



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 17, 2026 – 11:28 PM UTC

PDB ID : 6WP0 / pdb_00006wp0
Title : The Crystal Structure of Domain-Swapped Trimer Q108K:T51D variant of HCRBPII
Authors : Ghanbarpour, A.; Geiger, J.
Deposited on : 2020-04-26
Resolution : 2.78 Å (reported)

This is a wwPDB X-ray Structure Validation Summary 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

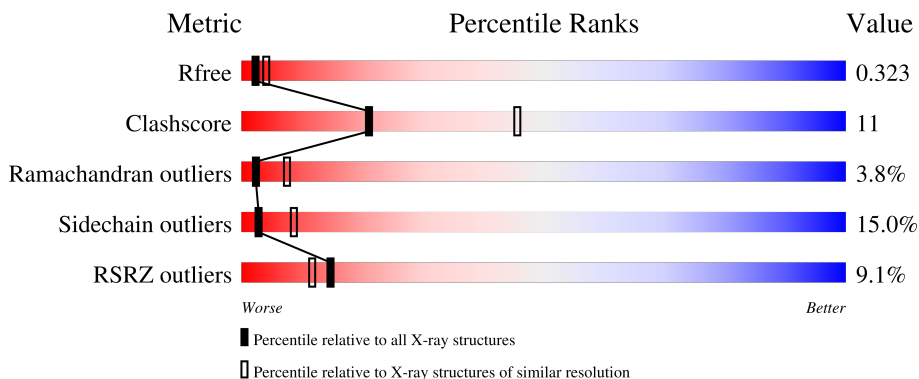
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.78 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	5248 (2.80-2.76)
Clashscore	190562	5693 (2.80-2.76)
Ramachandran outliers	187476	5590 (2.80-2.76)
Sidechain outliers	187428	5592 (2.80-2.76)
RSRZ outliers	180081	5251 (2.80-2.76)

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	133	
1	B	133	
1	C	133	
1	D	133	
1	E	133	

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Mol	Chain	Length	Quality of chain
1	F	133	
1	G	133	
1	H	133	
1	I	133	
1	J	133	
1	K	133	
1	L	133	

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 12908 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 Retinol-binding protein 2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	133	1076	675	185	211	5	0	0	0
1	B	133	1056	663	178	210	5	0	1	0
1	C	133	1078	679	181	213	5	0	1	0
1	D	133	1064	667	182	210	5	0	0	0
1	E	133	1050	659	176	210	5	0	0	0
1	F	133	1066	667	180	214	5	0	0	0
1	G	133	1058	667	177	209	5	0	0	0
1	H	133	1079	678	183	213	5	0	0	0
1	I	133	1046	655	177	209	5	0	0	0
1	J	133	1046	652	174	215	5	0	0	0
1	K	133	1052	661	174	212	5	0	0	0
1	L	133	1040	656	173	206	5	0	0	0

There are 24 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	51	ASP	THR	engineered mutation	UNP P50120
A	108	LYS	GLN	engineered mutation	UNP P50120
B	51	ASP	THR	engineered mutation	UNP P50120
B	108	LYS	GLN	engineered mutation	UNP P50120
C	51	ASP	THR	engineered mutation	UNP P50120

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Chain	Residue	Modelled	Actual	Comment	Reference
C	108	LYS	GLN	engineered mutation	UNP P50120
D	51	ASP	THR	engineered mutation	UNP P50120
D	108	LYS	GLN	engineered mutation	UNP P50120
E	51	ASP	THR	engineered mutation	UNP P50120
E	108	LYS	GLN	engineered mutation	UNP P50120
F	51	ASP	THR	engineered mutation	UNP P50120
F	108	LYS	GLN	engineered mutation	UNP P50120
G	51	ASP	THR	engineered mutation	UNP P50120
G	108	LYS	GLN	engineered mutation	UNP P50120
H	51	ASP	THR	engineered mutation	UNP P50120
H	108	LYS	GLN	engineered mutation	UNP P50120
I	51	ASP	THR	engineered mutation	UNP P50120
I	108	LYS	GLN	engineered mutation	UNP P50120
J	51	ASP	THR	engineered mutation	UNP P50120
J	108	LYS	GLN	engineered mutation	UNP P50120
K	51	ASP	THR	engineered mutation	UNP P50120
K	108	LYS	GLN	engineered mutation	UNP P50120
L	51	ASP	THR	engineered mutation	UNP P50120
L	108	LYS	GLN	engineered mutation	UNP P50120

- Molecule 2 is GLYCEROL (CCD ID: GOL) (formula: C₃H₈O₃).



