	3:F:9680:HOH:O	1.95	0.65
1:D:380:ALA:HB2	1:D:414:MET:HE1	1.79	0.64
1:C:363:ARG:O	1:C:367:GLU:HG3	1.97	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:339:GLU:O	1:E:343:LEU:HD13	1.96	0.64
1:C:439:ASN:C	1:C:439:ASN:HD22	2.02	0.64
1:E:390:MET:C	1:E:414:MET:HE2	2.23	0.63
1:C:478:MET:SD	1:C:479:GLU:N	2.72	0.62
1:F:467:SER:OG	2:I:578:SER:HB2	1.99	0.62
1:A:380:ALA:HB1	1:A:414:MET:HE1	1.79	0.62
1:B:482:ASN:HB3	3:B:9190:HOH:O	1.99	0.62
1:A:434:LEU:HB3	1:A:443:VAL:HB	1.81	0.61
1:D:390:MET:C	1:D:414:MET:HE2	2.26	0.61
1:F:380:ALA:HB2	1:F:414:MET:HE1	1.81	0.61
1:A:480:ALA:O	1:A:481:LYS:CB	2.49	0.61
1:B:478:MET:O	1:B:480:ALA:N	2.34	0.61
1:A:479:GLU:C	1:A:481:LYS:H	2.09	0.60
1:E:467:SER:OG	2:H:578:SER:HB2	2.01	0.60
1:E:478:MET:SD	1:E:479:GLU:N	2.74	0.60
1:C:434:LEU:HB3	1:C:443:VAL:HB	1.82	0.60
1:D:482:ASN:HB3	3:D:9647:HOH:O	2.01	0.60
3:C:9057:HOH:O	1:D:377:PHE:HE1	1.85	0.60
1:B:380:ALA:HB1	1:B:414:MET:HE1	1.84	0.59
1:B:434:LEU:HB3	1:B:443:VAL:HB	1.84	0.59
1:A:482:ASN:HB3	3:A:9404:HOH:O	2.02	0.59
1:C:478:MET:O	1:C:480:ALA:N	2.36	0.59
1:F:389:LYS:CG	1:F:414:MET:HE3	2.21	0.59
1:F:433:MET:HE2	1:F:444:ILE:HD12	1.84	0.59
1:A:478:MET:SD	1:A:479:GLU:N	2.76	0.58
1:F:363:ARG:O	1:F:367:GLU:HG3	2.03	0.58
1:F:390:MET:C	1:F:414:MET:HE2	2.28	0.58
1:D:389:LYS:CG	1:D:414:MET:HE3	2.22	0.58
1:C:380:ALA:HB1	1:C:414:MET:HE1	1.85	0.57
1:B:479:GLU:C	1:B:481:LYS:H	2.12	0.57
1:E:389:LYS:CG	1:E:414:MET:HE3	2.19	0.57
1:D:363:ARG:O	1:D:367:GLU:HG3	2.04	0.57
1:D:434:LEU:HB3	1:D:443:VAL:HB	1.87	0.56
1:F:377:PHE:HE1	3:F:9101:HOH:O	1.88	0.56
1:D:478:MET:SD	1:D:479:GLU:N	2.79	0.56
1:E:380:ALA:HB2	1:E:414:MET:HE1	1.88	0.56
1:F:478:MET:SD	1:F:479:GLU:N	2.78	0.56
1:A:479:GLU:O	1:A:481:LYS:N	2.39	0.55
1:A:478:MET:O	1:A:480:ALA:N	2.38	0.55
1:D:412:VAL:HG22	1:D:466:ALA:HB2	1.88	0.55
1:B:389:LYS:CG	1:B:414:MET:HE3	2.24	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:480:ALA:O	1:B:481:LYS:CB	2.55	0.54
1:E:363:ARG:O	1:E:367:GLU:HG3	2.07	0.54
1:F:486:ARG:HG3	1:F:486:ARG:HH11	1.73	0.54
1:D:480:ALA:O	1:D:481:LYS:CB	2.57	0.53
1:E:377:PHE:HE1	3:E:9043:HOH:O	1.89	0.53
1:F:434:LEU:HB3	1:F:443:VAL:HB	1.90	0.53
1:C:372:ARG:NH2	3:C:9537:HOH:O	2.41	0.53
1:F:412:VAL:HG22	1:F:466:ALA:HB2	1.90	0.53
1:A:451:VAL:HG12	1:A:451:VAL:O	2.07	0.53
1:C:439:ASN:C	1:C:439:ASN:ND2	2.67	0.52
1:C:479:GLU:O	1:C:481:LYS:N	2.35	0.52
1:E:377:PHE:HB2	3:E:9502:HOH:O	2.09	0.52
