



Full wwPDB X-ray Structure Validation Report ⓘ

Nov 2, 2021 – 06:58 PM EDT

PDB ID : 3I4C
Title : Crystal structure of Sulfolobus Solfataricus ADH(SsADH) double mutant (W95L,N249Y)
Authors : Esposito, L.; Pennacchio, A.; Zagari, A.; Rossi, M.; Raia, C.A.
Deposited on : 2009-07-01
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 following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.23.2
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.23.2

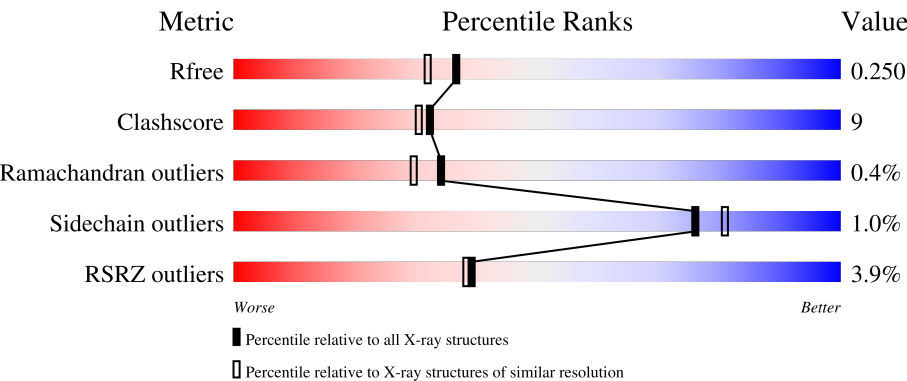
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.00 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}	130704	8085 (2.00-2.00)
Clashscore	141614	9178 (2.00-2.00)
Ramachandran outliers	138981	9054 (2.00-2.00)
Sidechain outliers	138945	9053 (2.00-2.00)
RSRZ outliers	127900	7900 (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	347	<div><div>3%</div><div>78%</div><div>19%</div><div>..</div></div>
1	B	347	<div><div>3%</div><div>72%</div><div>18%</div><div>10%</div></div>
1	C	347	<div><div>9%</div><div>66%</div><div>25%</div><div>9%</div></div>
1	D	347	<div><div>2%</div><div>79%</div><div>14%</div><div>6%</div></div>
1	E	347	<div><div>2%</div><div>79%</div><div>13%</div><div>8%</div></div>

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Mol	Chain	Length	Quality of chain
1	H	347	<div><div></div><div>3%</div><div>78%</div><div>18%</div><div>••</div></div>

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 15145 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 NAD-dependent alcohol dehydrogenase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	340	Total	C	N	O	S	0	0	0
			2575	1635	444	482	14			
1	B	312	Total	C	N	O	S	0	0	0
			2354	1495	403	442	14			
1	C	316	Total	C	N	O	S	0	0	0
			2378	1509	406	450	13			
1	D	327	Total	C	N	O	S	0	0	0
			2481	1576	427	464	14			
1	E	319	Total	C	N	O	S	0	0	0
			2412	1530	416	452	14			
1	H	334	Total	C	N	O	S	0	0	0
			2504	1591	429	470	14			

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	95	LEU	TRP	engineered mutation	UNP P39462
A	249	TYR	ASN	engineered mutation	UNP P39462
B	95	LEU	TRP	engineered mutation	UNP P39462
B	249	TYR	ASN	engineered mutation	UNP P39462
C	95	LEU	TRP	engineered mutation	UNP P39462
C	249	TYR	ASN	engineered mutation	UNP P39462
D	95	LEU	TRP	engineered mutation	UNP P39462
D	249	TYR	ASN	engineered mutation	UNP P39462
E	95	LEU	TRP	engineered mutation	UNP P39462
E	249	TYR	ASN	engineered mutation	UNP P39462
H	95	LEU	TRP	engineered mutation	UNP P39462
H	249	TYR	ASN	engineered mutation	UNP P39462

- Molecule 2 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	2	Total 2	Zn 2	0	0
2	B	2	Total 2	Zn 2	0	0
2	C	2	Total 2	Zn 2	0	0
2	D	2	Total 2	Zn 2	0	0
2	E	2	Total 2	Zn 2	0	0
2	H	2	Total 2	Zn 2	0	0

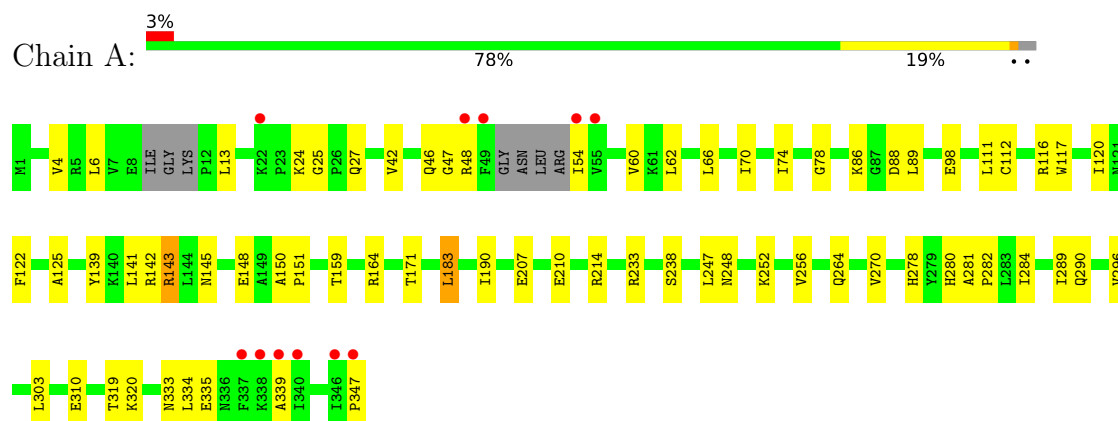
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	98	Total 98	O 98	0	0
3	B	60	Total 60	O 60	0	0
3	C	55	Total 55	O 55	0	0
3	D	102	Total 102	O 102	0	0
3	E	60	Total 60	O 60	0	0
3	H	54	Total 54	O 54	0	0

