



Full wwPDB X-ray Structure Validation Report ⓘ

Oct 30, 2023 – 10:10 AM EDT

PDB ID : 8SX1
Title : PARP4 catalytic domain
Authors : Frigon, L.; Pascal, J.M.
Deposited on : 2023-05-19
Resolution : 4.20 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 : 4.02b-467
Xtrriage (Phenix) : 1.13
EDS : 2.36
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) : 2.36

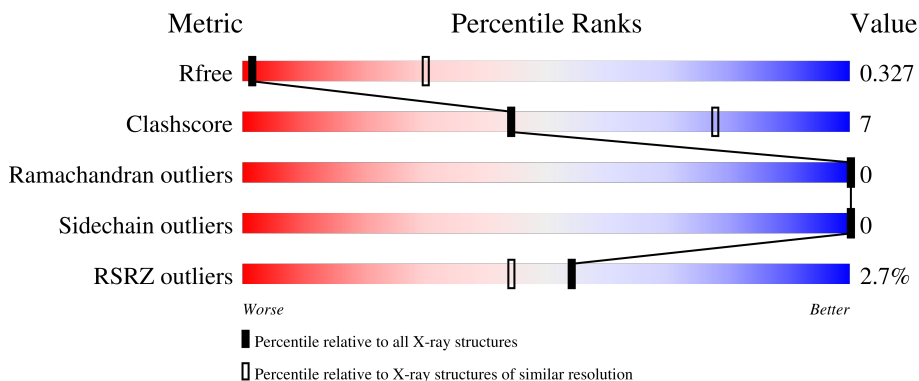
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 4.20 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.



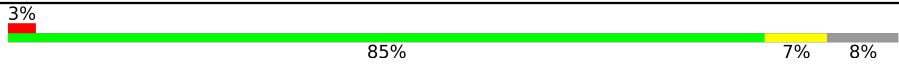

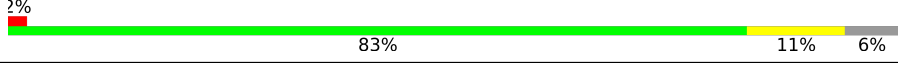
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	1005 (4.62-3.78)
Clashscore	141614	1044 (4.60-3.80)
Ramachandran outliers	138981	1000 (4.60-3.80)
Sidechain outliers	138945	1007 (4.62-3.78)
RSRZ outliers	127900	1063 (4.70-3.70)

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	333	 2% 85% 9% 6%
1	B	333	 2% 85% 9% 6%
1	C	333	 2% 84% 8% 8%
1	D	333	 2% 86% 7% 6%
1	E	333	 4% 85% 8% 6%

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Mol	Chain	Length	Quality of chain
1	F	333	 3% 85% 7% 8%
1	G	333	 3% 86% 8% 6%
1	H	333	 2% 83% 11% 6%

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 19491 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 mono-ADP-ribosyltransferase PARP4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	313	2448	1550	418	464	16	0	0	0
1	B	313	2448	1550	418	464	16	0	0	0
1	C	306	2400	1522	410	452	16	0	0	0
1	D	313	2448	1550	418	464	16	0	0	0
1	E	313	2448	1550	418	464	16	0	0	0
1	F	306	2400	1522	410	452	16	0	0	0
1	G	313	2448	1550	418	464	16	0	0	0
1	H	313	2448	1550	418	464	16	0	0	0

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	241	SER	-	expression tag	UNP Q9UKK3
B	241	SER	-	expression tag	UNP Q9UKK3
C	241	SER	-	expression tag	UNP Q9UKK3
D	241	SER	-	expression tag	UNP Q9UKK3
E	241	SER	-	expression tag	UNP Q9UKK3
F	241	SER	-	expression tag	UNP Q9UKK3
G	241	SER	-	expression tag	UNP Q9UKK3
H	241	SER	-	expression tag	UNP Q9UKK3

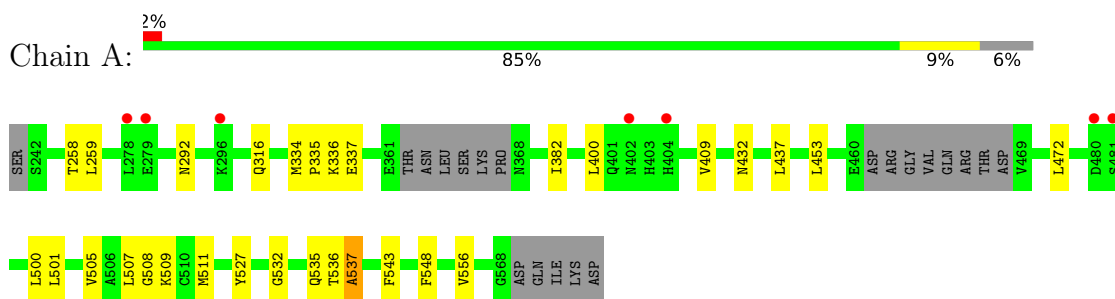
- Molecule 2 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	E	1	Total O 1 1	0	0
2	F	2	Total O 2 2	0	0

