



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 10:11 AM UTC

PDB ID : 8GRE / pdb_00008gre
Title : F-box protein in complex with skp1(FL) and substrate
Authors : Nishio, K.; Nakatsukasa, K.; Kamura, T.; Mizushima, T.
Deposited on : 2022-09-01
Resolution : 2.30 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

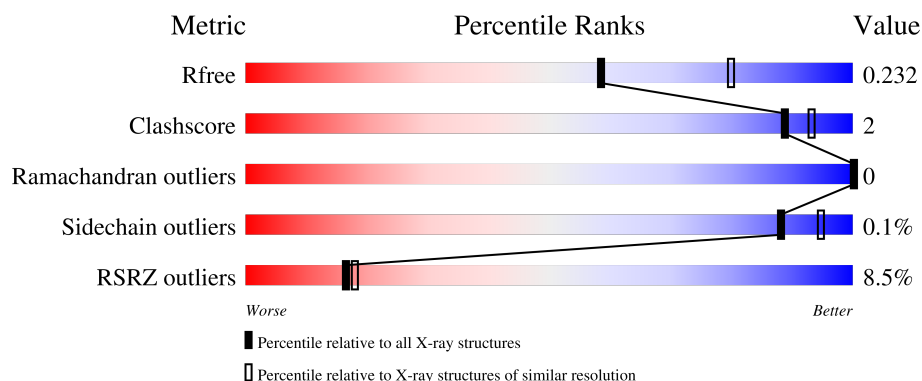
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.30 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	6319 (2.30-2.30)
Clashscore	190562	6919 (2.30-2.30)
Ramachandran outliers	187476	6854 (2.30-2.30)
Sidechain outliers	187428	6854 (2.30-2.30)
RSRZ outliers	180081	6325 (2.30-2.30)

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	460	4% 90% 6% 5%
1	B	460	5% 90% 5% 5%
2	C	369	6% 86% 5% 8%
3	D	194	24% 44% 52%

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 10749 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 Citrate synthase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	438	Total	C	N	O	S	0	0	0
			3460	2213	582	658	7			
1	B	438	Total	C	N	O	S	0	0	0
			3460	2212	583	658	7			

- Molecule 2 is a protein called F-box protein UCC1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	338	Total	C	N	O	S	0	0	0
			2785	1817	456	501	11			

- Molecule 3 is a protein called E3 ubiquitin ligase complex SCF subunit.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	D	94	Total	C	N	O	S	0	0	0
			776	489	134	150	3			

- Molecule 4 is GLYCEROL (CCD ID: GOL) (formula: C₃H₈O₃).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			6	3	3		
4	A	1	Total	C	O	0	0
			6	3	3		
4	C	1	Total	C	O	0	0
			6	3	3		
4	C	1	Total	C	O	0	0
			6	3	3		

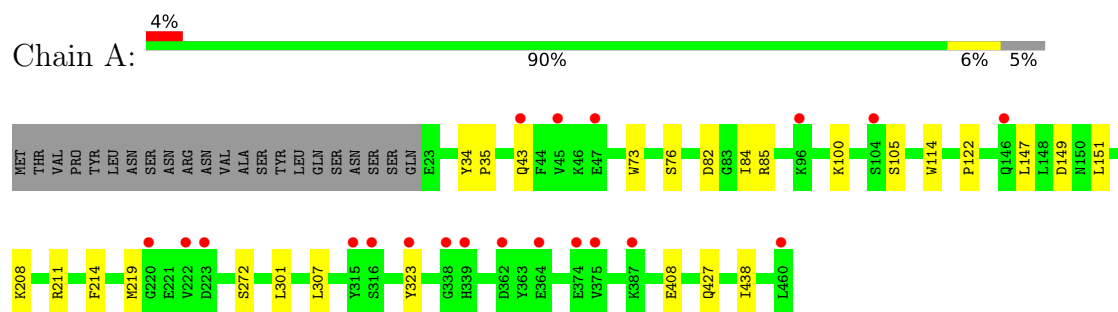
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	73	Total	O	0	0
			73	73		
5	B	68	Total	O	0	0
			68	68		
5	C	93	Total	O	0	0
			93	93		
5	D	10	Total	O	0	0
			10	10		