1:C:479:GLU:C	1:C:481:LYS:H	2.18	0.52
1:E:480:ALA:O	1:E:481:LYS:CB	2.57	0.52
1:B:412:VAL:HG22	1:B:466:ALA:HB2	1.92	0.52
1:E:419:ASP:HA	1:E:422:LEU:CD2	2.40	0.51
1:C:480:ALA:O	1:C:481:LYS:CB	2.57	0.51
1:F:480:ALA:O	1:F:481:LYS:CB	2.58	0.51
1:F:405:THR:OG1	1:F:406:HIS:HD2	1.92	0.51
1:C:451:VAL:O	1:C:451:VAL:HG12	2.09	0.51
1:E:479:GLU:O	1:E:481:LYS:N	2.44	0.51
1:C:339:GLU:O	1:C:343:LEU:HD23	2.10	0.51
1:F:372:ARG:NE	3:F:9505:HOH:O	2.44	0.50
1:E:414:MET:HG2	1:E:463:MET:HG2	1.94	0.50
1:C:482:ASN:HB3	3:C:9512:HOH:O	2.10	0.50
1:A:476:SER:O	1:A:480:ALA:HB3	2.12	0.50
1:E:376:ILE:HD11	3:E:9497:HOH:O	2.11	0.49
1:E:412:VAL:HG22	1:E:466:ALA:HB2	1.95	0.49
1:E:478:MET:O	1:E:480:ALA:N	2.45	0.49
1:B:479:GLU:O	1:B:481:LYS:N	2.38	0.49
1:E:434:LEU:HB3	1:E:443:VAL:HB	1.94	0.49
1:F:466:ALA:HB3	2:I:581:GLU:OE2	2.13	0.49
1:A:389:LYS:CG	1:A:414:MET:HE3	2.24	0.48
1:A:342:VAL:HG21	1:C:338:LEU:HD11	1.96	0.48
1:F:479:GLU:O	1:F:481:LYS:N	2.47	0.48
1:C:433:MET:HE2	1:C:444:ILE:HD12	1.95	0.47
1:D:341:LYS:O	1:D:345:MET:HG3	2.14	0.47
1:D:425:PRO:HG3	1:D:451:VAL:CG1	2.42	0.47
1:A:433:MET:HE2	1:A:444:ILE:HD12	1.96	0.47
1:E:394:ILE:CD1	1:E:407:LEU:HD11	2.40	0.47
1:B:437:GLN:CD	1:B:486:ARG:HB3	2.39	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:486:ARG:HH11	1:D:486:ARG:HG3	1.79	0.47
1:C:451:VAL:O	1:C:451:VAL:CG1	2.62	0.47
1:D:433:MET:HE2	1:D:444:ILE:HD12	1.97	0.47
1:F:377:PHE:CZ	1:F:393:ARG:NE	2.77	0.47
1:A:372:ARG:NH2	3:A:9425:HOH:O	2.46	0.47
1:D:478:MET:O	1:D:480:ALA:N	2.47	0.47
1:E:419:ASP:HA	1:E:422:LEU:HD22	1.97	0.47
1:C:439:ASN:ND2	1:C:439:ASN:O	2.48	0.47
1:D:419:ASP:HA	1:D:422:LEU:CD2	2.45	0.46
1:A:372:ARG:CG	3:A:9271:HOH:O	2.63	0.46
1:F:396:LEU:HA	1:F:407:LEU:HD12	1.97	0.46
1:A:366:GLN:HB3	3:A:9425:HOH:O	2.16	0.46
1:A:372:ARG:HD3	3:A:9271:HOH:O	2.14	0.46
1:B:372:ARG:CG	3:B:9266:HOH:O	2.63	0.46
1:A:486:ARG:HD2	3:C:9470:HOH:O	2.15	0.46
1:D:339:GLU:O	1:D:343:LEU:HD13	2.16	0.46
1:C:370:ALA:HB3	1:C:372:ARG:HD3	1.99	0.45
1:C:361:PHE:O	1:C:365:ARG:HB2	2.17	0.45
1:C:382:TYR:CD1	1:C:382:TYR:N	2.85	0.45
1:B:482:ASN:N	3:B:9643:HOH:O	2.49	0.45
1:F:479:GLU:C	1:F:481:LYS:H	2.25	0.45
1:A:454:SER:HA	1:A:457:GLN:HG2	1.99	0.44
1:B:361:PHE:O	1:B:365:ARG:HB2	2.18	0.44
1:D:414:MET:HG2	1:D:463:MET:HG2	1.99	0.44
1:C:486:ARG:HH11	1:C:486:ARG:HG3	1.82	0.44
1:F:396:LEU:HA	1:F:407:LEU:CD1	2.47	0.44
1:E:390:MET:CA	1:E:414:MET:HE2	2.48	0.44