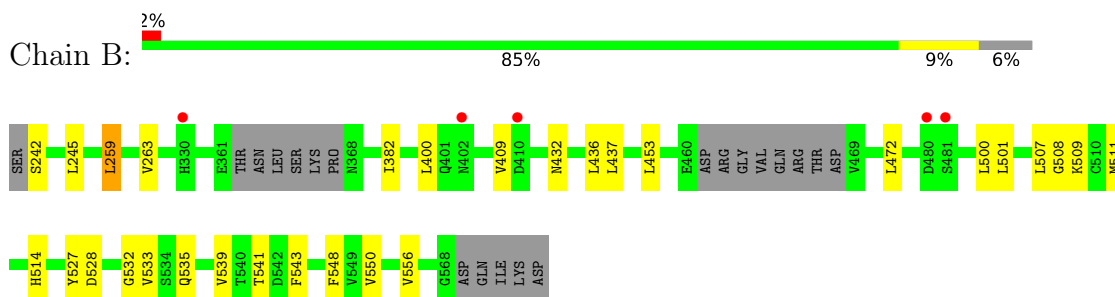
3 Residue-property plots [i](#)

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.

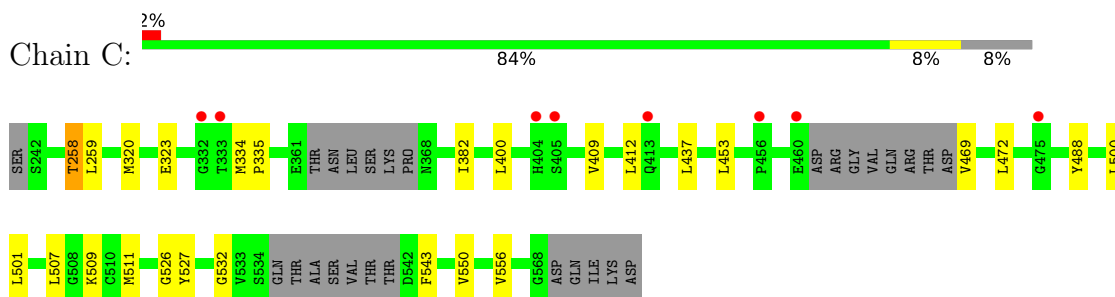
- Molecule 1: Protein mono-ADP-ribosyltransferase PARP4



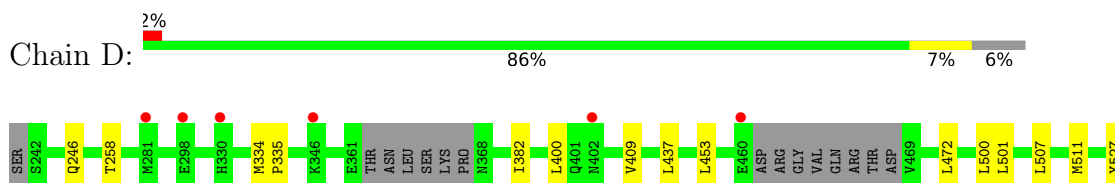
- Molecule 1: Protein mono-ADP-ribosyltransferase PARP4



- Molecule 1: Protein mono-ADP-ribosyltransferase PARP4

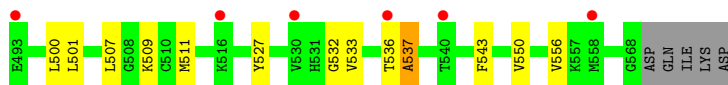
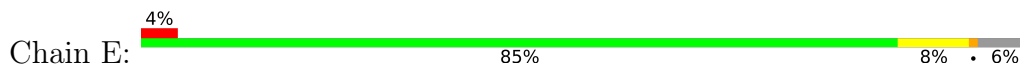


- Molecule 1: Protein mono-ADP-ribosyltransferase PARP4

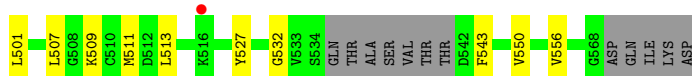
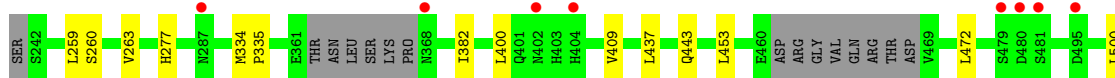
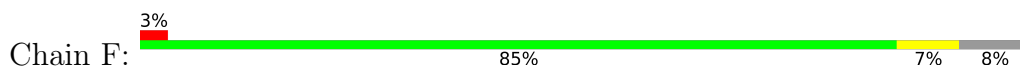




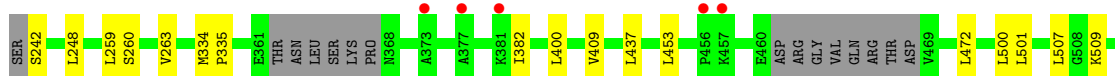
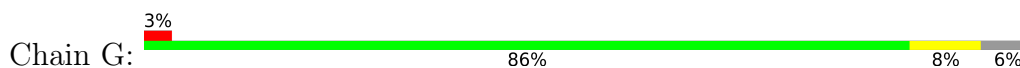
- Molecule 1: Protein mono-ADP-ribosyltransferase PARP4