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

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	C	O	0	0
			6	3	3		
2	A	1	Total	C	O	0	0
			6	3	3		
2	B	1	Total	C	O	0	0
			6	3	3		
2	B	1	Total	C	O	0	0
			6	3	3		
2	B	1	Total	C	O	0	0
			6	3	3		
2	B	1	Total	C	O	0	0
			6	3	3		
2	D	1	Total	C	O	0	0
			6	3	3		
2	E	1	Total	C	O	0	0
			6	3	3		
2	E	1	Total	C	O	0	0
			6	3	3		
2	G	1	Total	C	O	0	0
			6	3	3		
2	H	1	Total	C	O	0	0
			6	3	3		
2	J	1	Total	C	O	0	0
			6	3	3		
2	J	1	Total	C	O	0	0
			6	3	3		
2	J	1	Total	C	O	0	0
			6	3	3		
2	J	1	Total	C	O	0	0
			6	3	3		
2	K	1	Total	C	O	0	0
			6	3	3		
2	K	1	Total	C	O	0	0
			6	3	3		
2	L	1	Total	C	O	0	0
			6	3	3		
2	L	1	Total	C	O	0	0
			6	3	3		

- Molecule 3 is ACETATE ION (CCD ID: ACT) (formula: C₂H₃O₂).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	D	1	Total C O 4 2 2	0	0
3	J	1	Total C O 4 2 2	0	0

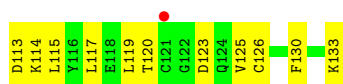
- Molecule 4 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	6	Total O 6 6	0	0
4	B	6	Total O 6 6	0	0
4	C	6	Total O 6 6	0	0
4	D	1	Total O 1 1	0	0
4	E	7	Total O 7 7	0	0
4	F	8	Total O 8 8	0	0
4	G	3	Total O 3 3	0	0
4	H	2	Total O 2 2	0	0
4	I	7	Total O 7 7	0	0
4	J	7	Total O 7 7	0	0

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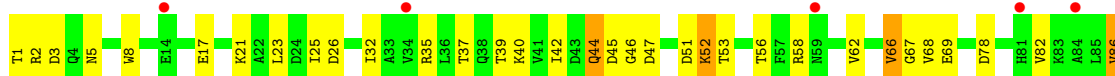
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	K	4	Total O 4 4	0	0
4	L	6	Total O 6 6	0	0



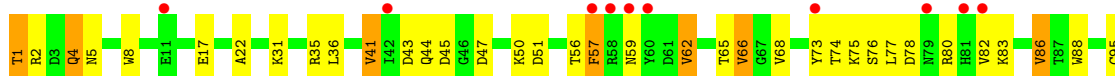
- Molecule 1: Retinol-binding protein 2



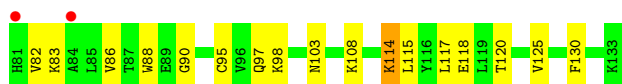
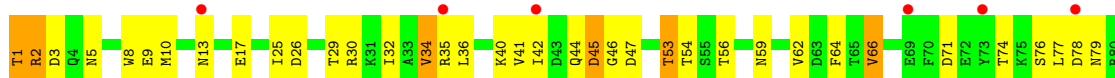
- Molecule 1: Retinol-binding protein 2