1:F:485:VAL:HG22	1:F:490:ILE:CG2	2.48	0.44
1:A:451:VAL:O	1:A:451:VAL:CG1	2.65	0.44
1:B:382:TYR:CD1	1:B:382:TYR:N	2.85	0.44
1:F:451:VAL:HG12	1:F:451:VAL:O	2.17	0.44
1:E:479:GLU:C	1:E:481:LYS:H	2.26	0.43
1:B:394:ILE:CD1	1:B:407:LEU:HD11	2.42	0.43
1:A:486:ARG:HH11	1:A:486:ARG:HG3	1.83	0.43
1:B:414:MET:HG2	1:B:463:MET:HG2	2.00	0.43
1:F:419:ASP:HA	1:F:422:LEU:HD22	2.01	0.43
1:A:438:ASN:HB2	1:A:483:SER:HB2	2.00	0.43
1:B:476:SER:O	1:B:480:ALA:HB3	2.19	0.43
1:D:479:GLU:C	1:D:481:LYS:H	2.26	0.43
1:F:365:ARG:O	1:F:369:VAL:HG23	2.18	0.43
1:E:437:GLN:CD	1:E:486:ARG:HB3	2.43	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:478:MET:O	1:F:480:ALA:N	2.52	0.42
1:D:466:ALA:HB3	2:G:581:GLU:OE2	2.18	0.42
1:D:382:TYR:CD1	1:D:382:TYR:N	2.87	0.42
1:E:382:TYR:CD1	1:E:382:TYR:N	2.88	0.42
1:B:338:LEU:HD11	1:C:342:VAL:HG21	2.01	0.42
1:C:370:ALA:CB	1:C:372:ARG:HD3	2.49	0.42
1:B:458:ARG:HA	1:B:459:PRO:HD3	1.92	0.42
1:B:473:CYS:HA	1:B:474:PRO:HD3	1.95	0.42
1:B:474:PRO:HD3	3:B:9458:HOH:O	2.20	0.42
1:B:469:CYS:HA	1:B:470:PRO:HD2	1.96	0.41
1:C:414:MET:HG2	1:C:463:MET:HG2	2.01	0.41
1:D:394:ILE:CD1	1:D:407:LEU:HD11	2.41	0.41
1:D:405:THR:OG1	1:D:406:HIS:HD2	2.03	0.41
1:E:479:GLU:C	1:E:481:LYS:N	2.78	0.41
1:B:439:ASN:O	1:B:439:ASN:CG	2.63	0.41
1:D:419:ASP:HA	1:D:422:LEU:HD22	2.02	0.41
1:E:365:ARG:NH2	1:E:475:VAL:HG11	2.36	0.41
1:D:478:MET:SD	1:D:479:GLU:CB	3.08	0.41
1:E:466:ALA:HB3	2:H:581:GLU:OE2	2.20	0.41
1:F:382:TYR:CD1	1:F:382:TYR:N	2.88	0.41
1:A:382:TYR:CD1	1:A:382:TYR:N	2.88	0.41
1:A:405:THR:C	1:A:406:HIS:HD2	2.29	0.41
1:E:437:GLN:NE2	1:E:486:ARG:HB3	2.35	0.41
1:C:414:MET:SD	3:C:9350:HOH:O	2.63	0.41
1:D:485:VAL:HG22	1:D:490:ILE:CG2	2.50	0.41
1:C:436:ASP:OD1	1:C:483:SER:HB2	2.22	0.40
1:E:396:LEU:HA	1:E:407:LEU:CD1	2.51	0.40
1:F:377:PHE:CE1	1:F:393:ARG:NE	2.80	0.40
1:D:479:GLU:C	1:D:481:LYS:N	2.80	0.40
1:F:444:ILE:HG12	1:F:445:ASP:N	2.35	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	166/168 (99%)	154 (93%)	7 (4%)	5 (3%)	3	1
1	B	166/168 (99%)	155 (93%)	6 (4%)	5 (3%)	3	1
1	C	166/168 (99%)	155 (93%)	6 (4%)	5 (3%)	3	1
1	D	166/168 (99%)	156 (94%)	6 (4%)	4 (2%)	4	2
1	E	166/168 (99%)	158 (95%)	3 (2%)	5 (3%)	3	1
1	F	166/168 (99%)	157 (95%)	4 (2%)	5 (3%)	3	1
2	G	7/9 (78%)	7 (100%)	0	0	100	100
2	H	7/9 (78%)	7 (100%)	0	0	100	100
2	I	7/9 (78%)	7 (100%)	0	0	100	100
All	All	1017/1035 (98%)	956 (94%)	32 (3%)	29 (3%)	3	1