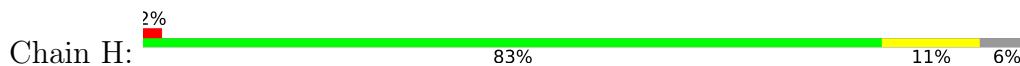
- Molecule 1: Protein mono-ADP-ribosyltransferase PARP4



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4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	126.58Å 71.58Å 163.97Å 90.00° 103.27° 90.00°	Depositor
Resolution (Å)	47.07 – 4.20 47.07 – 4.20	Depositor EDS
% Data completeness (in resolution range)	98.9 (47.07-4.20) 99.8 (47.07-4.20)	Depositor EDS
R_{merge}	0.16	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.87 (at 4.14Å)	Xtrriage
Refinement program	PHENIX 1.20.1_4487	Depositor
R, R_{free}	0.277 , 0.331 0.276 , 0.327	Depositor DCC
R_{free} test set	1070 reflections (5.03%)	wwPDB-VP
Wilson B-factor (Å ²)	139.4	Xtrriage
Anisotropy	0.453	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.24 , 117.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.40$, $\langle L^2 \rangle = 0.22$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.87	EDS
Total number of atoms	19491	wwPDB-VP
Average B, all atoms (Å ²)	187.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 41.56 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 2.3188e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

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

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	0.27	0/2486	0.53	3/3356 (0.1%)
1	B	0.29	0/2486	0.50	2/3356 (0.1%)
1	C	0.26	0/2437	0.50	3/3286 (0.1%)
1	D	0.27	0/2486	0.52	3/3356 (0.1%)
1	E	0.27	0/2486	0.54	5/3356 (0.1%)
1	F	0.28	0/2437	0.47	1/3286 (0.0%)
1	G	0.27	0/2486	0.50	2/3356 (0.1%)
1	H	0.28	0/2486	0.55	3/3356 (0.1%)
All	All	0.27	0/19790	0.51	22/26708 (0.1%)

There are no bond length outliers.

All (22) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	H	470	GLY	N-CA-C	-7.83	93.53	113.10
1	E	532	GLY	N-CA-C	-6.98	95.64	113.10
1	A	532	GLY	N-CA-C	-6.61	96.57	113.10
1	A	537	ALA	CB-CA-C	6.56	119.94	110.10
1	C	532	GLY	N-CA-C	-6.20	97.61	113.10
1	B	532	GLY	N-CA-C	-6.20	97.61	113.10
1	E	259	LEU	N-CA-CB	6.12	122.64	110.40
1	C	412	LEU	CB-CA-C	-5.99	98.82	110.20
1	D	537	ALA	CB-CA-C	5.88	118.92	110.10
1	H	532	GLY	N-CA-C	-5.85	98.48	113.10
1	A	537	ALA	N-CA-C	-5.70	95.61	111.00
1	D	258	THR	N-CA-C	-5.65	95.75	111.00
1	D	532	GLY	N-CA-C	-5.57	99.17	113.10
1	E	537	ALA	CB-CA-C	5.55	118.43	110.10
1	H	537	ALA	CB-CA-C	5.53	118.39	110.10
1	G	532	GLY	N-CA-C	-5.49	99.38	113.10
1	E	259	LEU	N-CA-C	-5.17	97.04	111.00
1	G	537	ALA	CB-CA-C	5.16	117.84	110.10
1	B	259	LEU	N-CA-CB	5.09	120.58	110.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	E	533	VAL	N-CA-C	-5.05	97.35	111.00
1	C	258	THR	N-CA-C	-5.04	97.39	111.00
1	F	532	GLY	N-CA-C	-5.01	100.56	113.10

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	2448	0	2501	54	0
1	B	2448	0	2501	34	1
1	C	2400	0	2452	29	0
1	D	2448	0	2501	43	0
1	E	2448	0	2501	29	1
1	F	2400	0	2452	25	0
1	G	2448	0	2501	32	1
1	H	2448	0	2501	53	0
2	E	1	0	0	0	0
2	F	2	0	0	0	0
All	All	19491	0	19910	259	2

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 7.

All (259) 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:505:VAL:HG12	1:A:507:LEU:CD1	1.45	1.43
1:A:505:VAL:CG1	1:A:507:LEU:HD11	1.63	1.28
1:F:277:HIS:CE1	1:F:443:GLN:OE1	1.88	1.27
1:A:505:VAL:CG1	1:A:507:LEU:CD1	2.19	1.20
1:A:505:VAL:HG12	1:A:507:LEU:HD12	1.14	1.08
1:C:258:THR:O	1:C:259:LEU:HD23	1.53	1.08
1:E:258:THR:O	1:E:259:LEU:HD23	1.58	1.04

