



Full wwPDB X-ray Structure Validation Report ⓘ

Jan 31, 2016 – 09:59 PM GMT

PDB ID : 1RJ8
Title : The crystal structure of TNF family member EDA-A2
Authors : Hymowitz, S.G.; Compaaan, D.M.; Yan, M.; Ackerly, H.; Dixit, V.M.; Starovasnik, M.A.; de Vos, A.M.
Deposited on : 2003-11-18
Resolution : 2.23 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
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467
Mogul : 1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026688
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

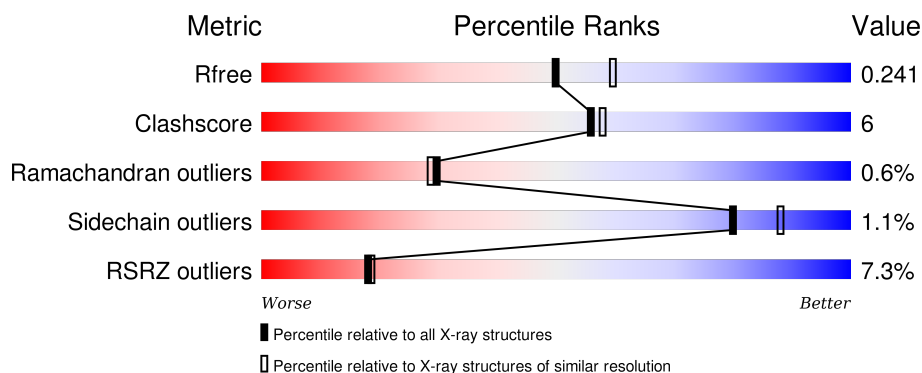
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.23 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}	91344	1611 (2.26-2.22)
Clashscore	102246	1764 (2.26-2.22)
Ramachandran outliers	100387	1724 (2.26-2.22)
Sidechain outliers	100360	1724 (2.26-2.22)
RSRZ outliers	91569	1616 (2.26-2.22)

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 on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. 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	164	<div> <div>3%</div> <div>73% 10% 15%</div> </div>
1	B	164	<div> <div>7%</div> <div>79% 6% 15%</div> </div>
1	D	164	<div> <div>5%</div> <div>73% 11% 15%</div> </div>
1	E	164	<div> <div>7%</div> <div>79% 7% 15%</div> </div>
1	F	164	<div> <div>10%</div> <div>66% 16% 15%</div> </div>

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Mol	Chain	Length	Quality of chain
1	G	164	 A horizontal bar chart showing the quality of chain G. The bar is divided into four segments: a small red segment at the beginning labeled '5%', a large green segment labeled '75%', a small yellow segment labeled '10%', and a small grey segment at the end labeled '15%'.

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 6776 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 ectodysplasin-A isoform EDA-A2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	140	Total	C	N	O	S	0	0	0
			1099	704	186	203	6			
1	B	140	Total	C	N	O	S	0	0	0
			1099	704	186	203	6			
1	D	140	Total	C	N	O	S	0	0	0
			1099	704	186	203	6			
1	E	140	Total	C	N	O	S	0	0	0
			1099	704	186	203	6			
1	F	140	Total	C	N	O	S	0	0	0
			1099	704	186	203	6			
1	G	140	Total	C	N	O	S	0	0	0
			1099	704	186	203	6			

There are 24 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	226	GLY	-	CLONING ARTIFACT	UNP Q92838
A	227	SER	-	CLONING ARTIFACT	UNP Q92838
A	228	HIS	-	CLONING ARTIFACT	UNP Q92838
A	229	MET	-	CLONING ARTIFACT	UNP Q92838
B	226	GLY	-	CLONING ARTIFACT	UNP Q92838
B	227	SER	-	CLONING ARTIFACT	UNP Q92838
B	228	HIS	-	CLONING ARTIFACT	UNP Q92838
B	229	MET	-	CLONING ARTIFACT	UNP Q92838
D	226	GLY	-	CLONING ARTIFACT	UNP Q92838
D	227	SER	-	CLONING ARTIFACT	UNP Q92838
D	228	HIS	-	CLONING ARTIFACT	UNP Q92838
D	229	MET	-	CLONING ARTIFACT	UNP Q92838
E	226	GLY	-	CLONING ARTIFACT	UNP Q92838
E	227	SER	-	CLONING ARTIFACT	UNP Q92838
E	228	HIS	-	CLONING ARTIFACT	UNP Q92838
E	229	MET	-	CLONING ARTIFACT	UNP Q92838
F	226	GLY	-	CLONING ARTIFACT	UNP Q92838