- Molecule 1: Retinol-binding protein 2

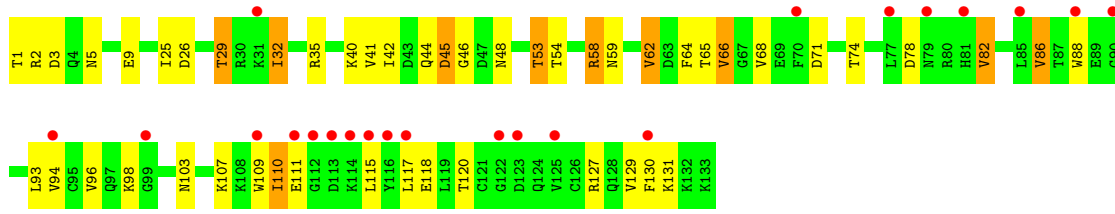


- Molecule 1: Retinol-binding protein 2

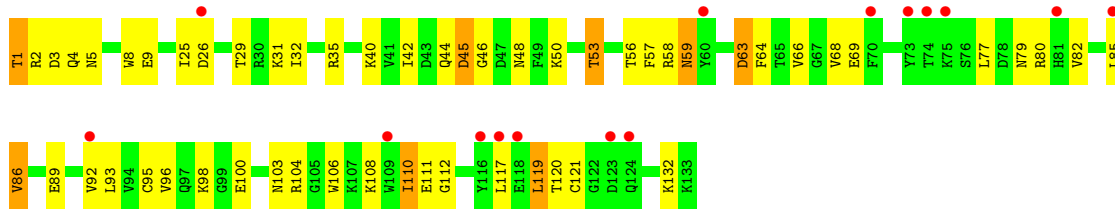


- Molecule 1: Retinol-binding protein 2

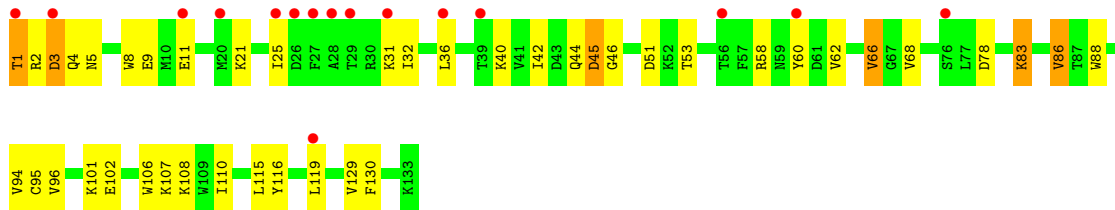




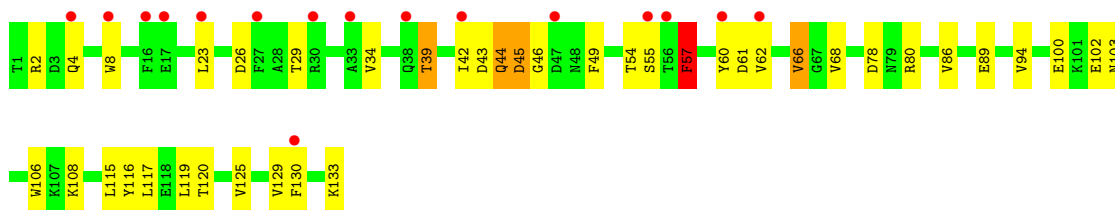
● Molecule 1: Retinol-binding protein 2



● Molecule 1: Retinol-binding protein 2



● Molecule 1: Retinol-binding protein 2



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	84.56Å 111.27Å 101.83Å 90.00° 112.89° 90.00°	Depositor
Resolution (Å)	46.90 – 2.78 46.90 – 2.78	Depositor EDS
% Data completeness (in resolution range)	99.4 (46.90-2.78) 99.3 (46.90-2.78)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.08 (at 2.77Å)	Xtrriage
Refinement program	PHENIX 1.14_3260, PHENIX 1.14_3260	Depositor
R, R_{free}	0.276 , 0.321 0.277 , 0.323	Depositor DCC
R_{free} test set	1990 reflections (4.54%)	wwPDB-VP
Wilson B-factor (Å ²)	60.6	Xtrriage
Anisotropy	0.481	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 38.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtrriage
Estimated twinning fraction	0.000 for h,-k,-h-l	Xtrriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	12908	wwPDB-VP
Average B, all atoms (Å ²)	74.0	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 50.88 % 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 6.0763e-05. 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](#)

Bond lengths and bond angles in the following residue types are not validated in this section: GOL, ACT