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:507:LEU:HD23	1:C:550:VAL:CG1	1.89	1.01
1:A:505:VAL:HG11	1:A:507:LEU:HD11	1.40	1.01
1:G:242:SER:HB2	1:H:509:LYS:HE3	1.46	0.97
1:D:511:MET:SD	1:D:527:TYR:CE1	2.59	0.96
1:C:511:MET:SD	1:C:527:TYR:CE1	2.59	0.95
1:C:507:LEU:CD2	1:C:550:VAL:HG13	1.95	0.95
1:E:511:MET:SD	1:E:527:TYR:CE1	2.60	0.95
1:B:511:MET:SD	1:B:527:TYR:CE1	2.61	0.94
1:H:511:MET:SD	1:H:527:TYR:CE1	2.61	0.94
1:A:511:MET:SD	1:A:527:TYR:CE1	2.61	0.94
1:D:511:MET:SD	1:D:527:TYR:CD1	2.61	0.93
1:G:507:LEU:HD23	1:G:550:VAL:CG1	1.97	0.93
1:C:511:MET:SD	1:C:527:TYR:CD1	2.62	0.93
1:E:511:MET:SD	1:E:527:TYR:CD1	2.62	0.92
1:D:507:LEU:HD23	1:D:550:VAL:CG1	2.00	0.91
1:H:511:MET:SD	1:H:527:TYR:CD1	2.64	0.91
1:B:511:MET:SD	1:B:527:TYR:CD1	2.64	0.91
1:A:511:MET:SD	1:A:527:TYR:CD1	2.64	0.91
1:D:511:MET:SD	1:D:527:TYR:CZ	2.65	0.90
1:C:511:MET:SD	1:C:527:TYR:CZ	2.65	0.90
1:E:507:LEU:HD23	1:E:550:VAL:CG1	2.02	0.89
1:E:511:MET:SD	1:E:527:TYR:CZ	2.65	0.89
1:B:511:MET:SD	1:B:527:TYR:CZ	2.66	0.89
1:A:511:MET:SD	1:A:527:TYR:CZ	2.65	0.89
1:H:509:LYS:CD	1:H:526:GLY:O	2.21	0.88
1:H:511:MET:SD	1:H:527:TYR:CZ	2.66	0.88
1:G:507:LEU:CD2	1:G:550:VAL:HG13	2.06	0.85
1:C:511:MET:SD	1:C:527:TYR:CG	2.71	0.84
1:D:511:MET:SD	1:D:527:TYR:CG	2.71	0.83
1:A:507:LEU:HD21	1:A:548:PHE:HB3	1.60	0.83
1:D:511:MET:SD	1:D:527:TYR:CE2	2.72	0.83
1:C:511:MET:SD	1:C:527:TYR:CE2	2.72	0.82
1:E:511:MET:SD	1:E:527:TYR:CG	2.72	0.82
1:H:511:MET:SD	1:H:527:TYR:CG	2.73	0.82
1:A:511:MET:SD	1:A:527:TYR:CE2	2.73	0.82
1:F:277:HIS:NE2	1:F:443:GLN:OE1	2.11	0.82
1:D:507:LEU:CD2	1:D:550:VAL:HG13	2.10	0.82
1:B:511:MET:SD	1:B:527:TYR:CE2	2.73	0.82
1:C:507:LEU:CD2	1:C:550:VAL:CG1	2.54	0.82
1:E:511:MET:SD	1:E:527:TYR:CE2	2.73	0.82
1:H:511:MET:SD	1:H:527:TYR:CE2	2.73	0.82