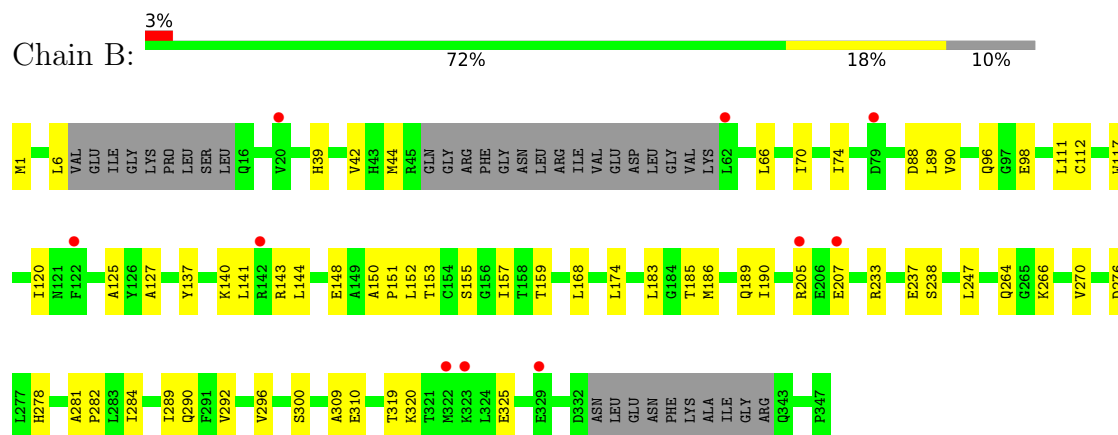
3 Residue-property plots [i](#)

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.

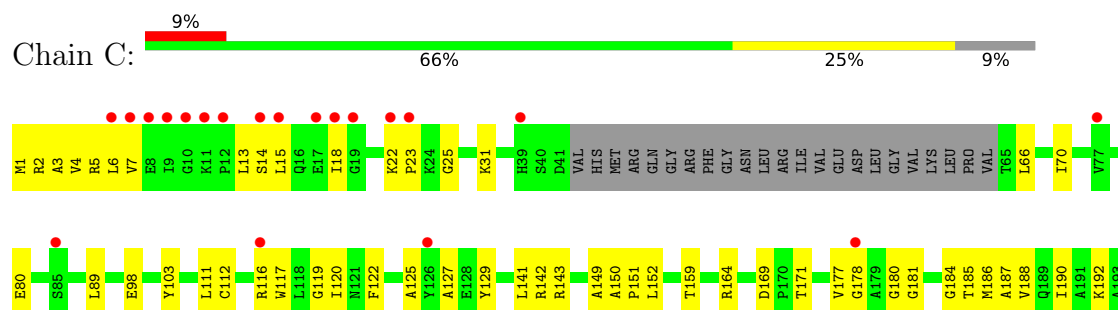
• Molecule 1: NAD-dependent alcohol dehydrogenase

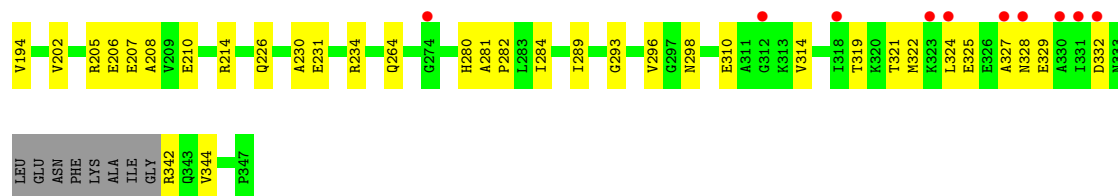


• Molecule 1: NAD-dependent alcohol dehydrogenase

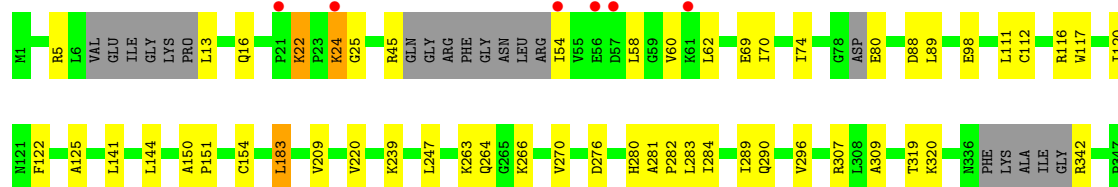
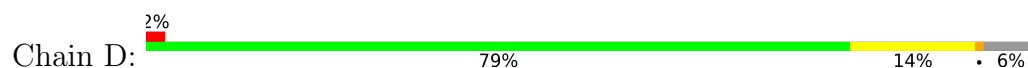