All (29) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	479	GLU
1	A	480	ALA
1	A	481	LYS
1	B	479	GLU
1	B	480	ALA
1	B	481	LYS
1	C	477	LYS
1	C	479	GLU
1	C	480	ALA
1	C	481	LYS
1	D	477	LYS
1	D	481	LYS
1	E	477	LYS
1	E	481	LYS
1	F	477	LYS
1	F	481	LYS
1	A	477	LYS
1	B	477	LYS
1	E	479	GLU
1	E	480	ALA
1	F	479	GLU
1	F	480	ALA
1	B	478	MET

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Mol	Chain	Res	Type
1	C	478	MET
1	D	479	GLU
1	D	480	ALA
1	E	478	MET
1	A	478	MET
1	F	478	MET

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	132/145 (91%)	127 (96%)	5 (4%)	29	29
1	B	132/145 (91%)	128 (97%)	4 (3%)	36	38
1	C	132/145 (91%)	129 (98%)	3 (2%)	44	49
1	D	132/145 (91%)	128 (97%)	4 (3%)	36	38
1	E	132/145 (91%)	128 (97%)	4 (3%)	36	38
1	F	132/145 (91%)	128 (97%)	4 (3%)	36	38
2	G	7/7 (100%)	7 (100%)	0	100	100
2	H	7/7 (100%)	7 (100%)	0	100	100
2	I	7/7 (100%)	7 (100%)	0	100	100
All	All	813/891 (91%)	789 (97%)	24 (3%)	36	38

All (24) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	343	LEU
1	A	365	ARG
1	A	366	GLN
1	A	409	LEU
1	A	422	LEU
1	B	365	ARG
1	B	366	GLN
1	B	409	LEU

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Mol	Chain	Res	Type
1	B	422	LEU
1	C	365	ARG
1	C	409	LEU
1	C	422	LEU
1	D	365	ARG
1	D	366	GLN
1	D	409	LEU
1	D	422	LEU
1	E	365	ARG
1	E	366	GLN
1	E	409	LEU
1	E	422	LEU
1	F	360	ASP
1	F	365	ARG
1	F	409	LEU
1	F	422	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (33) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	366	GLN
1	A	406	HIS
1	A	427	ASN
1	A	439	ASN
1	A	461	ASN
1	B	366	GLN
1	B	406	HIS
1	B	427	ASN
1	B	428	GLN
1	B	439	ASN
1	B	461	ASN
1	C	366	GLN
1	C	406	HIS
1	C	427	ASN
1	C	428	GLN
1	C	439	ASN
1	C	461	ASN
1	D	366	GLN
1	D	406	HIS
1	D	427	ASN
1	D	428	GLN
1	D	439	ASN

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Mol	Chain	Res	Type
1	D	461	ASN
1	E	406	HIS
1	E	427	ASN
1	E	428	GLN
1	E	439	ASN
1	E	461	ASN
1	F	366	GLN
1	F	406	HIS
1	F	427	ASN
1	F	439	ASN
1	F	461	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides 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 [i](#)

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	168/168 (100%)	-1.14	0 100 100	12, 20, 44, 51	0
1	B	168/168 (100%)	-1.12	0 100 100	11, 20, 42, 51	0
1	C	168/168 (100%)	-1.14	0 100 100	12, 20, 42, 52	0
1	D	168/168 (100%)	-1.12	0 100 100	12, 21, 37, 51	0
1	E	168/168 (100%)	-1.12	0 100 100	12, 20, 38, 51	0
1	F	168/168 (100%)	-1.13	0 100 100	12, 21, 37, 52	0
2	G	8/9 (88%)	-1.26	0 100 100	16, 18, 25, 30	0
2	H	8/9 (88%)	-1.12	0 100 100	15, 18, 25, 29	0
2	I	8/9 (88%)	-1.26	0 100 100	16, 18, 26, 30	0
All	All	1032/1035 (99%)	-1.13	0 100 100	11, 20, 42, 52	0

There are no RSRZ outliers to report.

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.