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:511:MET:SD	1:B:527:TYR:CG	2.73	0.81
1:A:511:MET:SD	1:A:527:TYR:CG	2.73	0.81
1:B:514:HIS:HA	1:B:541:THR:HG22	1.61	0.81
1:E:507:LEU:CD2	1:E:550:VAL:HG13	2.12	0.80
1:D:511:MET:SD	1:D:527:TYR:CD2	2.74	0.80
1:C:511:MET:SD	1:C:527:TYR:CD2	2.75	0.79
1:F:260:SER:OG	1:F:263:VAL:HG23	1.83	0.79
1:A:511:MET:SD	1:A:527:TYR:CD2	2.76	0.79
1:E:511:MET:SD	1:E:527:TYR:CD2	2.76	0.79
1:H:511:MET:SD	1:H:527:TYR:CD2	2.76	0.79
1:G:260:SER:OG	1:G:263:VAL:HG23	1.83	0.78
1:G:242:SER:HB2	1:H:509:LYS:CE	2.13	0.78
1:B:511:MET:SD	1:B:527:TYR:CD2	2.76	0.78
1:E:255:ASN:OD1	1:E:369:PRO:HG3	1.85	0.77
1:G:507:LEU:HD23	1:G:550:VAL:HG13	1.66	0.76
1:G:242:SER:HB3	1:H:509:LYS:HD2	1.67	0.75
1:G:242:SER:CB	1:H:509:LYS:HD2	2.16	0.75
1:H:509:LYS:HD2	1:H:526:GLY:O	1.84	0.75
1:F:507:LEU:HD23	1:F:550:VAL:CG1	2.17	0.75
1:A:535:GLN:HG3	1:C:469:VAL:HG12	1.69	0.75
1:A:336:LYS:CB	1:D:535:GLN:NE2	2.49	0.74
1:B:533:VAL:HB	1:B:541:THR:HG21	1.69	0.74
1:A:337:GLU:CB	1:D:536:THR:O	2.36	0.73
1:A:335:PRO:HA	1:D:538:SER:HA	1.71	0.72
1:H:260:SER:OG	1:H:263:VAL:HG23	1.90	0.72
1:H:509:LYS:HD3	1:H:526:GLY:O	1.90	0.71
1:D:507:LEU:CD2	1:D:550:VAL:CG1	2.68	0.71
1:A:336:LYS:HB3	1:D:535:GLN:NE2	2.06	0.71
1:B:507:LEU:HD13	1:B:548:PHE:CD1	2.27	0.70
1:F:277:HIS:CE1	1:F:443:GLN:CD	2.64	0.70
1:A:337:GLU:HB3	1:D:536:THR:O	1.92	0.70
1:G:248:LEU:HD23	1:H:427:LEU:HD22	1.72	0.70
1:A:292:ASN:OD1	1:H:258:THR:O	2.10	0.69
1:G:509:LYS:HD2	1:G:526:GLY:O	1.93	0.69
1:A:336:LYS:HB2	1:D:535:GLN:NE2	2.07	0.68
1:A:258:THR:O	1:A:259:LEU:HD23	1.96	0.66
1:G:242:SER:CB	1:H:509:LYS:CD	2.73	0.66
1:B:507:LEU:HD23	1:B:550:VAL:HG13	1.78	0.65
1:E:507:LEU:HD23	1:E:550:VAL:HG13	1.70	0.64
1:F:511:MET:SD	1:F:513:LEU:HD21	2.38	0.64
1:F:507:LEU:HD23	1:F:550:VAL:HG13	1.78	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:245:LEU:O	1:H:248:LEU:HG	1.99	0.63
1:G:507:LEU:CD2	1:G:550:VAL:CG1	2.69	0.62
1:F:260:SER:OG	1:F:263:VAL:CG2	2.46	0.62
1:F:507:LEU:CD2	1:F:550:VAL:HG13	2.29	0.62
1:A:337:GLU:HB2	1:D:536:THR:O	1.98	0.62
1:A:336:LYS:HB2	1:D:535:GLN:HE22	1.63	0.62
1:G:242:SER:HB3	1:H:509:LYS:CD	2.29	0.62
1:H:507:LEU:HD23	1:H:550:VAL:CG1	2.29	0.62
1:G:260:SER:OG	1:G:263:VAL:CG2	2.48	0.61
1:A:337:GLU:CB	1:D:536:THR:C	2.69	0.60
1:A:507:LEU:CD2	1:A:548:PHE:HB3	2.31	0.60
1:G:259:LEU:HD11	1:G:263:VAL:HG11	1.83	0.60
1:A:316:GLN:CD	1:H:246:GLN:OE1	2.41	0.59
1:A:536:THR:O	1:A:537:ALA:C	2.40	0.59
1:H:507:LEU:HD23	1:H:550:VAL:HG13	1.85	0.58
1:H:259:LEU:HD11	1:H:263:VAL:HG11	1.85	0.57
1:C:507:LEU:HD21	1:C:550:VAL:HG13	1.82	0.57
1:H:260:SER:OG	1:H:263:VAL:CG2	2.53	0.56
1:G:248:LEU:CD2	1:H:427:LEU:HD22	2.35	0.56
1:E:536:THR:O	1:E:537:ALA:C	2.45	0.55
1:A:334:MET:O	1:D:540:THR:HG22	2.06	0.55
1:A:316:GLN:HB3	1:H:246:GLN:OE1	2.06	0.55
1:D:536:THR:O	1:D:537:ALA:C	2.45	0.54
1:H:536:THR:O	1:H:537:ALA:C	2.45	0.54
1:G:536:THR:O	1:G:537:ALA:C	2.46	0.54
1:F:259:LEU:HD11	1:F:263:VAL:CG1	2.38	0.54
1:H:510:CYS:SG	1:H:531:HIS:HB2	2.47	0.54
1:B:507:LEU:HD23	1:B:550:VAL:CG1	2.37	0.53
1:F:509:LYS:HE2	1:F:527:TYR:CD2	2.44	0.53