• Molecule 1: NAD-dependent alcohol dehydrogenase

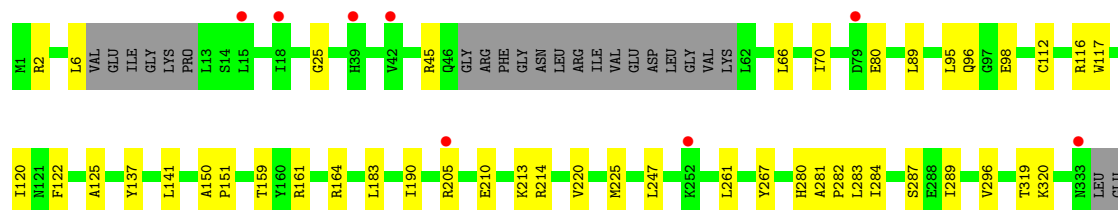
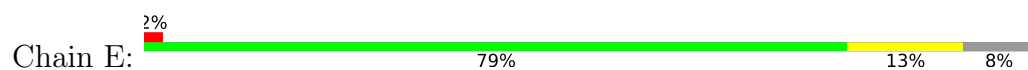




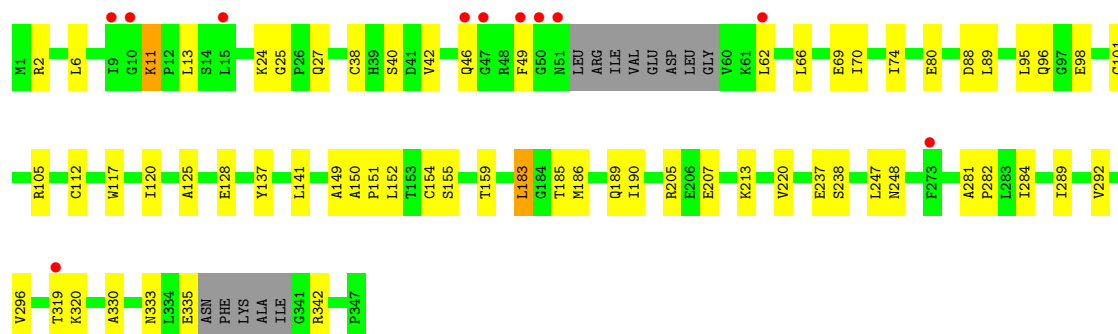
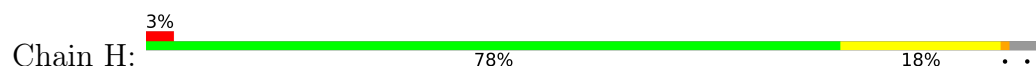
- Molecule 1: NAD-dependent alcohol dehydrogenase



- Molecule 1: NAD-dependent alcohol dehydrogenase



- Molecule 1: NAD-dependent alcohol dehydrogenase



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	215.73Å 91.55Å 118.37Å 90.00° 99.20° 90.00°	Depositor
Resolution (Å)	32.36 – 2.00 32.36 – 2.00	Depositor EDS
% Data completeness (in resolution range)	91.5 (32.36-2.00) 91.6 (32.36-2.00)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.09 (at 2.00Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.228 , 0.250 0.228 , 0.250	Depositor DCC
R_{free} test set	7574 reflections (5.05%)	wwPDB-VP
Wilson B-factor (Å ²)	22.0	Xtriage
Anisotropy	0.366	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 54.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	15145	wwPDB-VP
Average B, all atoms (Å ²)	30.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.20% 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](#)

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	0.32	0/2616	0.65	0/3535
1	B	0.32	0/2391	0.63	0/3235
1	C	0.32	0/2415	0.66	0/3266
1	D	0.32	0/2517	0.63	0/3400
1	E	0.30	0/2448	0.62	0/3308
1	H	0.30	0/2544	0.62	0/3443
All	All	0.31	0/14931	0.63	0/20187

There are no bond length outliers.

There are no bond angle outliers.

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	2575	0	2627	53	0
1	B	2354	0	2389	43	0
1	C	2378	0	2423	64	0
1	D	2481	0	2546	39	0
1	E	2412	0	2468	32	0
1	H	2504	0	2535	42	0
2	A	2	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	B	2	0	0	0	0
2	C	2	0	0	0	0
2	D	2	0	0	0	0
2	E	2	0	0	0	0
2	H	2	0	0	0	0
3	A	98	0	0	3	0
3	B	60	0	0	0	0
3	C	55	0	0	1	0
3	D	102	0	0	2	0
3	E	60	0	0	0	0
3	H	54	0	0	0	0
All	All	15145	0	14988	260	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 9.