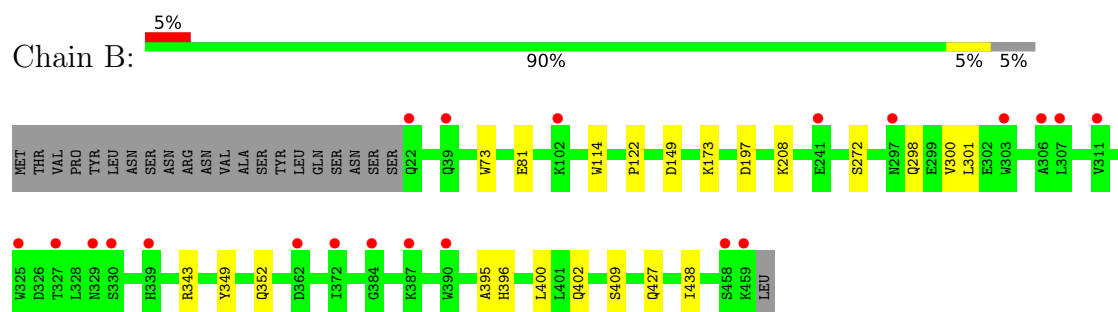
3 Residue-property plots [i](#)

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.

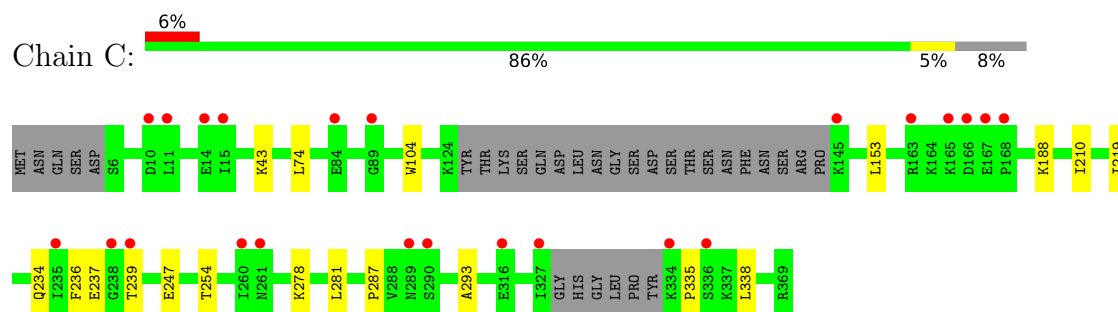
- Molecule 1: Citrate synthase



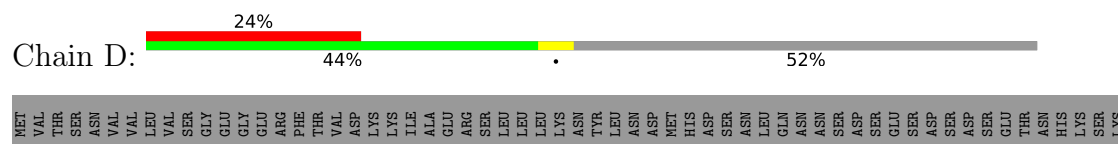
- Molecule 1: Citrate synthase

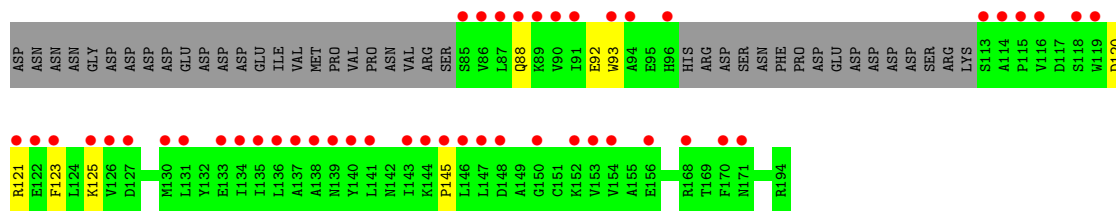


- Molecule 2: F-box protein UCC1



- Molecule 3: E3 ubiquitin ligase complex SCF subunit





4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	77.59Å 150.94Å 160.29Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	37.71 – 2.30 37.71 – 2.30	Depositor EDS
% Data completeness (in resolution range)	98.8 (37.71-2.30) 92.8 (37.71-2.30)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.40 (at 2.29Å)	Xtriage
Refinement program	PHENIX 1.18.2_3874	Depositor
R, R_{free}	0.206 , 0.232 0.207 , 0.232	Depositor DCC
R_{free} test set	1986 reflections (2.34%)	wwPDB-VP
Wilson B-factor (Å ²)	36.4	Xtriage
Anisotropy	0.302	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 37.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	10749	wwPDB-VP
Average B, all atoms (Å ²)	51.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.88% 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: GOL

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	0.09	0/3541	0.26	0/4795
1	B	0.08	0/3541	0.25	0/4796
2	C	0.10	0/2864	0.27	0/3896
3	D	0.09	0/790	0.29	0/1067
All	All	0.09	0/10736	0.26	0/14554

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	3460	0	3434	13	0
1	B	3460	0	3431	11	0
2	C	2785	0	2773	10	0
3	D	776	0	754	5	0
4	A	12	0	16	0	0
4	C	12	0	16	0	0
5	A	73	0	0	0	0
5	B	68	0	0	0	0
5	C	93	0	0	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	D	10	0	0	0	0
All	All	10749	0	10424	39	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 2.

All (39) 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)
2:C:293:ALA:HB1	2:C:338:LEU:HD11	1.83	0.60
1:B:272:SER:HB2	1:B:438:ILE:HA	1.92	0.51
2:C:219:ILE:HG13	2:C:287:PRO:HA	1.93	0.51
1:A:211:ARG:HG3	1:A:219:MET:HG2	1.93	0.51