1:A:337:GLU:HB3	1:D:536:THR:C	2.26	0.53
1:A:509:LYS:HE2	1:A:527:TYR:CD2	2.44	0.52
1:E:509:LYS:HE2	1:E:527:TYR:CD2	2.45	0.52
1:B:507:LEU:CD1	1:B:548:PHE:CD1	2.92	0.52
1:F:259:LEU:HD12	1:F:260:SER:N	2.25	0.52
1:F:259:LEU:HD11	1:F:263:VAL:HG11	1.91	0.52
1:B:242:SER:N	1:B:245:LEU:HD12	2.24	0.51
1:F:277:HIS:ND1	1:F:443:GLN:CD	2.63	0.51
1:B:436:LEU:HD11	1:B:507:LEU:HD11	1.93	0.51
1:H:259:LEU:HD11	1:H:263:VAL:CG1	2.39	0.51
1:H:509:LYS:HB2	1:H:527:TYR:HA	1.92	0.51
1:G:259:LEU:HD11	1:G:263:VAL:CG1	2.40	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:336:LYS:CB	1:D:535:GLN:HE22	2.18	0.50
1:C:507:LEU:HD23	1:C:550:VAL:HG11	1.82	0.50
1:A:337:GLU:N	1:D:535:GLN:OE1	2.44	0.50
1:D:453:LEU:HD12	1:D:556:VAL:HG11	1.93	0.49
1:A:336:LYS:HD2	1:D:541:THR:N	2.28	0.49
1:B:432:ASN:HB3	1:B:508:GLY:HA2	1.94	0.49
1:C:320:MET:HG2	1:E:250:LEU:HD11	1.94	0.49
1:G:242:SER:HB2	1:H:509:LYS:CD	2.40	0.49
1:A:453:LEU:HD12	1:A:556:VAL:HG11	1.95	0.49
1:E:453:LEU:HD12	1:E:556:VAL:HG11	1.94	0.49
1:H:453:LEU:HD12	1:H:556:VAL:HG11	1.94	0.49
1:F:453:LEU:HD12	1:F:556:VAL:HG11	1.94	0.49
1:G:453:LEU:HD12	1:G:556:VAL:HG11	1.95	0.49
1:G:242:SER:CB	1:H:509:LYS:CE	2.89	0.49
1:B:507:LEU:CD2	1:B:550:VAL:HG13	2.43	0.48
1:H:507:LEU:CD2	1:H:550:VAL:HG13	2.43	0.48
1:C:453:LEU:HD12	1:C:556:VAL:HG11	1.95	0.48
1:F:382:ILE:HD12	1:F:382:ILE:N	2.29	0.48
1:G:382:ILE:N	1:G:382:ILE:HD12	2.28	0.48
1:C:382:ILE:N	1:C:382:ILE:HD12	2.28	0.48
1:E:382:ILE:N	1:E:382:ILE:HD12	2.28	0.48
1:B:453:LEU:HD12	1:B:556:VAL:HG11	1.95	0.48
1:D:400:LEU:HD21	1:D:409:VAL:HG11	1.96	0.48
1:H:382:ILE:N	1:H:382:ILE:HD12	2.28	0.48
1:A:382:ILE:HD12	1:A:382:ILE:N	2.28	0.48
1:B:382:ILE:N	1:B:382:ILE:HD12	2.28	0.48
1:E:255:ASN:HB3	1:E:369:PRO:HG3	1.95	0.48
1:D:382:ILE:HD12	1:D:382:ILE:N	2.28	0.48
1:H:259:LEU:HD12	1:H:260:SER:N	2.28	0.48
1:F:400:LEU:HD21	1:F:409:VAL:HG11	1.95	0.48
1:A:400:LEU:HD21	1:A:409:VAL:HG11	1.96	0.48
1:H:400:LEU:HD21	1:H:409:VAL:HG11	1.95	0.48
1:G:400:LEU:HD21	1:G:409:VAL:HG11	1.96	0.48
1:A:336:LYS:HB2	1:D:535:GLN:CD	2.34	0.47
1:A:336:LYS:HG3	1:D:540:THR:HA	1.96	0.47
1:D:246:GLN:OE1	1:E:316:GLN:HB3	2.15	0.47
1:A:472:LEU:HD21	1:A:543:PHE:CZ	2.50	0.47
1:D:472:LEU:HD21	1:D:543:PHE:CZ	2.50	0.47
1:E:400:LEU:HD21	1:E:409:VAL:HG11	1.96	0.47
1:E:472:LEU:HD21	1:E:543:PHE:CZ	2.50	0.47
1:B:400:LEU:HD21	1:B:409:VAL:HG11	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:509:LYS:HE2	1:B:527:TYR:CD2	2.48	0.47
1:C:323:GLU:OE2	1:E:254:MET:CE	2.62	0.47
1:F:259:LEU:HD11	1:F:263:VAL:HB	1.97	0.47
1:H:248:LEU:HD12	1:H:249:LEU:N	2.30	0.47
1:C:400:LEU:HD21	1:C:409:VAL:HG11	1.96	0.47
1:C:472:LEU:HD21	1:C:543:PHE:CZ	2.50	0.47
1:A:336:LYS:CB	1:D:535:GLN:CD	2.84	0.46
1:H:472:LEU:HD21	1:H:543:PHE:CZ	2.50	0.46
1:B:472:LEU:HD21	1:B:543:PHE:CZ	2.50	0.46
1:F:472:LEU:HD21	1:F:543:PHE:CZ	2.50	0.46
1:E:334:MET:O	1:E:335:PRO:C	2.54	0.46
1:G:472:LEU:HD21	1:G:543:PHE:CZ	2.50	0.46
1:G:259:LEU:HD12	1:G:260:SER:N	2.31	0.46
1:H:334:MET:O	1:H:335:PRO:C	2.54	0.46
1:B:500:LEU:C	1:B:500:LEU:HD23	2.37	0.45
1:D:500:LEU:HD23	1:D:500:LEU:C	2.37	0.45
1:C:500:LEU:C	1:C:500:LEU:HD23	2.37	0.45