All (260) 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:C:159:THR:HG22	1:C:190:ILE:HD12	1.49	0.94
1:D:22:LYS:H	1:D:22:LYS:HD2	1.42	0.85
1:C:4:VAL:HG11	1:C:327:ALA:HB3	1.67	0.77
1:A:210:GLU:HG3	1:A:214:ARG:NH1	2.01	0.76
1:H:213:LYS:HG3	1:H:220:VAL:HG11	1.68	0.75
1:A:70:ILE:HG12	1:A:125:ALA:HB2	1.68	0.74
1:H:205:ARG:HH12	1:H:207:GLU:HB2	1.53	0.73
1:H:155:SER:O	1:H:186:MET:HE3	1.89	0.72
1:C:205:ARG:HD3	1:C:207:GLU:OE1	1.89	0.72
1:C:206:GLU:O	1:C:210:GLU:HG3	1.90	0.71
1:E:70:ILE:HG12	1:E:125:ALA:HB2	1.72	0.71
1:C:180:GLY:HA3	1:C:208:ALA:O	1.89	0.71
1:B:155:SER:O	1:B:186:MET:HE3	1.90	0.71
1:A:233:ARG:HG3	1:A:238:SER:HA	1.73	0.70
1:D:70:ILE:HG12	1:D:125:ALA:HB2	1.73	0.70
1:A:42:VAL:HG13	1:A:335:GLU:HG2	1.76	0.67
1:B:89:LEU:HG	1:B:141:LEU:HD12	1.77	0.67
1:C:2:ARG:HB3	1:C:15:LEU:HD11	1.76	0.67
1:B:70:ILE:HG12	1:B:125:ALA:HB2	1.77	0.67
1:E:98:GLU:HG3	1:E:112:CYS:SG	2.36	0.66
1:A:74:ILE:HD12	1:A:88:ASP:HB2	1.78	0.66
1:C:159:THR:CG2	1:C:190:ILE:HD12	2.25	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:74:ILE:HD12	1:B:88:ASP:HB2	1.78	0.65
1:B:143:ARG:HD2	1:B:310:GLU:O	1.98	0.64
1:B:98:GLU:HG3	1:B:112:CYS:SG	2.38	0.63
1:H:284:ILE:HA	1:H:289:ILE:HG12	1.80	0.63
1:E:183:LEU:HB3	1:E:247:LEU:HD13	1.80	0.63
1:H:98:GLU:HG3	1:H:112:CYS:SG	2.39	0.62
1:A:98:GLU:HG3	1:A:112:CYS:SG	2.40	0.62
1:A:333:ASN:HB3	1:A:339:ALA:HB2	1.81	0.62
1:C:7:VAL:HG21	1:C:14:SER:HB3	1.82	0.61
1:C:6:LEU:HB2	1:C:66:LEU:HD11	1.83	0.61
1:C:164:ARG:HH11	1:C:164:ARG:HB3	1.64	0.61
1:D:24:LYS:HD2	1:D:25:GLY:N	2.16	0.60
1:B:266:LYS:HE2	1:B:290:GLN:HE22	1.66	0.60
1:E:213:LYS:HG3	1:E:220:VAL:HG11	1.83	0.60
1:H:213:LYS:HD2	1:H:220:VAL:HG21	1.83	0.60
1:A:164:ARG:HH11	1:A:164:ARG:HB3	1.66	0.60
1:A:54:ILE:HB	1:A:60:VAL:HG21	1.83	0.60
1:A:333:ASN:CB	1:A:339:ALA:HB2	2.32	0.60
1:B:207:GLU:H	1:B:207:GLU:CD	2.04	0.60
1:C:143:ARG:HD2	1:C:310:GLU:O	2.00	0.60
1:H:2:ARG:HG3	1:H:128:GLU:OE2	2.02	0.60
1:A:210:GLU:HG3	1:A:214:ARG:HH11	1.66	0.60
1:C:25:GLY:C	1:C:80:GLU:HB2	2.22	0.60
1:H:25:GLY:C	1:H:80:GLU:HB2	2.21	0.60
1:B:266:LYS:HE2	1:B:290:GLN:NE2	2.18	0.59
1:E:117:TRP:HB3	1:E:120:ILE:HB	1.84	0.59
1:E:150:ALA:HB3	1:E:151:PRO:HD3	1.83	0.59
1:C:98:GLU:HG3	1:C:112:CYS:SG	2.43	0.59
1:E:25:GLY:C	1:E:80:GLU:HB2	2.23	0.58
1:H:205:ARG:NH1	1:H:207:GLU:HB2	2.18	0.58
1:H:159:THR:HG22	1:H:190:ILE:HD12	1.84	0.58
1:A:42:VAL:CG1	1:A:335:GLU:HG2	2.33	0.58
1:C:70:ILE:HG12	1:C:125:ALA:HB2	1.86	0.58
1:H:70:ILE:HG12	1:H:125:ALA:HB2	1.84	0.58
1:A:142:ARG:HD2	1:E:225:MET:HE1	1.86	0.58
1:E:284:ILE:HA	1:E:289:ILE:HG12	1.86	0.58
1:B:233:ARG:HG3	1:B:238:SER:HA	1.86	0.57
1:E:280:HIS:HB3	1:E:283:LEU:HG	1.86	0.57
1:A:24:LYS:HG2	1:A:27:GLN:OE1	2.05	0.57
1:B:6:LEU:HB2	1:B:66:LEU:HD11	1.85	0.57
1:C:4:VAL:HG11	1:C:327:ALA:CB	2.34	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:183:LEU:HB3	1:D:247:LEU:HD13	1.87	0.57
1:B:150:ALA:HB3	1:B:151:PRO:HD3	1.87	0.57