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	0.18	0/1095	0.43	0/1477
1	B	0.12	0/1078	0.41	0/1458
1	C	0.14	0/1100	0.44	0/1483
1	D	0.12	0/1082	0.38	0/1460
1	E	0.19	0/1069	0.46	0/1448
1	F	0.13	0/1083	0.39	0/1461
1	G	0.16	0/1077	0.47	0/1453
1	H	0.13	0/1098	0.45	0/1480
1	I	0.17	0/1062	0.48	0/1434
1	J	0.16	0/1063	0.48	0/1440
1	K	0.13	0/1070	0.40	0/1445
1	L	0.14	0/1058	0.43	0/1431
All	All	0.15	0/12935	0.44	0/17470

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	1076	0	1024	28	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	B	1056	0	977	23	0
1	C	1078	0	1030	33	0
1	D	1064	0	1008	26	0
1	E	1050	0	964	25	0
1	F	1066	0	1009	28	0
1	G	1058	0	995	27	0
1	H	1079	0	1030	38	0
1	I	1046	0	985	31	0
1	J	1046	0	956	26	0
1	K	1052	0	986	27	0
1	L	1040	0	974	22	0
2	A	24	0	32	0	0
2	B	24	0	32	0	0
2	D	6	0	8	0	0
2	E	12	0	16	0	0
2	G	6	0	8	0	0
2	H	6	0	8	0	0
2	J	24	0	32	0	0
2	K	12	0	16	0	0
2	L	12	0	16	0	0
3	D	4	0	3	0	0
3	J	4	0	3	0	0
4	A	6	0	0	0	0
4	B	6	0	0	1	0
4	C	6	0	0	0	0
4	D	1	0	0	0	0
4	E	7	0	0	0	0
4	F	8	0	0	0	0
4	G	3	0	0	0	0
4	H	2	0	0	0	0
4	I	7	0	0	0	0
4	J	7	0	0	0	0
4	K	4	0	0	0	0
4	L	6	0	0	0	0
All	All	12908	0	12112	275	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 11.

The worst 5 of 275 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:32:ILE:HG12	1:I:32:ILE:HD13	1.56	0.87
1:I:3:ASP:OD1	1:I:5:ASN:ND2	2.12	0.83
1:H:10:MET:HE2	1:H:13:ASN:HB3	1.61	0.83
1:E:86:VAL:HG13	1:E:95:CYS:HB2	1.63	0.80
1:I:109:TRP:HZ3	1:I:111:GLU:HB2	1.43	0.80

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	131/133 (98%)	119 (91%)	7 (5%)	5 (4%)	2	7
1	B	132/133 (99%)	120 (91%)	7 (5%)	5 (4%)	2	7
1	C	132/133 (99%)	120 (91%)	8 (6%)	4 (3%)	3	10
1	D	131/133 (98%)	119 (91%)	9 (7%)	3 (2%)	5	16
1	E	131/133 (98%)	118 (90%)	9 (7%)	4 (3%)	3	10
1	F	131/133 (98%)	118 (90%)	9 (7%)	4 (3%)	3	10
1	G	131/133 (98%)	119 (91%)	9 (7%)	3 (2%)	5	16
1	H	131/133 (98%)	117 (89%)	8 (6%)	6 (5%)	2	5
1	I	131/133 (98%)	119 (91%)	7 (5%)	5 (4%)	2	7
1	J	131/133 (98%)	117 (89%)	4 (3%)	10 (8%)	1	1
1	K	131/133 (98%)	118 (90%)	9 (7%)	4 (3%)	3	10
1	L	131/133 (98%)	118 (90%)	6 (5%)	7 (5%)	1	4
All	All	1574/1596 (99%)	1422 (90%)	92 (6%)	60 (4%)	2	7

5 of 60 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	46	GLY

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Mol	Chain	Res	Type
1	C	46	GLY
1	C	103	ASN
1	H	46	GLY
1	I	46	GLY