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Chain	Residue	Modelled	Actual	Comment	Reference
F	227	SER	-	CLONING ARTIFACT	UNP Q92838
F	228	HIS	-	CLONING ARTIFACT	UNP Q92838
F	229	MET	-	CLONING ARTIFACT	UNP Q92838
G	226	GLY	-	CLONING ARTIFACT	UNP Q92838
G	227	SER	-	CLONING ARTIFACT	UNP Q92838
G	228	HIS	-	CLONING ARTIFACT	UNP Q92838
G	229	MET	-	CLONING ARTIFACT	UNP Q92838

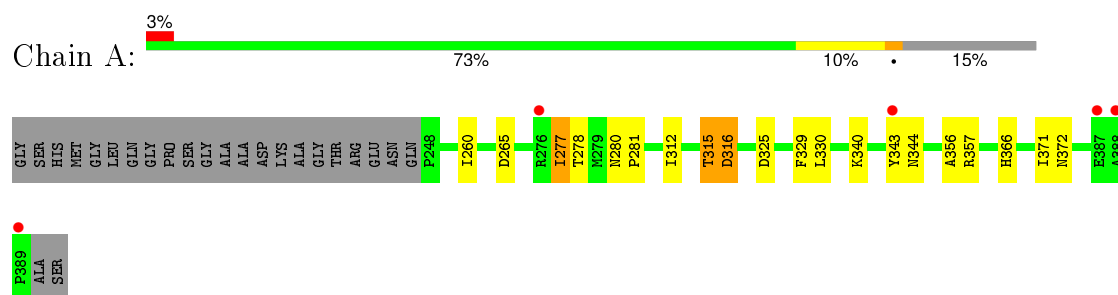
- Molecule 2 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	51	Total O 51 51	0	0
2	B	34	Total O 34 34	0	0
2	D	32	Total O 32 32	0	0
2	E	30	Total O 30 30	0	0
2	F	10	Total O 10 10	0	0
2	G	25	Total O 25 25	0	0

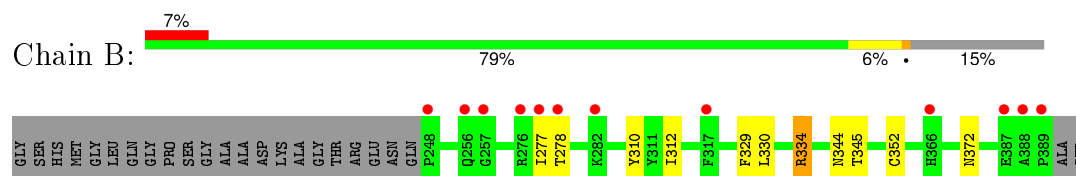
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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.

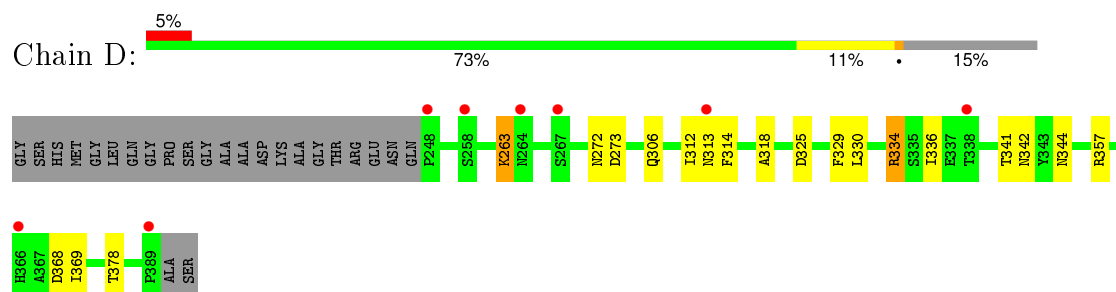
- Molecule 1: ectodysplasins-A isoform EDA-A2