1:C:4:VAL:HG21	1:C:324:LEU:O	2.04	0.56
1:C:150:ALA:HB3	1:C:151:PRO:HD3	1.86	0.56
1:C:1:MET:CE	1:C:127:ALA:HB1	2.36	0.56
1:A:334:LEU:HD23	1:A:339:ALA:HB3	1.87	0.56
1:D:98:GLU:HG3	1:D:112:CYS:SG	2.46	0.56
1:E:89:LEU:HG	1:E:141:LEU:HD12	1.88	0.56
1:H:24:LYS:HG2	1:H:27:GLN:OE1	2.05	0.56
1:D:117:TRP:HB3	1:D:120:ILE:HB	1.88	0.56
1:E:6:LEU:HB2	1:E:66:LEU:HD11	1.86	0.55
1:B:159:THR:HG22	1:B:190:ILE:HD12	1.87	0.55
1:B:117:TRP:HB3	1:B:120:ILE:HB	1.89	0.55
1:A:42:VAL:O	1:A:46:GLN:HG3	2.06	0.54
1:C:210:GLU:O	1:C:214:ARG:HD3	2.06	0.54
1:H:74:ILE:HD12	1:H:88:ASP:HB2	1.89	0.54
1:A:247:LEU:HD23	1:A:270:VAL:HB	1.89	0.54
1:H:330:ALA:HA	1:H:333:ASN:HD22	1.72	0.54
1:B:205:ARG:HH11	1:B:205:ARG:HG2	1.73	0.54
1:E:281:ALA:HB3	1:E:282:PRO:HD3	1.89	0.54
1:C:230:ALA:O	1:C:234:ARG:HG3	2.08	0.53
1:E:164:ARG:HG2	1:E:164:ARG:HH11	1.73	0.53
1:H:117:TRP:HB3	1:H:120:ILE:HB	1.90	0.53
1:A:252:LYS:HE3	1:A:256:VAL:HG21	1.91	0.53
1:B:325:GLU:CD	1:B:325:GLU:H	2.12	0.53
1:D:209:VAL:HG13	1:D:220:VAL:HB	1.91	0.53
1:H:281:ALA:HB3	1:H:282:PRO:HD3	1.89	0.53
1:B:284:ILE:HA	1:B:289:ILE:HG12	1.91	0.53
1:B:319:THR:HG22	1:B:320:LYS:N	2.24	0.53
1:A:143:ARG:HD2	1:A:310:GLU:O	2.09	0.52
1:H:95:LEU:HD13	1:H:117:TRP:CD2	2.44	0.52
1:D:280:HIS:HB3	1:D:283:LEU:HG	1.90	0.52
1:A:150:ALA:HB3	1:A:151:PRO:HD3	1.90	0.52
1:C:13:LEU:N	1:C:328:ASN:OD1	2.42	0.52
1:E:210:GLU:HG3	1:E:214:ARG:HH11	1.73	0.52
1:D:284:ILE:HA	1:D:289:ILE:HG12	1.91	0.52
1:C:164:ARG:HB3	1:C:164:ARG:NH1	2.24	0.51
1:A:264:GLN:HG3	1:B:111:LEU:CD1	2.41	0.51
1:H:42:VAL:HG13	1:H:335:GLU:HG2	1.92	0.51
1:A:62:LEU:HD12	1:A:62:LEU:N	2.26	0.51
1:A:290:GLN:HG2	1:B:292:VAL:HG12	1.92	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:329:GLU:O	1:C:332:ASP:HB2	2.10	0.51
1:C:89:LEU:HG	1:C:141:LEU:HD12	1.92	0.51
1:E:6:LEU:HD13	1:E:45:ARG:HA	1.93	0.51
1:A:142:ARG:NH1	1:E:225:MET:HE2	2.26	0.51
1:C:7:VAL:CG2	1:C:14:SER:HB3	2.40	0.50
1:C:142:ARG:HG3	1:C:142:ARG:HH11	1.76	0.50
1:C:181:GLY:O	1:C:185:THR:HG23	2.12	0.50
1:C:325:GLU:CD	1:C:325:GLU:H	2.15	0.50
1:A:47:GLY:O	1:A:54:ILE:HG23	2.12	0.50
1:A:164:ARG:HB3	1:A:164:ARG:NH1	2.26	0.50
1:C:103:TYR:CZ	1:D:263:LYS:HB2	2.47	0.50
1:D:22:LYS:H	1:D:22:LYS:CD	2.17	0.50
1:E:2:ARG:HG3	1:E:2:ARG:HH11	1.77	0.50
1:D:266:LYS:HE2	1:D:290:GLN:NE2	2.27	0.49
1:A:117:TRP:HB3	1:A:120:ILE:HB	1.94	0.49
1:E:66:LEU:N	1:E:66:LEU:HD12	2.26	0.49
1:D:24:LYS:HD2	1:D:24:LYS:C	2.32	0.49
1:A:171:THR:HA	1:D:307:ARG:HD3	1.94	0.49
1:C:116:ARG:HD2	1:C:122:PHE:CD1	2.48	0.49
1:C:111:LEU:CD1	1:D:264:GLN:HG3	2.42	0.49
1:D:116:ARG:HD2	1:D:122:PHE:CE1	2.48	0.49
1:D:150:ALA:HB3	1:D:151:PRO:HD3	1.93	0.49
1:H:150:ALA:HB3	1:H:151:PRO:HD3	1.93	0.49
1:H:13:LEU:HD11	1:H:66:LEU:HD22	1.94	0.48
1:A:183:LEU:HB3	1:A:247:LEU:HD13	1.95	0.48
1:B:155:SER:C	1:B:186:MET:HE3	2.34	0.48
1:D:58:LEU:HD12	1:D:58:LEU:N	2.29	0.48
1:A:159:THR:HG22	1:A:190:ILE:HD12	1.96	0.48
1:C:117:TRP:HB3	1:C:120:ILE:HB	1.96	0.48