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	115/120 (96%)	95 (83%)	20 (17%)	2	6
1	B	110/120 (92%)	91 (83%)	19 (17%)	2	6
1	C	116/120 (97%)	104 (90%)	12 (10%)	7	20
1	D	113/120 (94%)	97 (86%)	16 (14%)	3	10
1	E	109/120 (91%)	97 (89%)	12 (11%)	6	18
1	F	114/120 (95%)	95 (83%)	19 (17%)	2	7
1	G	111/120 (92%)	93 (84%)	18 (16%)	2	7
1	H	116/120 (97%)	102 (88%)	14 (12%)	5	14
1	I	110/120 (92%)	90 (82%)	20 (18%)	2	5
1	J	109/120 (91%)	85 (78%)	24 (22%)	1	3
1	K	111/120 (92%)	98 (88%)	13 (12%)	5	15
1	L	108/120 (90%)	94 (87%)	14 (13%)	4	12
All	All	1342/1440 (93%)	1141 (85%)	201 (15%)	3	9

5 of 201 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	G	114	LYS
1	I	78	ASP
1	L	102	GLU
1	H	17	GLU
1	I	1	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 9 such sidechains are listed below:

Mol	Chain	Res	Type
1	L	4	GLN
1	L	79	ASN
1	F	124	GLN
1	G	15	ASN
1	H	15	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

23 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	$\# Z > 2$
2	GOL	K	202	-	5,5,5	0.92	0	5,5,5	1.05	0
2	GOL	J	202	-	5,5,5	0.94	0	5,5,5	1.09	0
2	GOL	A	201	-	5,5,5	0.94	0	5,5,5	1.07	0
2	GOL	H	201	-	5,5,5	0.93	0	5,5,5	1.07	0
2	GOL	E	202	-	5,5,5	0.94	0	5,5,5	1.09	0
2	GOL	J	205	-	5,5,5	0.94	0	5,5,5	1.07	0
2	GOL	B	202	-	5,5,5	0.94	0	5,5,5	1.08	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	GOL	E	201	-	5,5,5	0.94	0	5,5,5	1.07	0
2	GOL	D	202	-	5,5,5	0.95	0	5,5,5	1.06	0
2	GOL	A	204	-	5,5,5	0.93	0	5,5,5	1.07	0
2	GOL	J	203	-	5,5,5	0.94	0	5,5,5	1.07	0
2	GOL	A	202	-	5,5,5	0.90	0	5,5,5	1.16	0
2	GOL	K	201	-	5,5,5	0.94	0	5,5,5	1.08	0
2	GOL	L	201	-	5,5,5	0.94	0	5,5,5	1.08	0
2	GOL	B	201	-	5,5,5	0.94	0	5,5,5	1.06	0
2	GOL	A	203	-	5,5,5	0.94	0	5,5,5	1.06	0
2	GOL	J	204	-	5,5,5	0.95	0	5,5,5	1.06	0
2	GOL	G	201	-	5,5,5	0.94	0	5,5,5	1.07	0
3	ACT	J	201	-	3,3,3	1.39	0	3,3,3	1.50	0
2	GOL	L	202	-	5,5,5	0.93	0	5,5,5	1.08	0
3	ACT	D	201	-	3,3,3	1.37	0	3,3,3	1.37	0
2	GOL	B	204	-	5,5,5	0.94	0	5,5,5	1.08	0
2	GOL	B	203	-	5,5,5	0.94	0	5,5,5	1.07	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
2	GOL	K	202	-	-	0/4/4/4	-
2	GOL	J	202	-	-	2/4/4/4	-
2	GOL	A	201	-	-	0/4/4/4	-
2	GOL	H	201	-	-	2/4/4/4	-
2	GOL	E	202	-	-	3/4/4/4	-
2	GOL	J	205	-	-	2/4/4/4	-
2	GOL	B	202	-	-	0/4/4/4	-
2	GOL	E	201	-	-	0/4/4/4	-
2	GOL	D	202	-	-	2/4/4/4	-
2	GOL	A	204	-	-	1/4/4/4	-
2	GOL	J	203	-	-	2/4/4/4	-
2	GOL	A	202	-	-	0/4/4/4	-
2	GOL	K	201	-	-	2/4/4/4	-
2	GOL	L	201	-	-	1/4/4/4	-
2	GOL	B	201	-	-	0/4/4/4	-
2	GOL	A	203	-	-	0/4/4/4	-
2	GOL	J	204	-	-	2/4/4/4	-
2	GOL	G	201	-	-	2/4/4/4	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	GOL	L	202	-	-	2/4/4/4	-
2	GOL	B	204	-	-	2/4/4/4	-
2	GOL	B	203	-	-	1/4/4/4	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