1:A:272:SER:HB2	1:A:438:ILE:HA	1.92	0.51
2:C:74:LEU:HD11	2:C:335:PRO:HG2	1.92	0.50
3:D:93:TRP:HH2	3:D:145:PRO:HB2	1.75	0.50
1:A:214:PHE:CD1	1:A:408:GLU:HG2	2.50	0.46
1:B:352:GLN:HB3	1:B:400:LEU:HD11	1.97	0.46
1:A:82:ASP:OD2	1:A:85:ARG:NH2	2.45	0.46
3:D:93:TRP:CH2	3:D:145:PRO:HB2	2.50	0.46
1:B:301:LEU:HD21	1:B:402:GLN:HE21	1.80	0.46
2:C:188:LYS:HB2	2:C:254:THR:HG22	1.98	0.46
1:B:73:TRP:CE3	1:B:427:GLN:HG2	2.52	0.45
3:D:120:ASP:HA	3:D:123:PHE:HB3	1.97	0.45
1:B:300:VAL:HG11	1:B:395:ALA:HA	1.99	0.45
1:B:81:GLU:OE1	1:B:343:ARG:NH1	2.50	0.45
1:B:149:ASP:OD1	1:B:208:LYS:HE3	2.17	0.44
2:C:153:LEU:HD23	2:C:247:GLU:HA	1.99	0.44
2:C:234:GLN:HA	2:C:237:GLU:HG3	1.99	0.44
1:A:76:SER:HB2	1:A:84:ILE:HD11	1.99	0.44
1:B:114:TRP:CD2	1:B:122:PRO:HB3	2.52	0.44
1:A:147:LEU:O	1:A:151:LEU:HG	2.17	0.44
1:A:307:LEU:HD13	1:A:323:TYR:CD1	2.54	0.43
3:D:121:ARG:O	3:D:125:LYS:HG3	2.19	0.43
2:C:210:ILE:HD11	2:C:281:LEU:HB3	2.01	0.42
2:C:278:LYS:NZ	5:C:505:HOH:O	2.51	0.42
2:C:43:LYS:HB2	2:C:104:TRP:CD1	2.55	0.42
1:B:173:LYS:NZ	1:B:197:ASP:OD2	2.51	0.42
2:C:236:PHE:O	2:C:239:THR:HG22	2.20	0.41
1:A:100:LYS:HD3	1:A:105:SER:HA	2.03	0.41
1:A:114:TRP:CD2	1:A:122:PRO:HB3	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:301:LEU:HD12	1:A:301:LEU:HA	1.93	0.41
1:A:149:ASP:OD1	1:A:208:LYS:HE3	2.21	0.41
1:B:298:GLN:HG3	1:B:409:SER:HB2	2.03	0.41
3:D:88:GLN:O	3:D:92:GLU:HG3	2.21	0.41
1:B:349:TYR:CD2	1:B:396:HIS:HB2	2.56	0.40
1:A:34:TYR:CG	1:A:35:PRO:HD3	2.57	0.40
1:A:73:TRP:CZ3	1:A:427:GLN:HG2	2.56	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	436/460 (95%)	426 (98%)	10 (2%)	0	100	100
1	B	436/460 (95%)	428 (98%)	8 (2%)	0	100	100
2	C	332/369 (90%)	325 (98%)	7 (2%)	0	100	100
3	D	90/194 (46%)	87 (97%)	3 (3%)	0	100	100
All	All	1294/1483 (87%)	1266 (98%)	28 (2%)	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	375/396 (95%)	374 (100%)	1 (0%)	86	93
1	B	375/396 (95%)	375 (100%)	0	100	100
2	C	309/337 (92%)	309 (100%)	0	100	100
3	D	83/179 (46%)	83 (100%)	0	100	100
All	All	1142/1308 (87%)	1141 (100%)	1 (0%)	88	95