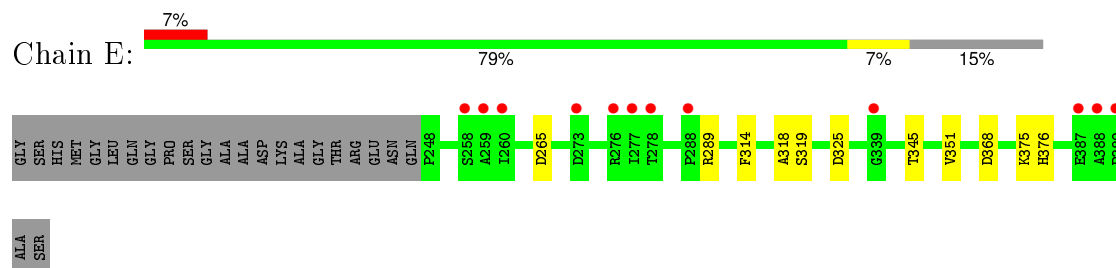
- Molecule 1: ectodysplasins-A isoform EDA-A2



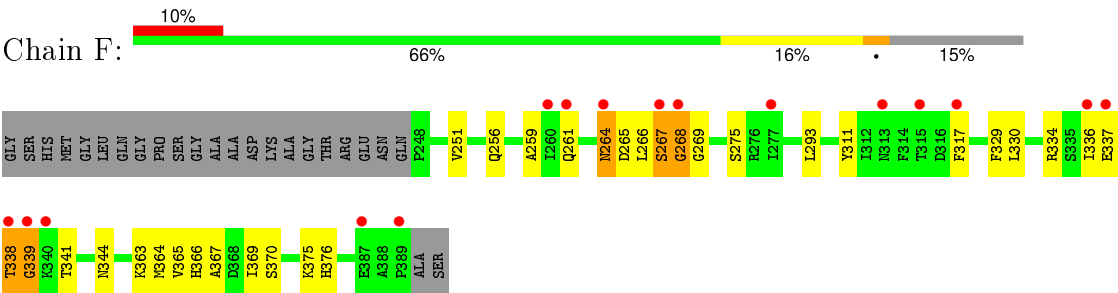
- Molecule 1: ectodysplasins-A isoform EDA-A2



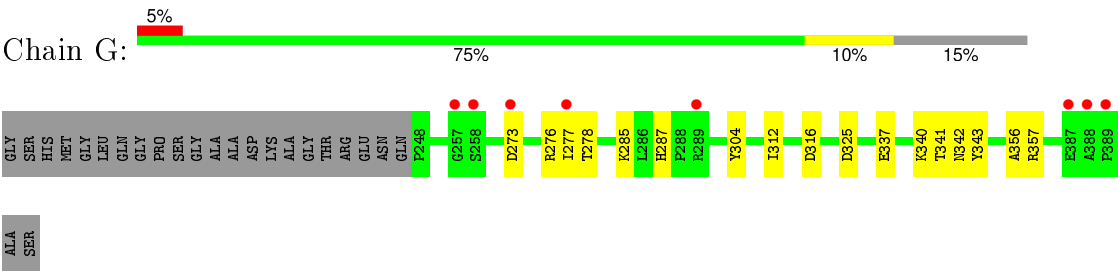
- Molecule 1: ectodysplasins-A isoform EDA-A2



● Molecule 1: ectodysplasins-A isoform EDA-A2



● Molecule 1: ectodysplasins-A isoform EDA-A2



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	50.72Å 161.34Å 51.02Å 90.00° 105.24° 90.00°	Depositor
Resolution (Å)	30.00 – 2.23 19.98 – 2.23	Depositor EDS
% Data completeness (in resolution range)	97.2 (30.00-2.23) 97.4 (19.98-2.23)	Depositor EDS
R_{merge}	0.03	Depositor
R_{sym}	0.04	Depositor
$\langle I/\sigma(I) \rangle$ ¹	10.36 (at 2.23Å)	Xtriage
Refinement program	REFMAC 5.1.07	Depositor
R, R_{free}	0.200 , 0.241 0.202 , 0.241	Depositor DCC
R_{free} test set	3700 reflections (11.04%)	DCC
Wilson B-factor (Å ²)	19.5	Xtriage
Anisotropy	0.284	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 39.2	EDS
Estimated twinning fraction	0.037 for l,-k,h	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.30$	Xtriage
Outliers	0 of 37223 reflections	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	6776	wwPDB-VP
Average B, all atoms (Å ²)	7.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.68% 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, 0.375 respectively for untwinned datasets, and 0.333, 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	0.37	0/1123	0.69	2/1521 (0.1%)
1	B	0.36	0/1123	0.70	2/1521 (0.1%)
1	D	0.37	0/1123	0.73	4/1521 (0.3%)
1	E	0.36	0/1123	0.67	2/1521 (0.1%)
1	F	0.36	0/1123	0.73	1/1521 (0.1%)
1	G	0.33	0/1123	0.67	3/1521 (0.2%)
All	All	0.36	0/6738	0.70	14/9126 (0.2%)

There are no bond length outliers.