1:D:144:LEU:HD11	1:D:309:ALA:HB1	1.95	0.48
1:A:143:ARG:HH11	1:A:143:ARG:HB2	1.79	0.48
1:C:264:GLN:HG3	1:D:111:LEU:CD1	2.43	0.48
1:C:281:ALA:HB3	1:C:282:PRO:HD3	1.95	0.47
1:D:281:ALA:HB3	1:D:282:PRO:HD3	1.95	0.47
1:B:39:HIS:O	1:B:42:VAL:HB	2.14	0.47
1:H:38:CYS:SG	1:H:40:SER:HB2	2.54	0.47
1:H:155:SER:HB3	1:H:186:MET:HE1	1.95	0.47
1:D:116:ARG:HD2	1:D:122:PHE:CD1	2.50	0.47
1:A:280:HIS:CD2	1:A:282:PRO:HD2	2.50	0.47
1:B:185:THR:O	1:B:189:GLN:HG3	2.14	0.47
1:C:1:MET:HE3	1:C:127:ALA:HB1	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:186:MET:HE1	1:C:314:VAL:HB	1.97	0.47
1:H:11:LYS:HD2	1:H:11:LYS:N	2.29	0.47
1:C:119:GLY:O	1:C:120:ILE:HD13	2.15	0.47
1:E:96:GLN:HG2	1:E:137:TYR:CE1	2.50	0.47
1:H:6:LEU:HB2	1:H:66:LEU:HD11	1.97	0.47
1:A:284:ILE:HA	1:A:289:ILE:HG12	1.97	0.46
1:A:319:THR:HG22	1:A:320:LYS:N	2.30	0.46
1:B:144:LEU:HD11	1:B:309:ALA:HB1	1.97	0.46
1:C:177:VAL:HA	1:C:202:VAL:HG13	1.96	0.46
1:E:116:ARG:HD2	1:E:122:PHE:CE1	2.50	0.46
1:H:319:THR:HG22	1:H:320:LYS:N	2.30	0.46
1:H:149:ALA:O	1:H:152:LEU:HB2	2.15	0.46
1:A:116:ARG:HD2	1:A:122:PHE:CD1	2.51	0.46
1:C:184:GLY:O	1:C:188:VAL:HG23	2.16	0.46
1:E:96:GLN:HG2	1:E:137:TYR:CZ	2.50	0.46
1:C:321:THR:C	1:C:322:MET:HG3	2.37	0.45
1:D:247:LEU:HD23	1:D:270:VAL:HB	1.98	0.45
1:H:319:THR:HG23	1:H:342:ARG:O	2.16	0.45
1:A:25:GLY:O	1:A:78:GLY:HA3	2.15	0.45
1:C:190:ILE:O	1:C:194:VAL:HG22	2.17	0.45
1:C:321:THR:HA	1:C:344:VAL:O	2.17	0.45
1:H:89:LEU:HG	1:H:141:LEU:HD12	1.98	0.45
1:H:101:CYS:O	1:H:105:ARG:HG3	2.16	0.45
1:H:330:ALA:HA	1:H:333:ASN:ND2	2.30	0.45
1:E:261:LEU:HD11	1:E:267:TYR:HB2	1.98	0.45
1:C:149:ALA:HA	1:C:152:LEU:HD13	1.99	0.45
1:A:6:LEU:HB2	1:A:66:LEU:HD11	1.99	0.45
1:H:96:GLN:HG2	1:H:137:TYR:CE1	2.52	0.45
1:A:74:ILE:HG22	1:A:86:LYS:HA	1.99	0.44
1:B:325:GLU:CD	1:B:325:GLU:N	2.70	0.44
1:H:42:VAL:CG1	1:H:335:GLU:HG2	2.47	0.44
1:C:159:THR:CG2	1:C:187:ALA:HA	2.47	0.44
1:H:96:GLN:HG2	1:H:137:TYR:CD1	2.52	0.44
1:B:44:MET:HE1	1:B:120:ILE:O	2.18	0.44
1:H:69:GLU:HG2	1:H:154:CYS:HB2	1.99	0.44
1:C:66:LEU:N	1:C:66:LEU:HD12	2.32	0.44
1:C:284:ILE:HA	1:C:289:ILE:HG12	1.99	0.44
1:D:62:LEU:HD12	1:D:62:LEU:N	2.32	0.44
1:C:5:ARG:NH1	1:C:18:ILE:HG21	2.33	0.44
1:D:69:GLU:HG2	1:D:154:CYS:HB2	1.98	0.44
1:D:239:LYS:HE2	3:D:418:HOH:O	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:281:ALA:HB3	1:B:282:PRO:HD3	1.98	0.44
1:C:293:GLY:HA3	1:D:284:ILE:HG22	2.00	0.44
1:E:95:LEU:HD13	1:E:117:TRP:CD2	2.53	0.44
1:E:161:ARG:NH1	1:E:164:ARG:HH22	2.17	0.43
1:A:319:THR:CG2	1:A:320:LYS:N	2.81	0.43
1:D:74:ILE:HD12	1:D:88:ASP:HB2	2.00	0.43
1:D:266:LYS:HE2	1:D:290:GLN:HE22	1.83	0.43
1:E:319:THR:HG22	1:E:320:LYS:N	2.33	0.43
1:A:111:LEU:CD1	1:B:264:GLN:HG3	2.48	0.43
1:C:3:ALA:O	1:C:5:ARG:HG3	2.19	0.43
1:B:153:THR:O	1:B:157:ILE:HD12	2.18	0.43
1:B:168:LEU:HD11	1:B:174:LEU:HD22	2.00	0.43
1:D:319:THR:HG23	1:D:342:ARG:O	2.18	0.43
1:A:89:LEU:HG	1:A:141:LEU:HD12	1.99	0.43
1:A:281:ALA:HB3	1:A:282:PRO:HD3	2.01	0.43