All (1) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	43	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (8) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	180	GLN
1	A	298	GLN
1	B	95	GLN
1	B	234	ASN
1	B	383	HIS
2	C	25	ASN
2	C	211	ASN
2	C	305	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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

4 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
4	GOL	C	402	-	5,5,5	0.91	0	5,5,5	1.10	0
4	GOL	A	501	-	5,5,5	0.93	0	5,5,5	1.10	0
4	GOL	C	401	-	5,5,5	0.92	0	5,5,5	1.07	0
4	GOL	A	502	-	5,5,5	0.94	0	5,5,5	1.08	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	GOL	C	402	-	-	0/4/4/4	-
4	GOL	A	501	-	-	2/4/4/4	-
4	GOL	C	401	-	-	2/4/4/4	-
4	GOL	A	502	-	-	0/4/4/4	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	501	GOL	O1-C1-C2-C3
4	C	401	GOL	O1-C1-C2-C3
4	A	501	GOL	O1-C1-C2-O2
4	C	401	GOL	O1-C1-C2-O2

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	438/460 (95%)	0.51	20 (4%) 37 39	25, 48, 72, 86	0
1	B	438/460 (95%)	0.59	21 (4%) 35 37	27, 50, 79, 96	0
2	C	338/369 (91%)	0.41	23 (6%) 23 25	26, 41, 71, 91	0
3	D	94/194 (48%)	2.28	47 (50%) 0 0	33, 88, 121, 129	0
All	All	1308/1483 (88%)	0.64	111 (8%) 16 18	25, 48, 83, 129	0

All (111) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	D	114	ALA	8.5
3	D	86	VAL	6.3
3	D	123	PHE	6.3
3	D	93	TRP	6.1
3	D	85	SER	5.8
3	D	126	VAL	5.6
3	D	94	ALA	5.4
3	D	145	PRO	5.2
3	D	140	TYR	5.2
3	D	119	TRP	4.8
3	D	138	ALA	4.6
2	C	166	ASP	4.6
3	D	144	LYS	4.6
3	D	127	ASP	4.6
3	D	96	HIS	4.5
3	D	87	LEU	4.5
3	D	143	ILE	4.5
1	A	460	LEU	4.4
1	B	330	SER	4.2
1	B	102	LYS	4.1
3	D	116	VAL	4.0