All (14) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	F	268	GLY	N-CA-C	-7.10	95.35	113.10
1	D	325	ASP	CB-CG-OD2	6.08	123.77	118.30
1	D	368	ASP	CB-CG-OD2	5.62	123.36	118.30
1	B	334	ARG	NE-CZ-NH2	-5.61	117.50	120.30
1	B	334	ARG	NE-CZ-NH1	5.52	123.06	120.30
1	G	325	ASP	CB-CG-OD2	5.21	122.99	118.30
1	G	316	ASP	CB-CG-OD2	5.15	122.94	118.30
1	G	273	ASP	CB-CG-OD2	5.10	122.89	118.30
1	A	325	ASP	CB-CG-OD2	5.10	122.89	118.30
1	E	325	ASP	CB-CG-OD2	5.09	122.88	118.30
1	D	273	ASP	CB-CG-OD2	5.08	122.87	118.30
1	D	334	ARG	NE-CZ-NH1	5.08	122.84	120.30
1	E	265	ASP	CB-CG-OD2	5.05	122.85	118.30
1	A	316	ASP	CB-CG-OD2	5.04	122.83	118.30

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	1099	0	1096	12	0
1	B	1099	0	1096	7	0
1	D	1099	0	1096	15	0
1	E	1099	0	1096	5	0
1	F	1099	0	1096	38	0
1	G	1099	0	1096	9	0
2	A	51	0	0	1	0
2	B	34	0	0	1	0
2	D	32	0	0	2	0
2	E	30	0	0	1	0
2	F	10	0	0	2	0
2	G	25	0	0	0	0
All	All	6776	0	6576	82	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 6.