5 of 26 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	B	204	GOL	O1-C1-C2-C3
2	E	202	GOL	C1-C2-C3-O3
2	J	202	GOL	O1-C1-C2-C3
2	J	205	GOL	O1-C1-C2-C3
2	K	201	GOL	O1-C1-C2-C3

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 [i](#)

6.1 Protein, DNA and RNA chains [i](#)

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	133/133 (100%)	0.65	10 (7%) 20 16	45, 60, 89, 102	0
1	B	133/133 (100%)	0.48	3 (2%) 61 53	36, 60, 84, 97	1 (0%)
1	C	133/133 (100%)	0.83	12 (9%) 15 12	47, 67, 97, 143	1 (0%)
1	D	133/133 (100%)	0.77	9 (6%) 23 18	44, 61, 88, 110	0
1	E	133/133 (100%)	0.97	16 (12%) 9 7	49, 76, 129, 180	0
1	F	133/133 (100%)	0.67	7 (5%) 32 26	46, 64, 97, 116	0
1	G	133/133 (100%)	0.99	12 (9%) 15 12	53, 79, 139, 174	0
1	H	133/133 (100%)	0.69	8 (6%) 27 23	46, 69, 106, 151	0
1	I	133/133 (100%)	1.05	22 (16%) 4 3	46, 79, 141, 158	0
1	J	133/133 (100%)	0.86	15 (11%) 10 8	45, 79, 137, 166	0
1	K	133/133 (100%)	0.92	16 (12%) 9 7	46, 77, 130, 176	0
1	L	133/133 (100%)	0.94	16 (12%) 9 7	47, 77, 123, 152	0
All	All	1596/1596 (100%)	0.82	146 (9%) 15 12	36, 69, 122, 180	2 (0%)

The worst 5 of 146 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	1	THR	5.1
1	K	28	ALA	5.0
1	J	73	TYR	4.9
1	E	71	ASP	4.8
1	G	73	TYR	4.8

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
2	GOL	J	202	6/6	0.50	0.18	68,87,92,93	0
2	GOL	E	201	6/6	0.51	0.17	83,93,99,111	0
2	GOL	E	202	6/6	0.54	0.14	52,94,101,102	0
3	ACT	J	201	4/4	0.55	0.17	59,70,70,78	0
2	GOL	K	201	6/6	0.65	0.13	64,85,89,96	0
2	GOL	L	201	6/6	0.67	0.11	74,94,101,107	0
2	GOL	J	203	6/6	0.68	0.12	74,79,98,109	0
2	GOL	G	201	6/6	0.69	0.15	50,74,92,109	0
2	GOL	A	202	6/6	0.70	0.20	73,100,105,113	0
2	GOL	A	203	6/6	0.74	0.20	46,84,92,99	0
2	GOL	J	204	6/6	0.77	0.11	65,79,91,93	0
3	ACT	D	201	4/4	0.78	0.11	71,81,81,84	0
2	GOL	B	204	6/6	0.78	0.12	62,71,90,97	0
2	GOL	B	201	6/6	0.79	0.14	55,72,74,77	0
2	GOL	B	203	6/6	0.80	0.09	73,80,82,86	0
2	GOL	A	201	6/6	0.81	0.09	66,73,90,92	0
2	GOL	A	204	6/6	0.82	0.09	60,69,74,76	0
2	GOL	D	202	6/6	0.82	0.13	69,81,88,95	0
2	GOL	K	202	6/6	0.83	0.13	48,82,86,89	0
2	GOL	J	205	6/6	0.83	0.10	50,60,65,74	0
2	GOL	H	201	6/6	0.84	0.24	76,82,104,104	0
2	GOL	B	202	6/6	0.84	0.13	79,88,92,94	0
2	GOL	L	202	6/6	0.86	0.08	71,77,79,87	0

6.5 Other polymers [i](#)

There are no such residues in this entry.