1:A:500:LEU:HD23	1:A:500:LEU:C	2.37	0.45
1:D:334:MET:O	1:D:335:PRO:C	2.54	0.45
1:E:500:LEU:C	1:E:500:LEU:HD23	2.37	0.45
1:B:509:LYS:CE	1:B:527:TYR:CD2	3.00	0.45
1:G:242:SER:N	1:H:528:ASP:OD1	2.50	0.45
1:C:509:LYS:HD2	1:C:526:GLY:O	2.16	0.45
1:G:334:MET:O	1:G:335:PRO:C	2.54	0.45
1:G:500:LEU:C	1:G:500:LEU:HD23	2.37	0.45
1:H:500:LEU:C	1:H:500:LEU:HD23	2.37	0.45
1:D:511:MET:HG2	1:D:527:TYR:CB	2.47	0.44
1:E:507:LEU:CD2	1:E:550:VAL:CG1	2.74	0.44
1:F:500:LEU:HD23	1:F:500:LEU:C	2.37	0.44
1:C:509:LYS:HD3	1:C:527:TYR:CD2	2.52	0.44
1:C:511:MET:HG2	1:C:527:TYR:CB	2.48	0.44
1:F:334:MET:O	1:F:335:PRO:C	2.55	0.44
1:A:334:MET:O	1:A:335:PRO:C	2.55	0.44
1:B:511:MET:HG2	1:B:527:TYR:CG	2.53	0.44
1:H:259:LEU:HD12	1:H:260:SER:H	1.83	0.44
1:A:511:MET:HG2	1:A:527:TYR:CG	2.53	0.44
1:C:511:MET:HG2	1:C:527:TYR:CG	2.53	0.44
1:A:511:MET:HG2	1:A:527:TYR:CB	2.48	0.44
1:B:535:GLN:NE2	1:B:539:VAL:HB	2.33	0.44
1:D:511:MET:HG2	1:D:527:TYR:CG	2.52	0.44
1:D:507:LEU:HD23	1:D:550:VAL:HG11	1.95	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:432:ASN:HB3	1:A:508:GLY:HA2	2.00	0.43
1:B:507:LEU:HD11	1:B:548:PHE:HB3	2.00	0.43
1:A:336:LYS:HE3	1:D:540:THR:HB	1.99	0.43
1:E:511:MET:HG2	1:E:527:TYR:CG	2.53	0.43
1:H:511:MET:HG2	1:H:527:TYR:CB	2.49	0.43
1:E:511:MET:HG2	1:E:527:TYR:CB	2.48	0.43
1:B:511:MET:HG2	1:B:527:TYR:CB	2.48	0.43
1:F:277:HIS:ND1	1:F:443:GLN:NE2	2.65	0.43
1:F:500:LEU:HD23	1:F:501:LEU:N	2.34	0.42
1:A:500:LEU:HD23	1:A:501:LEU:N	2.34	0.42
1:D:500:LEU:HD23	1:D:501:LEU:N	2.34	0.42
1:G:500:LEU:HD23	1:G:501:LEU:N	2.34	0.42
1:C:437:LEU:N	1:C:437:LEU:HD12	2.34	0.42
1:H:511:MET:HG2	1:H:527:TYR:CG	2.54	0.42
1:D:437:LEU:HD12	1:D:437:LEU:N	2.35	0.42
1:F:259:LEU:HD11	1:F:263:VAL:CB	2.50	0.42
1:E:500:LEU:HD23	1:E:501:LEU:N	2.34	0.42
1:H:437:LEU:N	1:H:437:LEU:HD12	2.35	0.42
1:F:437:LEU:HD12	1:F:437:LEU:N	2.34	0.42
1:G:242:SER:HB3	1:H:509:LYS:CG	2.49	0.42
1:H:259:LEU:HD11	1:H:263:VAL:CB	2.50	0.42
1:H:500:LEU:HD23	1:H:501:LEU:N	2.34	0.42
1:H:509:LYS:CB	1:H:527:TYR:HA	2.50	0.42
1:C:500:LEU:HD23	1:C:501:LEU:N	2.35	0.42
1:H:507:LEU:HD13	1:H:548:PHE:CD1	2.55	0.42
1:A:437:LEU:HD12	1:A:437:LEU:N	2.34	0.41
1:B:259:LEU:HD11	1:B:263:VAL:HG11	2.02	0.41
1:D:511:MET:CG	1:D:527:TYR:CG	3.02	0.41
1:E:437:LEU:N	1:E:437:LEU:HD12	2.34	0.41
1:B:436:LEU:CD1	1:B:507:LEU:HD11	2.50	0.41
1:G:437:LEU:N	1:G:437:LEU:HD12	2.34	0.41
1:A:336:LYS:CG	1:D:540:THR:HA	2.49	0.41
1:E:511:MET:CG	1:E:527:TYR:CG	3.04	0.41
1:B:437:LEU:N	1:B:437:LEU:HD12	2.34	0.41
1:C:334:MET:O	1:C:335:PRO:C	2.58	0.41
1:B:500:LEU:HD23	1:B:501:LEU:N	2.34	0.41
1:B:511:MET:CG	1:B:527:TYR:CG	3.04	0.41
1:A:511:MET:CG	1:A:527:TYR:CG	3.03	0.41
1:B:242:SER:OG	1:B:245:LEU:HG	2.20	0.41
1:C:511:MET:CG	1:C:527:TYR:CG	3.03	0.41
1:A:336:LYS:HD2	1:D:540:THR:HA	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:509:LYS:CE	1:A:527:TYR:CD2	3.04	0.40
1:H:257:SER:O	1:H:258:THR:C	2.60	0.40
1:B:535:GLN:N	1:B:543:PHE:O	2.54	0.40
1:G:509:LYS:HD3	1:G:527:TYR:CD2	2.57	0.40
1:H:259:LEU:HD11	1:H:263:VAL:HB	2.03	0.40
1:A:537:ALA:HB1	1:C:488:TYR:HE1	1.86	0.40