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Mol	Chain	Res	Type	RSRZ
2	C	145	LYS	4.0
3	D	141	LEU	3.9
1	B	384	GLY	3.8
3	D	122	GLU	3.8
3	D	118	SER	3.8
3	D	137	ALA	3.7
1	A	387	LYS	3.7
3	D	91	ILE	3.6
3	D	88	GLN	3.5
1	B	22	GLN	3.5
2	C	168	PRO	3.5
3	D	115	PRO	3.5
3	D	130	MET	3.5
1	B	339	HIS	3.3
3	D	147	LEU	3.3
3	D	170	PHE	3.2
1	A	315	TYR	3.2
1	A	220	GLY	3.1
3	D	113	SER	3.1
3	D	152	LYS	2.9
3	D	134	ILE	2.9
2	C	14	GLU	2.9
3	D	90	VAL	2.8
1	A	104	SER	2.8
1	B	458	SER	2.8
1	B	459	LYS	2.8
2	C	165	LYS	2.8
1	A	338	GLY	2.7
3	D	156	GLU	2.7
3	D	153	VAL	2.7
2	C	15	ILE	2.7
2	C	11	LEU	2.7
2	C	334	LYS	2.6
1	A	323	TYR	2.6
2	C	336	SER	2.6
1	B	329	ASN	2.6
1	B	362	ASP	2.6
3	D	148	ASP	2.6
2	C	327	ILE	2.6
3	D	146	LEU	2.5
1	B	327	THR	2.5
1	A	375	VAL	2.5

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Mol	Chain	Res	Type	RSRZ
2	C	260	ILE	2.5
1	B	307	LEU	2.5
2	C	238	GLY	2.5
3	D	121	ARG	2.5
3	D	135	ILE	2.5
1	B	306	ALA	2.5
3	D	131	LEU	2.4
2	C	289	ASN	2.4
3	D	139	ASN	2.4
1	A	45	VAL	2.4
3	D	136	LEU	2.4
2	C	89	GLY	2.4
1	A	362	ASP	2.4
1	A	223	ASP	2.3
2	C	235	ILE	2.3
3	D	133	GLU	2.3
1	B	303	TRP	2.3
3	D	89	LYS	2.3
3	D	171	ASN	2.3
3	D	168	ARG	2.3
1	B	39	GLN	2.3
1	A	222	VAL	2.3
1	A	316	SER	2.3
2	C	290	SER	2.3
1	A	364	GLU	2.3
2	C	167	GLU	2.2
2	C	10	ASP	2.2
1	A	146	GLN	2.2
1	A	339	HIS	2.2
2	C	316	GLU	2.2
1	B	325	TRP	2.2
1	B	387	LYS	2.2
2	C	163	ARG	2.1
1	A	96	LYS	2.1
1	A	43	GLN	2.1
3	D	125	LYS	2.1
2	C	84	GLU	2.1
1	B	297	ASN	2.1
2	C	261	ASN	2.1
1	B	390	TRP	2.1
3	D	150	GLY	2.1
3	D	154	VAL	2.1

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Mol	Chain	Res	Type	RSRZ
1	A	47	GLU	2.0
1	B	311	VAL	2.0
1	A	374	GLU	2.0
1	B	241	GLU	2.0
2	C	239	THR	2.0
1	B	372	ILE	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 oligosaccharides in this entry.

6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
4	GOL	A	502	6/6	0.68	0.16	68,74,75,76	0
4	GOL	C	402	6/6	0.71	0.21	55,59,62,64	0
4	GOL	A	501	6/6	0.88	0.15	36,46,50,51	0
4	GOL	C	401	6/6	0.89	0.14	56,58,61,72	0

6.5 Other polymers [i](#)

There are no such residues in this entry.