1:H:237:GLU:O	1:H:238:SER:HB2	2.18	0.43
1:H:186:MET:O	1:H:190:ILE:HG13	2.19	0.43
1:B:148:GLU:O	1:B:152:LEU:HD13	2.18	0.42
1:C:319:THR:HA	1:C:342:ARG:O	2.19	0.42
1:E:319:THR:CG2	1:E:320:LYS:N	2.81	0.42
1:H:6:LEU:O	1:H:62:LEU:HD22	2.19	0.42
1:B:96:GLN:HG2	1:B:137:TYR:CE1	2.54	0.42
1:A:62:LEU:H	1:A:62:LEU:CD1	2.32	0.42
1:C:1:MET:HE1	1:C:127:ALA:HB1	2.00	0.42
1:C:6:LEU:HA	1:C:13:LEU:HD23	2.00	0.42
1:E:287:SER:HB2	1:E:289:ILE:HG23	1.99	0.42
1:H:42:VAL:O	1:H:46:GLN:HG3	2.19	0.42
1:D:319:THR:CG2	1:D:320:LYS:N	2.82	0.42
1:B:44:MET:HE2	1:B:120:ILE:HA	2.01	0.42
1:A:4:VAL:HG12	1:A:13:LEU:HB3	2.02	0.42
1:B:1:MET:CE	1:B:127:ALA:HB1	2.49	0.42
1:C:4:VAL:HG23	1:C:324:LEU:HG	2.00	0.42
1:C:31:LYS:HA	1:C:129:TYR:CD1	2.54	0.42
1:C:231:GLU:OE2	1:C:234:ARG:NH1	2.52	0.42
1:A:164:ARG:NE	3:A:434:HOH:O	2.52	0.42
1:A:280:HIS:HA	1:B:276:ASP:OD1	2.20	0.42
1:D:25:GLY:C	1:D:80:GLU:HB2	2.40	0.42
1:A:139:TYR:HE2	1:A:303:LEU:HD12	1.85	0.42
1:E:96:GLN:HG2	1:E:137:TYR:CD1	2.54	0.42
1:B:90:VAL:HG12	1:B:140:LYS:HA	2.02	0.42
1:D:89:LEU:HG	1:D:141:LEU:HD12	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:247:LEU:HD23	1:A:270:VAL:CB	2.50	0.41
1:E:96:GLN:HG2	1:E:137:TYR:CE2	2.54	0.41
1:H:319:THR:CG2	1:H:320:LYS:N	2.83	0.41
1:A:290:GLN:NE2	3:A:378:HOH:O	2.49	0.41
1:B:152:LEU:N	1:B:152:LEU:HD12	2.34	0.41
1:H:183:LEU:HB3	1:H:247:LEU:HD13	2.02	0.41
1:A:347:PRO:HB2	3:A:417:HOH:O	2.20	0.41
1:B:159:THR:CG2	1:B:190:ILE:HD12	2.51	0.41
1:B:319:THR:CG2	1:B:320:LYS:N	2.83	0.41
1:C:22:LYS:HD3	1:C:22:LYS:C	2.41	0.41
1:C:280:HIS:HA	1:D:276:ASP:OD1	2.20	0.41
1:D:319:THR:HG22	1:D:320:LYS:N	2.35	0.41
1:H:159:THR:CG2	1:H:190:ILE:HD12	2.50	0.41
1:C:22:LYS:HD3	1:C:23:PRO:N	2.35	0.41
1:E:164:ARG:HG2	1:E:164:ARG:NH1	2.36	0.41
1:B:247:LEU:HD23	1:B:270:VAL:HB	2.03	0.41
1:B:300:SER:HB2	3:D:362:HOH:O	2.20	0.41
1:C:178:GLY:N	1:C:202:VAL:O	2.54	0.41
1:H:185:THR:O	1:H:189:GLN:HG3	2.21	0.41
1:A:145:ASN:OD1	1:A:148:GLU:HG3	2.20	0.41
1:A:284:ILE:HA	1:A:289:ILE:CG1	2.51	0.41
1:C:186:MET:HE3	1:C:190:ILE:HG13	2.03	0.41
1:C:314:VAL:O	1:C:314:VAL:HG23	2.20	0.41
1:D:54:ILE:O	1:D:60:VAL:HG23	2.21	0.41
1:E:159:THR:HG22	1:E:190:ILE:HD12	2.02	0.41
1:D:13:LEU:HG	1:D:45:ARG:HD3	2.03	0.41
1:C:298:ASN:HB2	3:C:351:HOH:O	2.20	0.40
1:A:278:HIS:ND1	1:B:278:HIS:ND1	2.53	0.40
1:C:169:ASP:OD1	1:C:171:THR:N	2.48	0.40
1:B:237:GLU:O	1:B:238:SER:HB2	2.21	0.40
1:C:280:HIS:CD2	1:C:282:PRO:HD2	2.57	0.40
1:D:5:ARG:HD3	1:D:16:GLN:NE2	2.37	0.40
1:D:22:LYS:HD2	1:D:22:LYS:N	2.20	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	334/347 (96%)	320 (96%)	13 (4%)	1 (0%)	41	37
1	B	304/347 (88%)	293 (96%)	10 (3%)	1 (0%)	41	37
1	C	310/347 (89%)	297 (96%)	12 (4%)	1 (0%)	41	37
1	D	317/347 (91%)	304 (96%)	12 (4%)	1 (0%)	41	37
1	E	311/347 (90%)	297 (96%)	13 (4%)	1 (0%)	41	37
1	H	328/347 (94%)	316 (96%)	10 (3%)	2 (1%)	25	19
All	All	1904/2082 (92%)	1827 (96%)	70 (4%)	7 (0%)	34	30