All (2) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:245:LEU:CD1	1:B:528:ASP:OD1[2_655]	1.55	0.65
1:E:337:GLU:OE2	1:G:538:SER:OG[2_646]	2.03	0.17

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	307/333 (92%)	293 (95%)	14 (5%)	0	100	100
1	B	307/333 (92%)	293 (95%)	14 (5%)	0	100	100
1	C	298/333 (90%)	287 (96%)	11 (4%)	0	100	100
1	D	307/333 (92%)	296 (96%)	11 (4%)	0	100	100
1	E	307/333 (92%)	295 (96%)	12 (4%)	0	100	100
1	F	298/333 (90%)	285 (96%)	13 (4%)	0	100	100
1	G	307/333 (92%)	294 (96%)	13 (4%)	0	100	100
1	H	307/333 (92%)	294 (96%)	13 (4%)	0	100	100
All	All	2438/2664 (92%)	2337 (96%)	101 (4%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains [i](#)

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	280/299 (94%)	280 (100%)	0	100	100
1	B	280/299 (94%)	280 (100%)	0	100	100
1	C	274/299 (92%)	274 (100%)	0	100	100
1	D	280/299 (94%)	280 (100%)	0	100	100
1	E	280/299 (94%)	280 (100%)	0	100	100
1	F	274/299 (92%)	274 (100%)	0	100	100
1	G	280/299 (94%)	280 (100%)	0	100	100
1	H	280/299 (94%)	280 (100%)	0	100	100
All	All	2228/2392 (93%)	2228 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	C	316	GLN
1	E	316	GLN
1	H	316	GLN

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](#)

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

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	313/333 (93%)	-0.09	7 (2%) 62 52	106, 178, 269, 395	0
1	B	313/333 (93%)	-0.11	5 (1%) 72 62	92, 170, 262, 381	0
1	C	306/333 (91%)	0.01	8 (2%) 56 45	95, 178, 259, 425	0
1	D	313/333 (93%)	0.06	8 (2%) 56 45	99, 197, 304, 491	0
1	E	313/333 (93%)	0.11	13 (4%) 36 29	97, 173, 272, 350	0
1	F	306/333 (91%)	0.11	9 (2%) 51 41	97, 182, 285, 397	0
1	G	313/333 (93%)	0.03	10 (3%) 47 37	134, 190, 290, 401	0
1	H	313/333 (93%)	-0.03	8 (2%) 56 45	92, 172, 270, 369	0
All	All	2490/2664 (93%)	0.01	68 (2%) 54 44	92, 182, 281, 491	0

All (68) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	E	540	THR	5.6
1	C	405	SER	5.2
1	E	402	ASN	5.2
1	F	480	ASP	4.6
1	F	402	ASN	4.5
1	F	481	SER	4.4
1	F	368	ASN	4.3
1	E	404	HIS	4.0
1	D	281	MET	4.0
1	B	480	ASP	3.9
1	C	460	GLU	3.6
1	G	536	THR	3.4
1	H	456	PRO	3.4
1	C	333	THR	3.4
1	B	410	ASP	3.3
1	H	555	GLN	3.3

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Mol	Chain	Res	Type	RSRZ
1	G	457	LYS	3.3
1	H	402	ASN	3.2
1	G	568	GLY	3.1
1	A	279	GLU	3.1
1	E	480	ASP	3.0
1	E	536	THR	3.0
1	C	404	HIS	3.0
1	E	516	LYS	2.9
1	D	536	THR	2.9
1	B	330	HIS	2.9
1	C	413	GLN	2.9
1	A	404	HIS	2.8
1	C	456	PRO	2.8
1	G	555	GLN	2.8
1	D	330	HIS	2.8
1	H	455	LEU	2.7
1	G	523	ALA	2.7
1	A	480	ASP	2.7
1	C	332	GLY	2.7
1	D	402	ASN	2.6
1	A	481	SER	2.6
1	E	530	VAL	2.6
1	D	540	THR	2.6
1	C	475	GLY	2.5
1	F	479	SER	2.4
1	G	373	ALA	2.4
1	E	493	GLU	2.3
1	D	346	LYS	2.3
1	G	381	LYS	2.3
1	E	558	MET	2.3
1	F	516	LYS	2.3
1	H	404	HIS	2.3
1	E	403	HIS	2.2
1	B	481	SER	2.2
1	G	551	TYR	2.2
1	D	460	GLU	2.2
1	E	405	SER	2.2
1	B	402	ASN	2.2
1	G	456	PRO	2.2
1	E	481	SER	2.2
1	F	404	HIS	2.2
1	F	287	ASN	2.1

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Mol	Chain	Res	Type	RSRZ
1	E	338	VAL	2.1
1	H	506	ALA	2.1
1	A	402	ASN	2.1
1	D	298	GLU	2.1
1	F	495	ASP	2.1
1	H	405	SER	2.1
1	A	278	LEU	2.1
1	H	373	ALA	2.1
1	A	296	LYS	2.0
1	G	377	ALA	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](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.