All (82) 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:F:267:SER:HB2	1:F:366:HIS:N	1.83	0.94
1:F:267:SER:HB3	1:F:366:HIS:CG	2.08	0.89
1:F:268:GLY:HA2	1:F:363:LYS:HE3	1.61	0.82
1:F:266:LEU:CD2	1:F:366:HIS:HD2	1.97	0.77
1:F:266:LEU:CD2	1:F:366:HIS:CD2	2.68	0.76
1:F:266:LEU:HD23	1:F:266:LEU:C	2.08	0.73
1:D:272:ASN:O	2:D:8:HOH:O	2.09	0.70
1:F:267:SER:HB3	1:F:366:HIS:CD2	2.26	0.70
1:F:267:SER:HB2	1:F:365:VAL:C	2.14	0.68
1:D:336:ILE:HD12	1:D:342:ASN:HB2	1.76	0.68
1:F:266:LEU:HD23	1:F:267:SER:N	2.10	0.66
1:F:265:ASP:O	1:F:269:GLY:HA3	1.97	0.65
1:F:266:LEU:HD22	1:F:366:HIS:HD2	1.62	0.64
1:F:266:LEU:CD2	1:F:366:HIS:HA	2.28	0.64
1:F:338:THR:O	1:F:339:GLY:O	2.16	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:266:LEU:HD21	1:F:366:HIS:CD2	2.36	0.60
1:F:267:SER:CB	1:F:366:HIS:CG	2.84	0.59
1:F:267:SER:HA	1:F:364:MET:O	2.02	0.59
1:F:266:LEU:HD21	1:F:366:HIS:HA	1.85	0.59
1:F:334:ARG:HD2	1:F:344:ASN:OD1	2.03	0.59
1:A:312:ILE:HG21	1:A:372:ASN:HB2	1.85	0.59
1:F:337:GLU:OE1	1:G:342:ASN:ND2	2.37	0.58
1:D:312:ILE:O	1:D:313:ASN:HB3	2.05	0.57
1:F:266:LEU:HD22	1:F:366:HIS:CD2	2.38	0.56
1:B:345:THR:O	1:D:334:ARG:NH2	2.38	0.56
1:F:266:LEU:CD2	1:F:266:LEU:C	2.75	0.55
1:B:334:ARG:HD2	1:B:344:ASN:OD1	2.06	0.55
1:F:266:LEU:HD11	2:F:83:HOH:O	2.06	0.55
1:G:276:ARG:HG3	1:G:276:ARG:O	2.06	0.55
1:F:336:ILE:HG13	1:F:336:ILE:O	2.06	0.55
1:F:266:LEU:HD21	1:F:366:HIS:HD2	1.68	0.55
1:D:263:LYS:HG3	2:D:170:HOH:O	2.07	0.54
1:F:266:LEU:HG	1:F:367:ALA:O	2.08	0.53
1:A:260:ILE:HG23	1:A:371:ILE:HG12	1.89	0.53
1:D:312:ILE:O	1:D:312:ILE:HG13	2.09	0.53
1:B:277:ILE:HG13	1:B:278:THR:H	1.75	0.52
2:A:167:HOH:O	1:D:341:THR:HG23	2.09	0.51
1:D:318:ALA:HA	1:D:369:ILE:HD13	1.92	0.51
1:A:265:ASP:HB2	1:A:366:HIS:CD2	2.46	0.50
1:F:267:SER:HB2	1:F:366:HIS:CA	2.41	0.50
1:A:340:LYS:HE2	2:B:134:HOH:O	2.11	0.50
1:D:318:ALA:HA	1:D:369:ILE:CD1	2.42	0.49
1:F:256:GLN:CG	1:F:275:SER:HB2	2.42	0.49
1:B:312:ILE:HG21	1:B:372:ASN:HB2	1.93	0.49
1:F:266:LEU:HD23	1:F:366:HIS:HA	1.94	0.48
1:F:251:VAL:HG11	1:F:293:LEU:HD21	1.95	0.48
1:A:312:ILE:O	1:A:343:TYR:CD2	2.67	0.48
1:G:356:ALA:O	1:G:357:ARG:HB2	2.15	0.47
1:E:314:PHE:CG	1:E:318:ALA:HB2	2.50	0.46
1:F:317:PHE:CE2	1:F:367:ALA:HB2	2.50	0.46
1:A:315:THR:HG22	1:A:316:ASP:OD2	2.15	0.46
1:D:334:ARG:HD2	1:D:344:ASN:OD1	2.16	0.46
1:A:260:ILE:CG2	1:A:371:ILE:CG1	2.94	0.46
1:F:264:ASN:O	1:F:265:ASP:HB2	2.16	0.46
1:F:311:TYR:CD1	1:F:369:ILE:HD11	2.51	0.46
1:G:312:ILE:HG23	1:G:343:TYR:CZ	2.51	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:312:ILE:O	1:A:343:TYR:CE2	2.69	0.46
1:D:314:PHE:CE2	1:D:336:ILE:HG22	2.51	0.45
1:E:345:THR:O	1:F:334:ARG:NH2	2.49	0.45
1:G:285:LYS:HE2	1:G:287:HIS:CE1	2.51	0.45
1:E:351:VAL:HG12	1:G:304:TYR:OH	2.17	0.44
1:F:267:SER:CB	1:F:366:HIS:CA	2.95	0.44
1:G:277:ILE:HG13	1:G:278:THR:N	2.32	0.44
1:B:329:PHE:CZ	1:B:352:CYS:HB3	2.54	0.43
1:B:310:TYR:CD2	1:B:372:ASN:HB3	2.54	0.43
1:F:259:ALA:HA	2:F:48:HOH:O	2.18	0.43
1:B:329:PHE:CD2	1:B:330:LEU:HG	2.53	0.43
1:D:306:GLN:O	1:D:378:THR:HA	2.19	0.42
1:D:313:ASN:OD1	1:D:314:PHE:N	2.52	0.42
1:F:329:PHE:CD2	1:F:330:LEU:HG	2.55	0.42
1:A:277:ILE:HG13	1:A:278:THR:N	2.35	0.42
1:D:329:PHE:CD2	1:D:330:LEU:HG	2.54	0.42
1:A:329:PHE:CD2	1:A:330:LEU:HG	2.55	0.42
1:F:261:GLN:HG3	1:F:370:SER:HB3	2.02	0.42
1:D:263:LYS:HG3	1:D:263:LYS:H	1.61	0.42
1:A:356:ALA:O	1:A:357:ARG:HB2	2.20	0.42
1:G:277:ILE:HG13	1:G:278:THR:H	1.84	0.41
1:A:280:ASN:HA	1:A:281:PRO:HD3	1.95	0.41
1:E:368:ASP:HB3	2:E:60:HOH:O	2.20	0.41
1:F:375:LYS:HG3	1:F:376:HIS:CE1	2.57	0.40
1:E:375:LYS:HG3	1:E:376:HIS:CE1	2.57	0.40
1:G:337:GLU:HG3	1:G:340:LYS:CB	2.51	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	138/164 (84%)	130 (94%)	8 (6%)	0	100	100
1	B	138/164 (84%)	132 (96%)	6 (4%)	0	100	100
1	D	138/164 (84%)	126 (91%)	12 (9%)	0	100	100
1	E	138/164 (84%)	129 (94%)	9 (6%)	0	100	100
1	F	138/164 (84%)	120 (87%)	13 (9%)	5 (4%)	4	1
1	G	138/164 (84%)	127 (92%)	11 (8%)	0	100	100
All	All	828/984 (84%)	764 (92%)	59 (7%)	5 (1%)	30	29