All (7) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	H	49	PHE
1	C	296	VAL
1	E	296	VAL
1	A	296	VAL
1	B	296	VAL
1	D	296	VAL
1	H	296	VAL

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	271/278 (98%)	266 (98%)	5 (2%)	59	63

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	B	246/278 (88%)	245 (100%)	1 (0%)	91	93
1	C	250/278 (90%)	248 (99%)	2 (1%)	81	86
1	D	263/278 (95%)	260 (99%)	3 (1%)	73	78
1	E	254/278 (91%)	253 (100%)	1 (0%)	91	93
1	H	260/278 (94%)	256 (98%)	4 (2%)	65	69
All	All	1544/1668 (93%)	1528 (99%)	16 (1%)	76	81

All (16) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	48	ARG
1	A	143	ARG
1	A	183	LEU
1	A	207	GLU
1	A	248	ASN
1	B	183	LEU
1	C	192	LYS
1	C	226	GLN
1	D	22	LYS
1	D	24	LYS
1	D	183	LEU
1	E	205	ARG
1	H	11	LYS
1	H	183	LEU
1	H	248	ASN
1	H	292	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (12) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	290	GLN
1	C	16	GLN
1	C	226	GLN
1	C	343	GLN
1	D	16	GLN
1	D	226	GLN
1	D	290	GLN
1	E	248	ASN
1	E	290	GLN

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Mol	Chain	Res	Type
1	E	328	ASN
1	H	16	GLN
1	H	248	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 monosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 12 ligands modelled in this entry, 12 are 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 [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

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	340/347 (97%)	0.06	11 (3%) 47 46	10, 23, 59, 78	0
1	B	312/347 (89%)	0.15	10 (3%) 47 46	15, 28, 55, 62	0
1	C	316/347 (91%)	0.44	30 (9%) 8 7	15, 29, 60, 75	0
1	D	327/347 (94%)	-0.07	6 (1%) 68 66	11, 23, 55, 81	0
1	E	319/347 (91%)	-0.03	8 (2%) 57 56	15, 27, 54, 66	0
1	H	334/347 (96%)	0.09	11 (3%) 46 45	16, 30, 61, 96	0
All	All	1948/2082 (93%)	0.10	76 (3%) 39 38	10, 27, 57, 96	0

All (76) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	H	50	GLY	8.5
1	A	339	ALA	7.4
1	A	338	LYS	6.9
1	A	337	PHE	6.2
1	C	9	ILE	5.9
1	C	10	GLY	5.7
1	C	327	ALA	4.8
1	C	332	ASP	4.8
1	C	274	GLY	4.7
1	H	9	ILE	4.7
1	C	331	ILE	4.5
1	A	347	PRO	4.5
1	A	340	ILE	4.2
1	C	11	LYS	3.9
1	D	57	ASP	3.7
1	H	51	ASN	3.6
1	H	62	LEU	3.4
1	C	39	HIS	3.4
1	B	62	LEU	3.3

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Mol	Chain	Res	Type	RSRZ
1	A	48	ARG	3.3
1	H	46	GLN	3.2
1	C	178	GLY	3.2
1	C	330	ALA	3.1
1	B	323	LYS	3.1
1	C	6	LEU	3.0
1	B	329	GLU	2.9
1	A	55	VAL	2.9
1	B	79	ASP	2.9
1	D	61	LYS	2.9
1	H	47	GLY	2.9
1	C	22	LYS	2.9
1	B	142	ARG	2.8
1	C	8	GLU	2.8
1	B	207	GLU	2.8
1	C	23	PRO	2.7
1	E	15	LEU	2.6
1	H	15	LEU	2.6
1	C	12	PRO	2.6
1	D	24	LYS	2.6
1	E	18	ILE	2.5
1	A	346	ILE	2.5
1	A	54	ILE	2.5
1	C	15	LEU	2.5
1	C	7	VAL	2.4
1	C	77	VAL	2.4
1	C	328	ASN	2.4
1	B	122	PHE	2.4
1	D	54	ILE	2.4
1	E	79	ASP	2.4
1	D	56	GLU	2.3
1	A	49	PHE	2.3
1	H	273	PHE	2.3
1	A	22	LYS	2.3
1	B	205	ARG	2.2
1	C	14	SER	2.2
1	C	323	LYS	2.2
1	B	322	MET	2.2
1	E	252	LYS	2.2
1	C	318	ILE	2.2
1	H	49	PHE	2.2
1	C	116	ARG	2.2

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Mol	Chain	Res	Type	RSRZ
1	C	324	LEU	2.2
1	E	39	HIS	2.2
1	E	333	ASN	2.2
1	C	312	GLY	2.2
1	E	205	ARG	2.2
1	B	20	VAL	2.1
1	H	319	THR	2.1
1	D	21	PRO	2.1
1	C	85	SER	2.1
1	C	17	GLU	2.1
1	C	18	ILE	2.1
1	C	19	GLY	2.0
1	H	10	GLY	2.0
1	C	126	TYR	2.0
1	E	42	VAL	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 monosaccharides 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
2	ZN	B	500	1/1	0.96	0.07	36,36,36,36	0
2	ZN	C	500	1/1	0.98	0.04	35,35,35,35	0
2	ZN	A	400	1/1	0.99	0.07	19,19,19,19	0
2	ZN	A	500	1/1	0.99	0.05	23,23,23,23	0
2	ZN	D	400	1/1	0.99	0.05	19,19,19,19	0
2	ZN	D	500	1/1	0.99	0.05	24,24,24,24	0
2	ZN	E	400	1/1	0.99	0.04	23,23,23,23	0
2	ZN	E	500	1/1	0.99	0.07	33,33,33,33	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
2	ZN	H	400	1/1	0.99	0.04	23,23,23,23	0
2	ZN	B	400	1/1	1.00	0.04	20,20,20,20	0
2	ZN	C	400	1/1	1.00	0.05	20,20,20,20	0
2	ZN	H	500	1/1	1.00	0.05	32,32,32,32	0

6.5 Other polymers [i](#)

There are no such residues in this entry.