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	F	267	SER
1	F	339	GLY
1	F	338	THR
1	F	341	THR
1	F	264	ASN

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	121/136 (89%)	118 (98%)	3 (2%)	55	65
1	B	121/136 (89%)	121 (100%)	0	100	100
1	D	121/136 (89%)	119 (98%)	2 (2%)	68	78
1	E	121/136 (89%)	119 (98%)	2 (2%)	68	78
1	F	121/136 (89%)	121 (100%)	0	100	100
1	G	121/136 (89%)	120 (99%)	1 (1%)	86	92
All	All	726/816 (89%)	718 (99%)	8 (1%)	80	88

All (8) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	277	ILE
1	A	315	THR
1	A	344	ASN
1	D	263	LYS
1	D	357	ARG
1	E	289	ARG
1	E	319	SER
1	G	341	THR

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

Mol	Chain	Res	Type
1	A	376	HIS
1	E	280	ASN
1	F	376	HIS
1	G	254	GLN
1	G	280	ASN
1	G	313	ASN
1	G	366	HIS

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 carbohydrates 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	140/164 (85%)	-0.09	5 (3%) 46 49	2, 5, 16, 22	0
1	B	140/164 (85%)	0.23	12 (8%) 13 14	2, 5, 16, 23	0
1	D	140/164 (85%)	-0.01	8 (5%) 27 28	2, 6, 15, 19	0
1	E	140/164 (85%)	0.32	12 (8%) 13 14	2, 6, 15, 18	0
1	F	140/164 (85%)	0.68	16 (11%) 7 6	2, 5, 15, 19	0
1	G	140/164 (85%)	0.22	8 (5%) 27 28	2, 5, 13, 18	0
All	All	840/984 (85%)	0.23	61 (7%) 18 19	2, 6, 15, 23	0

All (61) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	F	338	THR	7.8
1	A	389	PRO	7.1
1	F	267	SER	7.0
1	F	268	GLY	6.8
1	E	277	ILE	6.5
1	B	257	GLY	5.9
1	B	277	ILE	5.9
1	F	340	LYS	5.8
1	E	339	GLY	5.6
1	F	317	PHE	5.4
1	G	289	ARG	5.3
1	A	388	ALA	4.9
1	F	261	GLN	4.7
1	G	389	PRO	4.5
1	B	389	PRO	4.4
1	E	258	SER	4.3
1	F	339	GLY	4.2
1	G	388	ALA	4.2
1	B	278	THR	4.0

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Mol	Chain	Res	Type	RSRZ
1	F	336	ILE	3.9
1	F	315	THR	3.7
1	E	278	THR	3.4
1	D	248	PRO	3.4
1	F	277	ILE	3.4
1	A	343	TYR	3.4
1	F	260	ILE	3.4
1	B	276	ARG	3.3
1	B	366	HIS	3.1
1	E	276	ARG	3.1
1	A	276	ARG	3.1
1	D	264	ASN	3.1
1	E	288	PRO	3.0
1	B	317	PHE	3.0
1	E	389	PRO	2.9
1	G	387	GLU	2.9
1	B	388	ALA	2.8
1	E	388	ALA	2.8
1	F	387	GLU	2.8
1	B	282	LYS	2.7
1	F	389	PRO	2.7
1	G	273	ASP	2.6
1	E	273	ASP	2.5
1	A	387	GLU	2.5
1	D	267	SER	2.4
1	B	387	GLU	2.4
1	D	338	THR	2.4
1	G	258	SER	2.4
1	B	256	GLN	2.3
1	F	337	GLU	2.3
1	D	313	ASN	2.3
1	G	277	ILE	2.3
1	G	257	GLY	2.2
1	F	313	ASN	2.2
1	B	248	PRO	2.2
1	E	259	ALA	2.2
1	E	260	ILE	2.2
1	D	366	HIS	2.2
1	E	387	GLU	2.2
1	F	264	ASN	2.1
1	D	389	PRO	2.1
1	D	258	SER	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 carbohydrates 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.